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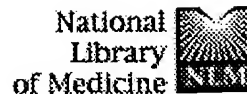
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
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
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

















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
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
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
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

















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
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
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
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
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
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
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
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TI Expression of \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
\*\*\*transporter\*\*\* CHT1 in the \*\*\*human\*\*\* leukemic T cell line  
MOLT-3.  
AU Fujii, Takeshi [Reprint Author]; Okuda, Takashi; Haga, Tatsuya; Kawashima,  
Koichiro [Reprint Author]  
CS Dept. Pharmacol., Kyoritsu Col. Pharmacy, Tokyo, 105-8512, Japan  
SO Journal of Pharmacological Sciences, (2004) Vol. 94, No. Supplement 1, pp.  
202P. print.  
Meeting Info.: 77th Annual Meeting of the Japanese Pharmacological  
Society. Osaka, Japan. March 08-10, 2004. Japanese Pharmacological  
Society.  
ISSN: 1347-8613 (ISSN print).  
DT Conference; (Meeting)  
Conference; Abstract; (Meeting Abstract)  
LA English  
ED Entered STN: 14 Apr 2004  
Last Updated on STN: 14 Apr 2004

L3 ANSWER 2 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 2004:114768 BIOSIS  
DN PREV200400104871  
TI The lymphocytic cholinergic system and its contribution to the regulation  
of immune activity.  
AU Kawashima, Koichiro [Reprint Author]; Fujii, Takeshi  
CS Department of Pharmacology, Kyoritsu College of Pharmacy, 1-5-30  
Shibakoen, Minato, Tokyo, 105-8512, Japan  
kawashima-ki@kyoritsu-ph.ac.jp  
SO Life Sciences, (December 26 2003) Vol. 74, No. 6, pp. 675-696. print.  
ISSN: 0024-3205 (ISSN print).  
DT Article  
General Review; (Literature Review)  
LA English  
ED Entered STN: 25 Feb 2004  
Last Updated on STN: 25 Feb 2004

L3 ANSWER 3 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 2004:79232 BIOSIS  
DN PREV200400080163  
TI Characterization of the \*\*\*human\*\*\* \*\*\*high\*\*\* - \*\*\*affinity\*\*\*  
\*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
AU Haga, T. [Reprint Author]; Okuda, T.; Kaitsuka, C. [Reprint Author];  
Okamura, M.; Osawa, C. [Reprint Author]; Nishiyama, N. [Reprint Author];  
Yamada, H. [Reprint Author]; Nakamura, T. [Reprint Author]; Kobayashi, Y.  
CS Gakushuin University, Institute of Biomolecular Science, Tokyo, Japan  
SO Journal of Neurochemistry, (December 2003) Vol. 87, No. Supplement 1, pp.  
43. print.  
Meeting Info.: Meeting of the International Society for Neurochemistry  
(ISN). Hong Kong, China. August 03-08, 2003. International Society for  
Neurochemistry.  
CODEN: JONRA9. ISSN: 0022-3042.  
DT Conference; (Meeting)  
Conference; Abstract; (Meeting Abstract)  
LA English  
ED Entered STN: 4 Feb 2004  
Last Updated on STN: 4 Feb 2004

L3 ANSWER 4 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 2004:65466 BIOSIS  
DN PREV200400066534  
TI Expression of the \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
\*\*\*transporter\*\*\* CHT1 in rat and \*\*\*human\*\*\* arteries.  
AU Lips, Katrin S. [Reprint Author]; Pfeil, Uwe; Reiners, Katja; Rimasch,

CS Rainer V.; Schmidt, Rupert; Kummer, Wolfgang  
Inst. for Anatomy and Cell Biology, Justus-Liebig-University, Aulweg 123,  
D-35385, Giessen, Germany  
Katr.S.Lips@anatomie.med.uni-giessen.de

SO Journal of Histochemistry & Cytochemistry, (December 2003) Vol. 51, No.  
12, pp. 1645-1654. print.  
ISSN: 0022-1554 (ISSN print).

DT Article  
LA English  
ED Entered STN: 28 Jan 2004  
Last Updated on STN: 28 Jan 2004

L3 ANSWER 5 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 2003:577555 BIOSIS  
DN PREV200300581998  
TI Expression of acetylcholine in lymphocytes and modulation of an  
independent lymphocytic cholinergic activity by immunological stimulation.

AU Fujii, Takeshi; Watanabe, Yoshihiro; Fujimoto, Kazuko; Kawashima, Koichiro  
[Reprint Author]

CS Department of Pharmacology, Kyoritsu College of Pharmacy, 1-5-30  
Shibakoen, Minato-ku, Tokyo, 105-8512, Japan  
kawashima-ki@kyoritsu-ph.ac.jp

SO Biogenic Amines, (2003) Vol. 17, No. 4-6, pp. 373-386. print.  
CODEN: BIAME7. ISSN: 0168-8561.

DT Article  
LA English  
ED Entered STN: 10 Dec 2003  
Last Updated on STN: 10 Dec 2003

L3 ANSWER 6 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 2003:533308 BIOSIS  
DN PREV200300536831  
TI The hemicholinium-3 sensitive \*\*\*high\*\*\* \*\*\*affinity\*\*\*  
\*\*\*choline\*\*\* \*\*\*transporter\*\*\* is internalized by clathrin-mediate  
endocytosis and is present in endosomes and synaptic vesicles.

AU Ribeiro, F. M.; Alves-Silva, J.; Volkandt, W.; Martins-Silva, C.; Mahmud,  
H.; Wilhelm, A.; Gomez, M. V.; Rylett, R. J.; Ferguson, S. S. G.; Prado,  
V. F.; Prado, M. A. M. [Reprint Author]

CS Laboratorio de Neurofarmacologia, Departamento de Farmacologia, ICB,  
Universidade Federal de Minas Gerais, Avenue Antonio Carlos 6627,  
31270-910, Belo Horizonte, MG, Brazil  
mprado@icb.ufmg.br

SO Journal of Neurochemistry, (October 2003) Vol. 87, No. 1, pp. 136-146.  
print.  
CODEN: JONRA9. ISSN: 0022-3042.

DT Article  
LA English  
ED Entered STN: 12 Nov 2003  
Last Updated on STN: 12 Nov 2003

L3 ANSWER 7 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 2003:441016 BIOSIS  
DN PREV200300441016  
TI Distribution of \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
\*\*\*transporter\*\*\* immunoreactivity in the primate central nervous  
system.

AU Kus, Laura; Borys, Ewa; Chu, Ya Ping; Ferguson, Shawn M.; Blakely, Randy  
D.; Emborg, Marina E.; Kordower, Jeffrey H.; Levey, Allan I.; Mufson,  
Elliott J. [Reprint Author]

CS Department of Neurological Sciences, 2242 W Harrison Street, Suite 200,  
Chicago, IL, 60612, USA  
emufson@rush.edu

SO Journal of Comparative Neurology, (August 25 2003) Vol. 463, No. 3, pp.  
341-357. print.  
ISSN: 0021-9967 (ISSN print).

DT Article  
LA English  
ED Entered STN: 24 Sep 2003  
Last Updated on STN: 24 Sep 2003

L3 ANSWER 8 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 2003:326967 BIOSIS  
DN PREV200300326967  
TI \*\*\*HIGH\*\*\* - \*\*\*AFFINITY\*\*\* \*\*\*CHOLINE\*\*\* \*\*\*TRANSPORTER\*\*\*  
IMMUNOREACTIVE PROFILES IN MONKEY AND \*\*\*HUMAN\*\*\* BRAIN.



[Reprint Author]; Kordower, J. H. [Reprint Author]; Levey, A. I.; Mufson, E. J. [Reprint Author]  
 CS Neurological Sciences, Rush Medical Center, Chicago, IL, USA  
 SO Society for Neuroscience Abstract Viewer and Itinerary Planner, (2002)  
 Vol. 2002, pp. Abstract No. 785.6. <http://sfn.scholarone.com>. cd-rom.  
 Meeting Info.: 32nd Annual Meeting of the Society for Neuroscience.  
 Orlando, Florida, USA. November 02-07, 2002. Society for Neuroscience.  
 DT Conference; (Meeting)  
 Conference; (Meeting Poster)  
 Conference; Abstract; (Meeting Abstract)  
 LA English  
 ED Entered STN: 16 Jul 2003  
 Last Updated on STN: 16 Jul 2003

L3 ANSWER 9 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
 AN 2003:283258 BIOSIS  
 DN PREV200300283258  
 TI A CHOLINERGIC AUTOCRINE LOOP REGULATES THE GROWTH OF SMALL CELL LUNG  
 CARCINOMA ( SCLC ) CELL LINES.  
 AU Song, P. [Reprint Author]; Sekhon, H. S. [Reprint Author]; Kuryatov, A.;  
 Blusztajn, J. K.; Mark, G. P.; Lindstrom, J.; Spindel, E. R. [Reprint  
 Author]  
 CS Div Neurosci, Dept Path, Dept Behav Neurosci, OHSU/ORPRC, Beaverton, OR,  
 USA  
 SO Society for Neuroscience Abstract Viewer and Itinerary Planner, (2002)  
 Vol. 2002, pp. Abstract No. 238.2. <http://sfn.scholarone.com>. cd-rom.  
 Meeting Info.: 32nd Annual Meeting of the Society for Neuroscience.  
 Orlando, Florida, USA. November 02-07, 2002. Society for Neuroscience.  
 DT Conference; (Meeting)  
 Conference; Abstract; (Meeting Abstract)  
 Conference; (Meeting Poster)  
 LA English  
 ED Entered STN: 19 Jun 2003  
 Last Updated on STN: 19 Jun 2003

L3 ANSWER 10 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
 AN 2003:282043 BIOSIS  
 DN PREV200300282043  
 TI TARGETED DISRUPTION OF THE MURINE \*\*\*HIGH\*\*\* \*\*\*AFFINITY\*\*\*  
 \*\*\*CHOLINE\*\*\* \*\*\*TRANSPORTER\*\*\* GENE.  
 AU Blakely, R. D. [Reprint Author]; Ferguson, S. M. [Reprint Author]; Wright,  
 J. [Reprint Author]; Bazalakova, M. [Reprint Author]; Apparsundaram, S.  
 CS Dept. of Pharmacology, Ctr. for Mol. Neurosci., Vanderbilt University  
 School of Medicine, Nashville, TN, USA  
 SO Society for Neuroscience Abstract Viewer and Itinerary Planner, (2002)  
 Vol. 2002, pp. Abstract No. 144.3. <http://sfn.scholarone.com>. cd-rom.  
 Meeting Info.: 32nd Annual Meeting of the Society for Neuroscience.  
 Orlando, Florida, USA. November 02-07, 2002. Society for Neuroscience.  
 DT Conference; (Meeting)  
 Conference; (Meeting Poster)  
 Conference; Abstract; (Meeting Abstract)  
 LA English  
 ED Entered STN: 19 Jun 2003  
 Last Updated on STN: 19 Jun 2003

L3 ANSWER 11 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
 AN 2003:164774 BIOSIS  
 DN PREV200300164774  
 TI Detection of the \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* in the MOLT-3 \*\*\*human\*\*\* leukemic T-cell line.  
 AU Fujii, Takeshi; Okuda, Takashi; Haga, Tatsuya; Kawashima, Koichiro  
 [Reprint Author]  
 CS Department of Pharmacology, Kyoritsu College of Pharmacy, 1-5-30  
 Shibakoen, Minato-ku, Tokyo, 105-8512, Japan  
 kawashima-ki@kyoritsu-ph.ac.jp  
 SO Life Sciences, (March 28 2003) Vol. 72, No. 18-19, pp. 2131-2134. print.  
 ISSN: 0024-3205 (ISSN print).  
 DT Article  
 LA English  
 ED Entered STN: 2 Apr 2003  
 Last Updated on STN: 2 Apr 2003

L3 ANSWER 12 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
 AN 2003:164766 BIOSIS  
 DN PREV200300164766

\*\*\*transporter\*\*\* CHT1 in epithelia.  
 AU Pfeil, Uwe; Haberberger, Rainer V.; Lips, Katrin S.; Eberling, Lars; Grau, Veronika; Kummer, Wolfgang [Reprint Author]  
 CS Institute for Anatomy and Cell Biology, Justus-Liebig-University, Aulweg 123, 35385, Giessen, Germany  
 SO wolfgang.kummer@anatomie.med.uni-giessen.de  
 Life Sciences, (March 28 2003) Vol. 72, No. 18-19, pp. 2087-2090. print.  
 ISSN: 0024-3205 (ISSN print).  
 DT Article  
 LA English  
 ED Entered STN: 2 Apr 2003  
 Last Updated on STN: 2 Apr 2003

L3 ANSWER 13 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
 AN 2003:85974 BIOSIS  
 DN PREV200300085974  
 TI \*\*\*Human\*\*\* \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\*  
 AU Wu, Dong-Hai [Inventor, Reprint Author]; Gu, Yunrong [Inventor]; Millard, William James [Inventor]; He, Yun-Ju [Inventor]  
 CS Gainesville, FL, USA  
 ASSIGNEE: University of Florida  
 PI US 6500643 December 31, 2002  
 SO Official Gazette of the United States Patent and Trademark Office Patents, (Dec 31 2002) Vol. 1265, No. 5. <http://www.uspto.gov/web/menu/patdata.html>  
 . e-file.  
 ISSN: 0098-1133 (ISSN print).  
 DT Patent  
 LA English  
 ED Entered STN: 6 Feb 2003  
 Last Updated on STN: 6 Feb 2003

L3 ANSWER 14 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
 AN 2003:55673 BIOSIS  
 DN PREV200300055673  
 TI Single nucleotide polymorphism of the \*\*\*human\*\*\* \*\*\*high\*\*\*  
 \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\* alters transport rate.  
 AU Okuda, Takashi; Okamura, Michiko; Kaitsuka, China; Haga, Tatsuya [Reprint Author]; Gurwitz, David  
 CS Faculty of Science, Institute for Biomolecular Science, Gakushuin University, 1-5-1 Mejiro, Toshima-ku, Tokyo, 171-8588, Japan  
 SO tatsuya.haga@gakushuin.ac.jp  
 Journal of Biological Chemistry, (November 22 2002) Vol. 277, No. 47, pp. 45315-45322. print.  
 CODEN: JBCHA3. ISSN: 0021-9258.  
 DT Article  
 LA English  
 ED Entered STN: 22 Jan 2003  
 Last Updated on STN: 22 Jan 2003

L3 ANSWER 15 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
 AN 2003:10758 BIOSIS  
 DN PREV200300010758  
 TI Expression of the \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\*, CHT1, in the neuronal and non-neuronal cholinergic system of \*\*\*human\*\*\* and rat skin.  
 AU Haberberger, Rainer Viktor [Reprint Author]; Pfeil, Uwe; Lips, Katrin  
 CS Susanne; Kummer, Wolfgang  
 Aulweg 123, 35385, Giessen, Germany  
 SO rainer.v.haberberger@anatomie.med.uni-giessen.de  
 Journal of Investigative Dermatology, (October 2002) Vol. 119, No. 4, pp. 943-948. print.  
 ISSN: 0022-202X (ISSN print).  
 DT Article  
 LA English  
 ED Entered STN: 18 Dec 2002  
 Last Updated on STN: 18 Dec 2002

L3 ANSWER 16 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
 AN 2002:319227 BIOSIS  
 DN PREV200200319227  
 TI Spinal endogenous acetylcholine contributes to the analgesic effect of systemic morphine in rats.  
 AU Chen, Shao-rui; Pan, Hui-lin [Reprint author]

Medicine, 500 University Drive, H187, Hershey, PA, 17033-0850, USA  
hpan@psu.edu

SO Anesthesiology (Hagerstown), (August, 2001) Vol. 95, No. 2, pp. 525-530.  
print.  
CODEN: ANESAV. ISSN: 0003-3022.

DT Article  
LA English  
ED Entered STN: 5 Jun 2002  
Last Updated on STN: 5 Jun 2002

L3 ANSWER 17 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 2002:167549 BIOSIS  
DN PREV200200167549  
TI Distribution of the \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
\*\*\*transporter\*\*\* in the \*\*\*human\*\*\* and macaque monkey spinal cord  
AU Kobayashi, Yasushi [Reprint author]; Okuda, Takashi; Fujioka, Yasunori;  
Matsumura, George; Nishimura, Yu; Haga, Tatsuya  
CS Department of Anatomy, Kyorin University School of Medicine, Mitaka,  
Tokyo, 181-8611, Japan  
yasushi@kyorin-u.ac.jp  
SO Neuroscience Letters, (January 4, 2002) Vol. 317, No. 1, pp. 25-28. print.  
CODEN: NELED5. ISSN: 0304-3940.  
DT Article  
LA English  
ED Entered STN: 5 Mar 2002  
Last Updated on STN: 5 Mar 2002

L3 ANSWER 18 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 2002:4241 BIOSIS  
DN PREV200200004241  
TI A single nucleotide polymorphism affects the transport rate of the  
\*\*\*human\*\*\* \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
\*\*\*transporter\*\*\*  
AU Okuda, T. [Reprint author]; Haga, T.  
CS Dept Neurochem, Fac Med, Univ Tokyo, Tokyo, Japan  
SO Society for Neuroscience Abstracts, (2001) Vol. 27, No. 2, pp. 2433.  
print.  
Meeting Info.: 31st Annual Meeting of the Society for Neuroscience. San  
Diego, California, USA. November 10-15, 2001.  
ISSN: 0190-5295.  
DT Conference; (Meeting)  
Conference; Abstract; (Meeting Abstract)  
LA English  
ED Entered STN: 28 Dec 2001  
Last Updated on STN: 25 Feb 2002

L3 ANSWER 19 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 2002:4240 BIOSIS  
DN PREV200200004240  
TI The use of polyclonal antibodies to partially confirm predicted topology  
of a putative choline cotransporter from Limulus.  
AU Wang, Y. [Reprint author]; Cao, Z.; McAdory, B. [Reprint author]; Newkirk,  
R. F. [Reprint author]; Ivy, M. T. [Reprint author]; Townsel, J. G.  
CS Biol. Sci., Tenn. St. Univ., Nashville, TN, USA  
SO Society for Neuroscience Abstracts, (2001) Vol. 27, No. 2, pp. 2432.  
print.  
Meeting Info.: 31st Annual Meeting of the Society for Neuroscience. San  
Diego, California, USA. November 10-15, 2001.  
ISSN: 0190-5295.  
DT Conference; (Meeting)  
Conference; Abstract; (Meeting Abstract)  
LA English  
ED Entered STN: 28 Dec 2001  
Last Updated on STN: 25 Feb 2002

L3 ANSWER 20 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 2001:434607 BIOSIS  
DN PREV200100434607  
TI Distribution of the \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
\*\*\*transporter\*\*\* in the central nervous system of the rat.  
AU Misawa, H. [Reprint author]; Nakata, K.; Matsuura, J.; Nagao, M.; Okuda,  
T.; Haga, T.  
CS Department of Neurology, Tokyo Metropolitan Institute for Neuroscience,  
2-6 Musashidai, Fuchu City, Tokyo, 183-8526, Japan  
hmisawa@tmin.ac.jp

CODEN: NRSCDN. ISSN: 0306-4522.

DT Article  
LA English  
ED Entered STN: 12 Sep 2001  
Last Updated on STN: 22 Feb 2002

L3 ANSWER 21 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 2001:252320 BIOSIS  
DN PREV200100252320

TI Spinal cholinergic system mediates the analgesic effect of systemic morphine in rats.

AU Chen, Shao-Rui [Reprint author]; Pan, Hui-Lin [Reprint author]  
CS Penn State College of Medicine, 500 University Drive, Hershey, PA, 17033, USA

SO FASEB Journal, (March 8, 2001) Vol. 15, No. 5, pp. A810. print.  
Meeting Info.: Annual Meeting of the Federation of American Societies for Experimental Biology on Experimental Biology 2001. Orlando, Florida, USA. March 31-April 04, 2001.

CODEN: FAJOEC. ISSN: 0892-6638.

DT Conference; (Meeting)  
Conference; Abstract; (Meeting Abstract)

LA English  
ED Entered STN: 23 May 2001  
Last Updated on STN: 19 Feb 2002

L3 ANSWER 22 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 2001:125719 BIOSIS  
DN PREV200100125719

TI Molecular cloning and characterization of \*\*\*human\*\*\* affinity choline transporter.

AU Wu, D. [Reprint author]; Gu, Y.; Millard, W.; He, Y.; Lian, W.  
CS University of Florida, Gainesville, FL, USA

SO Society for Neuroscience Abstracts, (2000) Vol. 26, No. 1-2, pp. Abstract No.-805.3. print.

Meeting Info.: 30th Annual Meeting of the Society of Neuroscience. New Orleans, LA, USA. November 04-09, 2000. Society for Neuroscience. ISSN: 0190-5295.

DT Conference; (Meeting)  
Conference; Abstract; (Meeting Abstract)

LA English  
ED Entered STN: 14 Mar 2001  
Last Updated on STN: 15 Feb 2002

L3 ANSWER 23 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 2001:109007 BIOSIS  
DN PREV200100109007

TI Cloning of the \*\*\*human\*\*\* \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*.

AU Okuda, T. [Reprint author]; Haga, T.  
CS Univ. of Tokyo, Tokyo, Japan

SO Society for Neuroscience Abstracts, (2000) Vol. 26, No. 1-2, pp. Abstract No.-625.2. print.

Meeting Info.: 30th Annual Meeting of the Society of Neuroscience. New Orleans, LA, USA. November 04-09, 2000. Society for Neuroscience. ISSN: 0190-5295.

DT Conference; (Meeting)  
Conference; Abstract; (Meeting Abstract)

LA English  
ED Entered STN: 28 Feb 2001  
Last Updated on STN: 15 Feb 2002

L3 ANSWER 24 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 2001:97086 BIOSIS  
DN PREV200100097086

TI Molecular cloning and characterization of \*\*\*human\*\*\* and murine \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporters\*\*\*.

AU Apparsundaram, S. [Reprint author]; Ferguson, S.; Blakely, R. D.  
CS Vanderbilt University, Nashville, TN, USA

SO Society for Neuroscience Abstracts, (2000) Vol. 26, No. 1-2, pp. Abstract No.-306.5. print.

Meeting Info.: 30th Annual Meeting of the Society of Neuroscience. New Orleans, LA, USA. November 04-09, 2000. Society for Neuroscience. ISSN: 0190-5295.

DT Conference; (Meeting)  
Conference; Abstract; (Meeting Abstract)

ED Entered STN: 21 Feb 2001  
Last Updated on STN: 15 Feb 2002

L3 ANSWER 25 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 2001:21058 BIOSIS  
DN PREV200100021058  
TI Functional characterization of the \*\*\*human\*\*\* \*\*\*high\*\*\* -  
\*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
AU Okuda, Takashi [Reprint author]; Haga, Tatsuya  
CS Department of Neurochemistry, Faculty of Medicine, University of Tokyo,  
7-3-1 Hongo, Bunkyo-ku, Tokyo, 113-0033, Japan  
okuda@m.u-tokyo.ac.jp  
SO FEBS Letters, (3 November, 2000) Vol. 484, No. 2, pp. 92-97. print.  
CODEN: FEBLAL. ISSN: 0014-5793.  
DT Article  
LA English  
ED Entered STN: 3 Jan 2001  
Last Updated on STN: 12 Feb 2002

L3 ANSWER 26 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 2000:382237 BIOSIS  
DN PREV200000382237  
TI Modeling adolescent nicotine exposure: Effects on cholinergic systems in  
rat brain regions.  
AU Trauth, Jennifer A.; McCook, Everett C.; Seidler, Frederic J.; Slotkin,  
Theodore A. [Reprint author]  
CS Department of Pharmacology and Cancer Biology, Duke University Medical  
Center, DUMC, Durham, NC, 27710, USA  
SO Brain Research, (4 August, 2000) Vol. 873, No. 1, pp. 18-25. print.  
CODEN: BRREAP. ISSN: 0006-8993.  
DT Article  
LA English  
ED Entered STN: 6 Sep 2000  
Last Updated on STN: 8 Jan 2002

L3 ANSWER 27 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 2000:309579 BIOSIS  
DN PREV200000309579  
TI No evidence for cholinergic problems in apolipoprotein E knockout and  
apolipoprotein E4 transgenic mice.  
AU Bronfman, F. C.; Tesseur, I.; Hofker, M. H.; Havekens, L. M.; Van Leuven,  
F. [Reprint author]  
CS Experimental Genetics Group, Center for Human Genetics, Flemish Institute  
for Biotechnology, K. U. Leuven, Campus Gasthuisberg, B-3000, Leuven,  
Belgium  
SO Neuroscience, (16 May, 2000) Vol. 97, No. 3, pp. 411-417. print.  
CODEN: NRSCDN. ISSN: 0306-4522.  
DT Article  
LA English  
ED Entered STN: 19 Jul 2000  
Last Updated on STN: 7 Jan 2002

L3 ANSWER 28 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 1996:299739 BIOSIS  
DN PREV199699022095  
TI \*\*\*High\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
status in Alzheimer's disease tissue from rapid autopsy.  
AU Bissette, G.; Seidler, F. J.; Nemeroff, C. B.; Slotkin, T. A. [Reprint  
author]  
CS Duke Univ. Med. Cent., Durham, NC 27710, USA  
SO Wurtman, Richard J. [Editor]; Corkin, Suzanne [Editor]; Crowdon, John H.  
[Editor]; Nitsch, Roger M. [Editor]. Ann. N. Y. Acad. Sci., (1996) pp.  
197-204. Annals of the New York Academy of Sciences; The neurobiology of  
Alzheimer's disease.  
Publisher: New York Academy of Sciences, 2 East 63rd Street, New York, New  
York 10021, USA. Series: Annals of the New York Academy of Sciences.  
Meeting Info.: Eighth Meeting of the International Study Group on the  
Pharmacology of Memory Disorders Associated with Aging. Zurich,  
Switzerland. February 17-19, 1995.  
CODEN: ANYAA9. ISSN: 0077-8923. ISBN: 0-89766-974-6 (paper), 0-89766-973-8  
(cloth).  
DT Book  
Conference; (Meeting)  
Book; (Book Chapter)  
Conference; (Meeting Paper)

ED Entered STN: 2 Jul 1996  
Last Updated on STN: 2 Jul 1996

L3 ANSWER 29 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 1994:473136 BIOSIS  
DN PREV199497486136  
TI Cloning and sequencing of a putative \*\*\*high\*\*\* \*\*\*affinity\*\*\*  
\*\*\*choline\*\*\* \*\*\*transporter\*\*\* cDNA from \*\*\*human\*\*\* brain.  
AU Barnwell, L. F. S.; Gresham, A. M.; Chaudhuri, G.; Townsel, J. G.  
CS Div. Biomedical Sci., Physiol. Dep., Meharry Med. Coll., Nashville, TN  
37208, USA  
SO Society for Neuroscience Abstracts, (1994) Vol. 20, No. 1-2, pp. 533.  
Meeting Info.: 24th Annual Meeting of the Society for Neuroscience. Miami  
Beach, Florida, USA. November 13-18, 1994.  
ISSN: 0190-5295.  
DT Conference; (Meeting)  
Conference; Abstract; (Meeting Abstract)  
Conference; (Meeting Poster)  
LA English  
ED Entered STN: 31 Oct 1994  
Last Updated on STN: 1 Nov 1994

L3 ANSWER 30 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 1993:392990 BIOSIS  
DN PREV199396068290  
TI Pharmacokinetics of two partial benzodiazepine receptor agonistic  
beta-carboline derivatives in healthy volunteers.  
AU Krause, W. [Reprint author]; Dorow, R.  
CS Postfach 65 03 11, W-1000 Berlin 65, Germany  
SO Arzneimittel-Forschung, (1993) Vol. 43, No. 5, pp. 511-515.  
CODEN: ARZNAD. ISSN: 0004-4172.  
DT Article  
LA English  
ED Entered STN: 23 Aug 1993  
Last Updated on STN: 28 Sep 1993

L3 ANSWER 31 OF 111 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN  
AN 2003-28812 BIOTECHDS  
TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
\*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
polypeptide, useful in gene therapy to increase cholinergic function in a  
cell of a patient suffering from Alzheimer's disease;  
recombinant protein, encoding gene, and monoclonal antibody for use in  
Parkinson disease, Huntington chorea, Alzheimer disease,  
schizophrenia, dysautonomia, myasthenia gravis diagnosis, therapy,  
gene therapy and drug screening  
AU BLAKELY R D; APPARSUNDARAM S; FERGUSON S  
PA BLAKELY R D; APPARSUNDARAM S; FERGUSON S  
PI US 2003114399 19 Jun 2003  
AI US 2001-911077 23 Jul 2001  
PRAI US 2001-911077 23 Jul 2001; US 2001-911077 23 Jul 2001  
DT Patent  
LA English  
OS WPI: 2003-810914 [76]

L3 ANSWER 32 OF 111 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN  
AN 2003-08295 BIOTECHDS  
TI New transporter array with a non-conserved region of a transporter  
polynucleotide, useful for identifying therapeutic, prophylactic or toxic  
agents in diseases with alteration in the expression profile of  
transporter polypeptides;  
DNA array, RNA array, peptide nucleic acid array, locked nucleic acid  
array, cDNA array, application in drug screening, diagnosis, gene  
therapy, prophylaxis and nucleic acid vaccine  
AU JENSEN J B; MADSEN L S; GETHER U; JENSEN B S  
PA AZIGN BIOSCIENCE AS  
PI WO 2002095064 28 Nov 2002  
AI WO 2002-DK336 21 May 2002  
PRAI DK 2001-803 18 May 2001; DK 2001-803 18 May 2001  
DT Patent  
LA English  
OS WPI: 2003-129438 [12]

L3 ANSWER 33 OF 111 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN  
AN 2001-08236 BIOTECHDS

\*\*\*choline\*\*\*      \*\*\*transporters\*\*\* , useful in diagnosis of  
Alzheimer's disease and screening promoters as drugs for treating  
Alzheimer's disease;  
recombinant protein production via plasmid expression in host cell for  
gene therapy

AU Haga T; Okuda T  
PA Japan-Sci.Technol.  
LO Saitama, Japan.  
PI WO 2001016315 8 Mar 2001  
AI WO 2000-JP5545 18 Aug 2000  
PRAI JP 1999-368991 27 Dec 1999; JP 1999-240642 27 Aug 1999  
DT Patent  
LA Japanese  
OS WPI: 2001-226688 [23]

L3 ANSWER 34 OF 111 CAPLUS COPYRIGHT 2004 ACS on STN  
AN 2004:361532 CAPLUS  
DN 140:352129  
TI Organic cation transporters  
AU Koepsell, H.; Schmitt, B. M.; Gorboulev, V.  
CS Institut fuer Anatomie und Zellbiologie, Bayerischen Julius-Maximilians-  
Universitaet, Wuerzburg, 97070, Germany  
SO Reviews of Physiology, Biochemistry and Pharmacology (2004), Volume Date  
2003, 150, 36-90  
CODEN: RPBEA5; ISSN: 0303-4240  
PB Springer-Verlag  
DT Journal; General Review  
LA English  
RE.CNT 313 THERE ARE 313 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 35 OF 111 CAPLUS COPYRIGHT 2004 ACS on STN  
AN 2004:213088 CAPLUS  
TI Localization of cholinergic innervation in guinea pig heart by  
immunohistochemistry for \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
\*\*\*transporters\*\*\*  
AU Hoover, Donald B.; Ganote, Charles E.; Ferguson, Shawn M.; Blakely, Randy  
D.; Parsons, Rodney L.  
CS James H. Quillen College of Medicine, Department of Pharmacology, East  
Tennessee State University, Johnson City, TN, 37614, USA  
SO Cardiovascular Research (2004), 62(1), 112-121  
CODEN: CVREAU; ISSN: 0008-6363  
PB Elsevier Science B.V.  
DT Journal  
LA English  
RE.CNT 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 36 OF 111 CAPLUS COPYRIGHT 2004 ACS on STN  
AN 2004:194824 CAPLUS  
DN 140:319635  
TI An independent, non-neuronal cholinergic system in lymphocytes and its  
roles in regulation of immune function  
AU Fujii, Takeshi  
CS Dep. Pharmacol, Kyoritsu Coll. Pharmacy, Tokyo, 105-8512, Japan  
SO Nippon Yakurigaku Zasshi (2004), 123(3), 179-188  
CODEN: NYKZAU; ISSN: 0015-5691  
PB Nippon Yakuri Gakkai  
DT Journal; General Review  
LA Japanese

L3 ANSWER 37 OF 111 CAPLUS COPYRIGHT 2004 ACS on STN  
AN 2001:635466 CAPLUS  
DN 135:206448  
TI Identification of a gene encoding a \*\*\*human\*\*\* salt-dependent  
\*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\* 1  
sequence homology  
IN Bruess, Michael; Boenisch, Heinz  
PA Germany  
SO Ger. Offen., 12 pp.  
CODEN: GWXXBX  
DT Patent  
LA German  
FAN.CNT 1  
PATENT NO.      KIND      DATE      APPLICATION NO.      DATE

PI DE 10009055 A1 20010830 DE 2000-10009055 20000228  
PRAI DE 2000-10009055 20000228

L3 ANSWER 38 OF 111 DISSABS COPYRIGHT (C) 2004 ProQuest Information and  
Learning Company; All Rights Reserved on STN  
AN 93:38034 DISSABS Order Number: AAR9318723  
TI ISOLATION AND CHARACTERIZATION OF A SODIUM- AND CHLORIDE-DEPENDENT GABA  
TRANSPORTER CDNA FROM TORPEDO CALIFORNICA (SODIUM DEPENDENT)  
AU SWANSON, GEOFFREY TODD [PH.D.]; CHO, ARTHUR K. [advisor]  
CS UNIVERSITY OF CALIFORNIA, LOS ANGELES (0031)  
SO Dissertation Abstracts International, (1993) Vol. 54, No. 3B, p. 1245.  
Order No.: AAR9318723. 159 pages.  
DT Dissertation  
FS DAI  
LA English  
ED Entered STN: 19930817  
Last Updated on STN: 19930817

L3 ANSWER 39 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
AN ADD50662 peptide DGENE  
TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
\*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
polypeptide, useful in gene therapy to increase cholinergic function in  
a cell of a patient suffering from Alzheimer's disease.  
IN Blakely R D; Apparsundaram S; Ferguson S  
PA (BLAK-I) BLAKELY R D.  
(APPA-I) APPARSUNDARAM S.  
(FERG-I) FERGUSON S.  
PI US 2003114399 A1 20030619 74p  
AI US 2001-911077 20010723  
PRAI US 2001-911077 20010723  
DT Patent  
LA English  
OS 2003-810914 [76]  
DESC C-terminal peptide of \*\*\*human\*\*\* , mouse and rat CHT.

L3 ANSWER 40 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
AN ADD50647 protein DGENE  
TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
\*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
polypeptide, useful in gene therapy to increase cholinergic function in  
a cell of a patient suffering from Alzheimer's disease.  
IN Blakely R D; Apparsundaram S; Ferguson S  
PA (BLAK-I) BLAKELY R D.  
(APPA-I) APPARSUNDARAM S.  
(FERG-I) FERGUSON S.  
PI US 2003114399 A1 20030619 74p  
AI US 2001-911077 20010723  
PRAI US 2001-911077 20010723  
DT Patent  
LA English  
OS 2003-810914 [76]  
DESC \*\*\*High\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
(CHT) associated protein sequence #1.

L3 ANSWER 41 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
AN ADD50643 protein DGENE  
TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
\*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
polypeptide, useful in gene therapy to increase cholinergic function in  
a cell of a patient suffering from Alzheimer's disease.  
IN Blakely R D; Apparsundaram S; Ferguson S  
PA (BLAK-I) BLAKELY R D.  
(APPA-I) APPARSUNDARAM S.  
(FERG-I) FERGUSON S.  
PI US 2003114399 A1 20030619 74p  
AI US 2001-911077 20010723  
PRAI US 2001-911077 20010723  
DT Patent  
LA English  
OS 2003-810914 [76]  
CR N-PSDB: ADD50642  
DESC Rat \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
\*\*\*transporter\*\*\* (rCHT).



AN ADD50648 protein DGENE  
 TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
 \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 polypeptide, useful in gene therapy to increase cholinergic function in  
 a cell of a patient suffering from Alzheimer's disease.  
 IN Blakely R D; Apparsundaram S; Ferguson S  
 PA (BLAK-I) BLAKELY R D.  
 (APPA-I) APPARSUNDARAM S.  
 (FERG-I) FERGUSON S.  
 PI US 2003114399 A1 20030619 74p  
 AI US 2001-911077 20010723  
 PRAI US 2001-911077 20010723  
 DT Patent  
 LA English  
 OS 2003-810914 [76]  
 DESC \*\*\*High\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 (CHT) associated protein sequence #2.

L3 ANSWER 43 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ADD50639 protein DGENE  
 TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
 \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 polypeptide, useful in gene therapy to increase cholinergic function in  
 a cell of a patient suffering from Alzheimer's disease.  
 IN Blakely R D; Apparsundaram S; Ferguson S  
 PA (BLAK-I) BLAKELY R D.  
 (APPA-I) APPARSUNDARAM S.  
 (FERG-I) FERGUSON S.  
 PI US 2003114399 A1 20030619 74p  
 AI US 2001-911077 20010723  
 PRAI US 2001-911077 20010723  
 DT Patent  
 LA English  
 OS 2003-810914 [76]  
 CR N-PSDB: ADD50638  
 DESC \*\*\*Human\*\*\* \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* (hCHT).

L3 ANSWER 44 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ADD50649 protein DGENE  
 TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
 \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 polypeptide, useful in gene therapy to increase cholinergic function in  
 a cell of a patient suffering from Alzheimer's disease.  
 IN Blakely R D; Apparsundaram S; Ferguson S  
 PA (BLAK-I) BLAKELY R D.  
 (APPA-I) APPARSUNDARAM S.  
 (FERG-I) FERGUSON S.  
 PI US 2003114399 A1 20030619 74p  
 AI US 2001-911077 20010723  
 PRAI US 2001-911077 20010723  
 DT Patent  
 LA English  
 OS 2003-810914 [76]  
 DESC \*\*\*High\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 (CHT) associated protein sequence #3.

L3 ANSWER 45 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ADD50645 protein DGENE  
 TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
 \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 polypeptide, useful in gene therapy to increase cholinergic function in  
 a cell of a patient suffering from Alzheimer's disease.  
 IN Blakely R D; Apparsundaram S; Ferguson S  
 PA (BLAK-I) BLAKELY R D.  
 (APPA-I) APPARSUNDARAM S.  
 (FERG-I) FERGUSON S.  
 PI US 2003114399 A1 20030619 74p  
 AI US 2001-911077 20010723  
 PRAI US 2001-911077 20010723  
 DT Patent  
 LA English  
 OS 2003-810914 [76]  
 DESC C. elegans CHOI protein.

AN ADD50661 protein DGENE  
 TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
 \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 polypeptide, useful in gene therapy to increase cholinergic function in  
 a cell of a patient suffering from Alzheimer's disease.  
 IN Blakely R D; Apparsundaram S; Ferguson S  
 PA (BLAK-I) BLAKELY R D.  
 (APPA-I) APPARSUNDARAM S.  
 (FERG-I) FERGUSON S.  
 PI US 2003114399 A1 20030619 74p  
 AI US 2001-911077 20010723  
 PRAI US 2001-911077 20010723  
 DT Patent  
 LA English  
 OS 2003-810914 [76]  
 CR N-PSDB: ADD50660  
 DESC Mouse \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* (mCHT) #2.

L3 ANSWER 47 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ADD50641 protein DGENE  
 TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
 \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 polypeptide, useful in gene therapy to increase cholinergic function in  
 a cell of a patient suffering from Alzheimer's disease.  
 IN Blakely R D; Apparsundaram S; Ferguson S  
 PA (BLAK-I) BLAKELY R D.  
 (APPA-I) APPARSUNDARAM S.  
 (FERG-I) FERGUSON S.  
 PI US 2003114399 A1 20030619 74p  
 AI US 2001-911077 20010723  
 PRAI US 2001-911077 20010723  
 DT Patent  
 LA English  
 OS 2003-810914 [76]  
 CR N-PSDB: ADD50640  
 DESC Mouse \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* (mCHT) #1.

L3 ANSWER 48 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ABU08980 Protein DGENE  
 TI Novel isolated polynucleotide (I) that encodes \*\*\*high\*\*\*  
 \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\* protein, useful  
 for preventing, treating or ameliorating neurological and cognitive  
 disorders such as Alzheimer's or Parkinson's disease -  
 IN Wu D; Gu Y; Millard W J; He Y  
 PA (UYFL) UNIV FLORIDA.  
 PI US 6500643 B1 20021231 20p  
 AI US 2000-657252 20000907  
 PRAI US 2000-657252 20000907  
 DT Patent  
 LA English  
 OS 2003-361535 [34]  
 CR N-PSDB: ABX94339  
 DESC \*\*\*Human\*\*\* choline acetyltransferase.

L3 ANSWER 49 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ABU08979 Protein DGENE  
 TI Novel isolated polynucleotide (I) that encodes \*\*\*high\*\*\*  
 \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\* protein, useful  
 for preventing, treating or ameliorating neurological and cognitive  
 disorders such as Alzheimer's or Parkinson's disease -  
 IN Wu D; Gu Y; Millard W J; He Y  
 PA (UYFL) UNIV FLORIDA.  
 PI US 6500643 B1 20021231 20p  
 AI US 2000-657252 20000907  
 PRAI US 2000-657252 20000907  
 DT Patent  
 LA English  
 OS 2003-361535 [34]  
 CR N-PSDB: ABX94338  
 DESC \*\*\*Human\*\*\* \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\*, HACT.

L3 ANSWER 50 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN

TI New rat and \*\*\*human\*\*\* spinal cord \*\*\*high\*\*\* \*\*\*affinity\*\*\*  
 \*\*\*choline\*\*\* \*\*\*transporters\*\*\* , useful in diagnosis of  
 Alzheimer's disease and screening promoters as drugs for treating  
 Alzheimer's disease -  
 IN Haga T; Okuda T  
 PA (NISC-N) JAPAN SCI & TECHNOLOGY CORP.  
 PI WO 2001016315 A1 20010308 90p  
 AI WO 2000-JP5545 20000818  
 PRAI JP 1999-240642 19990827  
 JP 1999-368991 19991227  
 DT Patent  
 LA Japanese  
 OS 2001-226688 [23]  
 CR N-PSDB: AAF81713  
 DESC Mouse \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* protein.

L3 ANSWER 51 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN AAB74665 Protein DGENE  
 TI New rat and \*\*\*human\*\*\* spinal cord \*\*\*high\*\*\* \*\*\*affinity\*\*\*  
 \*\*\*choline\*\*\* \*\*\*transporters\*\*\* , useful in diagnosis of  
 Alzheimer's disease and screening promoters as drugs for treating  
 Alzheimer's disease -  
 IN Haga T; Okuda T  
 PA (NISC-N) JAPAN SCI & TECHNOLOGY CORP.  
 PI WO 2001016315 A1 20010308 90p  
 AI WO 2000-JP5545 20000818  
 PRAI JP 1999-240642 19990827  
 JP 1999-368991 19991227  
 DT Patent  
 LA Japanese  
 OS 2001-226688 [23]  
 CR N-PSDB: AAF81712  
 DESC \*\*\*Human\*\*\* \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* protein.

L3 ANSWER 52 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN AAB74664 Protein DGENE  
 TI New rat and \*\*\*human\*\*\* spinal cord \*\*\*high\*\*\* \*\*\*affinity\*\*\*  
 \*\*\*choline\*\*\* \*\*\*transporters\*\*\* , useful in diagnosis of  
 Alzheimer's disease and screening promoters as drugs for treating  
 Alzheimer's disease -  
 IN Haga T; Okuda T  
 PA (NISC-N) JAPAN SCI & TECHNOLOGY CORP.  
 PI WO 2001016315 A1 20010308 90p  
 AI WO 2000-JP5545 20000818  
 PRAI JP 1999-240642 19990827  
 JP 1999-368991 19991227  
 DT Patent  
 LA Japanese  
 OS 2001-226688 [23]  
 CR N-PSDB: AAF81711  
 DESC Rat \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* protein.

L3 ANSWER 53 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN AAB74663 Protein DGENE  
 TI New rat and \*\*\*human\*\*\* spinal cord \*\*\*high\*\*\* \*\*\*affinity\*\*\*  
 \*\*\*choline\*\*\* \*\*\*transporters\*\*\* , useful in diagnosis of  
 Alzheimer's disease and screening promoters as drugs for treating  
 Alzheimer's disease -  
 IN Haga T; Okuda T  
 PA (NISC-N) JAPAN SCI & TECHNOLOGY CORP.  
 PI WO 2001016315 A1 20010308 90p  
 AI WO 2000-JP5545 20000818  
 PRAI JP 1999-240642 19990827  
 JP 1999-368991 19991227  
 DT Patent  
 LA Japanese  
 OS 2001-226688 [23]  
 CR N-PSDB: AAF81710  
 DESC C. elegans \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* protein.

L3 ANSWER 54 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN

TI Identifying genes having altered expression level in presence of non-conventional transmissible agent, e.g. prion, useful for diagnosis and drug screening.  
 IN Mouthon F; Nouvel V; Deslys J P  
 PA (COMS) COMMISSARIAT ENERGIE ATOMIQUE.  
 PI FR 2839081 A1 20031031 100p  
 AI FR 2002-5392 20020429  
 PRAI FR 2002-5392 20020429  
 DT Patent  
 LA French  
 OS 2004-045747 [05]  
 DESC NaCl dependent \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* PCR primer, SEQ ID 125.

L3 ANSWER 55 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ADF08397 DNA DGENE  
 TI Identifying genes having altered expression level in presence of non-conventional transmissible agent, e.g. prion, useful for diagnosis and drug screening.  
 IN Mouthon F; Nouvel V; Deslys J P  
 PA (COMS) COMMISSARIAT ENERGIE ATOMIQUE.  
 PI FR 2839081 A1 20031031 100p  
 AI FR 2002-5392 20020429  
 PRAI FR 2002-5392 20020429  
 DT Patent  
 LA French  
 OS 2004-045747 [05]  
 DESC NaCl dependent \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* PCR primer, SEQ ID 126.

L3 ANSWER 56 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ADD50653 DNA DGENE  
 TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
 \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 polypeptide, useful in gene therapy to increase cholinergic function in a cell of a patient suffering from Alzheimer's disease.  
 IN Blakely R D; Apparsundaram S; Ferguson S  
 PA (BLAK-I) BLAKELY R D.  
 (APPA-I) APPARSUNDARAM S.  
 (FERG-I) FERGUSON S.  
 PI US 2003114399 A1 20030619 74p  
 AI US 2001-911077 20010723  
 PRAI US 2001-911077 20010723  
 DT Patent  
 LA English  
 OS 2003-810914 [76]  
 DESC PCR primer #2 for \*\*\*human\*\*\* \*\*\*high\*\*\* - \*\*\*affinity\*\*\*  
 \*\*\*choline\*\*\* \*\*\*transporter\*\*\* (hCHT) cDNA.

L3 ANSWER 57 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ADD50650 DNA DGENE  
 TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
 \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 polypeptide, useful in gene therapy to increase cholinergic function in a cell of a patient suffering from Alzheimer's disease.  
 IN Blakely R D; Apparsundaram S; Ferguson S  
 PA (BLAK-I) BLAKELY R D.  
 (APPA-I) APPARSUNDARAM S.  
 (FERG-I) FERGUSON S.  
 PI US 2003114399 A1 20030619 74p  
 AI US 2001-911077 20010723  
 PRAI US 2001-911077 20010723  
 DT Patent  
 LA English  
 OS 2003-810914 [76]  
 DESC BAC sequence #1 containing hCHT DNA.

L3 ANSWER 58 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ADD50664 DNA DGENE  
 TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
 \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 polypeptide, useful in gene therapy to increase cholinergic function in a cell of a patient suffering from Alzheimer's disease.  
 IN Blakely R D; Apparsundaram S; Ferguson S  
 PA (BLAK-I) BLAKELY R D.

(FERG-I) FERGUSON S.  
PI US 2003114399 A1 20030619 74p  
AI US 2001-911077 20010723  
PRAI US 2001-911077 20010723  
DT Patent  
LA English  
OS 2003-810914 [76]  
DESC PCR primer #2 for mouse \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
\*\*\*transporter\*\*\* (mCHT) cDNA.

L3 ANSWER 59 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
AN ADD50660 cDNA DGENE  
TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
\*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
polypeptide, useful in gene therapy to increase cholinergic function in  
a cell of a patient suffering from Alzheimer's disease.  
IN Blakely R D; Apparsundaram S; Ferguson S  
PA (BLAK-I) BLAKELY R D.  
(APPA-I) APPARSUNDARAM S.  
(FERG-I) FERGUSON S.

PI US 2003114399 A1 20030619 74p  
AI US 2001-911077 20010723  
PRAI US 2001-911077 20010723  
DT Patent  
LA English  
OS 2003-810914 [76]  
CR P-PSDB: ADD50661  
DESC cDNA encoding mouse \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
\*\*\*transporter\*\*\* (mCHT) #2.

L3 ANSWER 60 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
AN ADD50646 DNA DGENE  
TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
\*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
polypeptide, useful in gene therapy to increase cholinergic function in  
a cell of a patient suffering from Alzheimer's disease.  
IN Blakely R D; Apparsundaram S; Ferguson S  
PA (BLAK-I) BLAKELY R D.  
(APPA-I) APPARSUNDARAM S.  
(FERG-I) FERGUSON S.

PI US 2003114399 A1 20030619 74p  
AI US 2001-911077 20010723  
PRAI US 2001-911077 20010723  
DT Patent  
LA English  
OS 2003-810914 [76]  
DESC \*\*\*High\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
(CHT) associated DNA sequence #2.

L3 ANSWER 61 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
AN ADD50652 DNA DGENE  
TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
\*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
polypeptide, useful in gene therapy to increase cholinergic function in  
a cell of a patient suffering from Alzheimer's disease.  
IN Blakely R D; Apparsundaram S; Ferguson S  
PA (BLAK-I) BLAKELY R D.  
(APPA-I) APPARSUNDARAM S.  
(FERG-I) FERGUSON S.

PI US 2003114399 A1 20030619 74p  
AI US 2001-911077 20010723  
PRAI US 2001-911077 20010723  
DT Patent  
LA English  
OS 2003-810914 [76]  
DESC PCR primer #1 for \*\*\*human\*\*\* \*\*\*high\*\*\* - \*\*\*affinity\*\*\*  
\*\*\*choline\*\*\* \*\*\*transporter\*\*\* (hCHT) cDNA.

L3 ANSWER 62 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
AN ADD50651 DNA DGENE  
TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
\*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
polypeptide, useful in gene therapy to increase cholinergic function in  
a cell of a patient suffering from Alzheimer's disease.  
IN Blakely R D; Apparsundaram S; Ferguson S

(APPA-I) APPARSUNDARAM S.  
 (FERG-I) FERGUSON S.  
 PI US 2003114399 A1 20030619 74p  
 AI US 2001-911077 20010723  
 PRAI US 2001-911077 20010723  
 DT Patent  
 LA English  
 OS 2003-810914 [76]  
 DESC BAC sequence #2 containing hCHT DNA.

L3 ANSWER 63 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ADD50644 DNA DGENE  
 TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
 \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 polypeptide, useful in gene therapy to increase cholinergic function in  
 a cell of a patient suffering from Alzheimer's disease.  
 IN Blakely R D; Apparsundaram S; Ferguson S  
 PA (BLAK-I) BLAKELY R D.  
 (APPA-I) APPARSUNDARAM S.  
 (FERG-I) FERGUSON S.  
 PI US 2003114399 A1 20030619 74p  
 AI US 2001-911077 20010723  
 PRAI US 2001-911077 20010723  
 DT Patent  
 LA English  
 OS 2003-810914 [76]  
 DESC \*\*\*High\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 (CHT) associated DNA sequence #1.

L3 ANSWER 64 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ADD50657 DNA DGENE  
 TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
 \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 polypeptide, useful in gene therapy to increase cholinergic function in  
 a cell of a patient suffering from Alzheimer's disease.  
 IN Blakely R D; Apparsundaram S; Ferguson S  
 PA (BLAK-I) BLAKELY R D.  
 (APPA-I) APPARSUNDARAM S.  
 (FERG-I) FERGUSON S.  
 PI US 2003114399 A1 20030619 74p  
 AI US 2001-911077 20010723  
 PRAI US 2001-911077 20010723  
 DT Patent  
 LA English  
 OS 2003-810914 [76]  
 DESC \*\*\*Human\*\*\* chromosome 2 marker D2S340.

L3 ANSWER 65 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ADD50663 DNA DGENE  
 TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
 \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 polypeptide, useful in gene therapy to increase cholinergic function in  
 a cell of a patient suffering from Alzheimer's disease.  
 IN Blakely R D; Apparsundaram S; Ferguson S  
 PA (BLAK-I) BLAKELY R D.  
 (APPA-I) APPARSUNDARAM S.  
 (FERG-I) FERGUSON S.  
 PI US 2003114399 A1 20030619 74p  
 AI US 2001-911077 20010723  
 PRAI US 2001-911077 20010723  
 DT Patent  
 LA English  
 OS 2003-810914 [76]  
 DESC PCR primer #1 for mouse \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* (mCHT) cDNA.

L3 ANSWER 66 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ADD50638 cDNA DGENE  
 TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
 \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 polypeptide, useful in gene therapy to increase cholinergic function in  
 a cell of a patient suffering from Alzheimer's disease.  
 IN Blakely R D; Apparsundaram S; Ferguson S  
 PA (BLAK-I) BLAKELY R D.  
 (APPA-I) APPARSUNDARAM S.

PI US 2003114399 A1 20030619 74p  
AI US 2001-911077 20010723  
PRAI US 2001-911077 20010723  
DT Patent  
LA English  
OS 2003-810914 [76]  
CR P-PSDB: ADD50639  
DESC cDNA encoding \*\*\*human\*\*\* \*\*\*high\*\*\* - \*\*\*affinity\*\*\*  
\*\*\*choline\*\*\* \*\*\*transporter\*\*\* (hCHT).

L3 ANSWER 67 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
AN ADD50658 DNA DGENE  
TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
\*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
polypeptide, useful in gene therapy to increase cholinergic function in  
a cell of a patient suffering from Alzheimer's disease.  
IN Blakely R D; Apparsundaram S; Ferguson S  
PA (BLAK-I) BLAKELY R D.  
(APPA-I) APPARSUNDARAM S.  
(FERG-I) FERGUSON S.

PI US 2003114399 A1 20030619 74p  
AI US 2001-911077 20010723  
PRAI US 2001-911077 20010723  
DT Patent  
LA English  
OS 2003-810914 [76]  
DESC \*\*\*Human\*\*\* chromosome 2 marker D2S176.

L3 ANSWER 68 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
AN ADD50656 DNA DGENE  
TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
\*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
polypeptide, useful in gene therapy to increase cholinergic function in  
a cell of a patient suffering from Alzheimer's disease.  
IN Blakely R D; Apparsundaram S; Ferguson S  
PA (BLAK-I) BLAKELY R D.  
(APPA-I) APPARSUNDARAM S.  
(FERG-I) FERGUSON S.

PI US 2003114399 A1 20030619 74p  
AI US 2001-911077 20010723  
PRAI US 2001-911077 20010723  
DT Patent  
LA English  
OS 2003-810914 [76]  
DESC BAC sequence containing hCHT gene.

L3 ANSWER 69 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
AN ADD50655 DNA DGENE  
TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
\*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
polypeptide, useful in gene therapy to increase cholinergic function in  
a cell of a patient suffering from Alzheimer's disease.  
IN Blakely R D; Apparsundaram S; Ferguson S  
PA (BLAK-I) BLAKELY R D.  
(APPA-I) APPARSUNDARAM S.  
(FERG-I) FERGUSON S.

PI US 2003114399 A1 20030619 74p  
AI US 2001-911077 20010723  
PRAI US 2001-911077 20010723  
DT Patent  
LA English  
OS 2003-810914 [76]  
DESC PCR primer #2 for \*\*\*human\*\*\* \*\*\*high\*\*\* - \*\*\*affinity\*\*\*  
\*\*\*choline\*\*\* \*\*\*transporter\*\*\* (hCHT) gene.

L3 ANSWER 70 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
AN ADD50642 cDNA DGENE  
TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
\*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
polypeptide, useful in gene therapy to increase cholinergic function in  
a cell of a patient suffering from Alzheimer's disease.  
IN Blakely R D; Apparsundaram S; Ferguson S  
PA (BLAK-I) BLAKELY R D.  
(APPA-I) APPARSUNDARAM S.  
(FERG-I) FERGUSON S.

AI US 2001-911077 20010723  
PRAI US 2001-911077 20010723  
DT Patent  
LA English  
OS 2003-810914 [76]  
CR P-PSDB: ADD50643  
DESC cDNA encoding rat \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
\*\*\*transporter\*\*\* (rCHT).

L3 ANSWER 71 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
AN ADD50640 cDNA DGENE  
TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
\*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
polypeptide, useful in gene therapy to increase cholinergic function in  
a cell of a patient suffering from Alzheimer's disease.  
IN Blakely R D; Apparsundaram S; Ferguson S  
PA (BLAK-I) BLAKELY R D.  
(APPA-I) APPARSUNDARAM S.  
(FERG-I) FERGUSON S.

PI US 2003114399 A1 20030619 74p  
AI US 2001-911077 20010723  
PRAI US 2001-911077 20010723  
DT Patent  
LA English  
OS 2003-810914 [76]  
CR P-PSDB: ADD50641  
DESC cDNA encoding mouse \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
\*\*\*transporter\*\*\* (mCHT) #1.

L3 ANSWER 72 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
AN ADD50654 DNA DGENE  
TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
\*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
polypeptide, useful in gene therapy to increase cholinergic function in  
a cell of a patient suffering from Alzheimer's disease.  
IN Blakely R D; Apparsundaram S; Ferguson S  
PA (BLAK-I) BLAKELY R D.  
(APPA-I) APPARSUNDARAM S.  
(FERG-I) FERGUSON S.

PI US 2003114399 A1 20030619 74p  
AI US 2001-911077 20010723  
PRAI US 2001-911077 20010723  
DT Patent  
LA English  
OS 2003-810914 [76]  
DESC PCR primer #1 for \*\*\*human\*\*\* \*\*\*high\*\*\* - \*\*\*affinity\*\*\*  
\*\*\*choline\*\*\* \*\*\*transporter\*\*\* (hCHT) gene.

L3 ANSWER 73 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
AN ADD50659 DNA DGENE  
TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
\*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
polypeptide, useful in gene therapy to increase cholinergic function in  
a cell of a patient suffering from Alzheimer's disease.  
IN Blakely R D; Apparsundaram S; Ferguson S  
PA (BLAK-I) BLAKELY R D.  
(APPA-I) APPARSUNDARAM S.  
(FERG-I) FERGUSON S.

PI US 2003114399 A1 20030619 74p  
AI US 2001-911077 20010723  
PRAI US 2001-911077 20010723  
DT Patent  
LA English  
OS 2003-810914 [76]  
DESC \*\*\*Human\*\*\* chromosome 2 marker D2S1893.

L3 ANSWER 74 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
AN ABX94341 DNA DGENE  
TI Novel isolated polynucleotide (I) that encodes \*\*\*high\*\*\*  
\*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\* protein, useful  
for preventing, treating or ameliorating neurological and cognitive  
disorders such as Alzheimer's or Parkinson's disease -  
IN Wu D; Gu Y; Millard W J; He Y  
PA (UYFL) UNIV FLORIDA.  
PI US 6500643 B1 20021231 20p



PRAI US 2000-657252 20000907  
 DT Patent  
 LA English  
 OS 2003-361535 [34]  
 DESC \*\*\*Human\*\*\* \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* , HACT, PCR primer #2.

L3 ANSWER 75 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ABX94340 DNA DGENE  
 TI Novel isolated polynucleotide (I) that encodes \*\*\*high\*\*\*  
 \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\* protein, useful  
 for preventing, treating or ameliorating neurological and cognitive  
 disorders such as Alzheimer's or Parkinson's disease -  
 IN Wu D; Gu Y; Millard W J; He Y  
 PA (UYFL) UNIV FLORIDA.  
 PI US 6500643 B1 20021231 20p  
 AI US 2000-657252 20000907  
 PRAI US 2000-657252 20000907  
 DT Patent  
 LA English  
 OS 2003-361535 [34]  
 DESC \*\*\*Human\*\*\* \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* , HACT, PCR primer #1.

L3 ANSWER 76 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ABX94339 cDNA DGENE  
 TI Novel isolated polynucleotide (I) that encodes \*\*\*high\*\*\*  
 \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\* protein, useful  
 for preventing, treating or ameliorating neurological and cognitive  
 disorders such as Alzheimer's or Parkinson's disease -  
 IN Wu D; Gu Y; Millard W J; He Y  
 PA (UYFL) UNIV FLORIDA.  
 PI US 6500643 B1 20021231 20p  
 AI US 2000-657252 20000907  
 PRAI US 2000-657252 20000907  
 DT Patent  
 LA English  
 OS 2003-361535 [34]  
 CR P-PSDB: ABU08980  
 DESC \*\*\*Human\*\*\* cDNA encoding choline acetyltransferase.

L3 ANSWER 77 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ABX94338 cDNA DGENE  
 TI Novel isolated polynucleotide (I) that encodes \*\*\*high\*\*\*  
 \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\* protein, useful  
 for preventing, treating or ameliorating neurological and cognitive  
 disorders such as Alzheimer's or Parkinson's disease -  
 IN Wu D; Gu Y; Millard W J; He Y  
 PA (UYFL) UNIV FLORIDA.  
 PI US 6500643 B1 20021231 20p  
 AI US 2000-657252 20000907  
 PRAI US 2000-657252 20000907  
 DT Patent  
 LA English  
 OS 2003-361535 [34]  
 CR P-PSDB: ABU08979  
 DESC \*\*\*Human\*\*\* cDNA encoding \*\*\*high\*\*\* \*\*\*affinity\*\*\*  
 \*\*\*choline\*\*\* \*\*\*transporter\*\*\* , HACT.

L3 ANSWER 78 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN AAF81713 cDNA DGENE  
 TI New rat and \*\*\*human\*\*\* spinal cord \*\*\*high\*\*\* \*\*\*affinity\*\*\*  
 \*\*\*choline\*\*\* \*\*\*transporters\*\*\* , useful in diagnosis of  
 Alzheimer's disease and screening promoters as drugs for treating  
 Alzheimer's disease -  
 IN Haga T; Okuda T  
 PA (NISC-N) JAPAN SCI & TECHNOLOGY CORP.  
 PI WO 2001016315 A1 20010308 90p  
 AI WO 2000-JP5545 20000818  
 PRAI JP 1999-240642 19990827  
 JP 1999-368991 19991227  
 DT Patent  
 LA Japanese  
 OS 2001-226688 [23]  
 CR P-PSDB: AAB74666

\*\*\*transporter\*\*\* protein encoding cDNA.

L3 ANSWER 79 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN AAF81712 cDNA DGENE  
 TI New rat and \*\*\*human\*\*\* spinal cord \*\*\*high\*\*\* \*\*\*affinity\*\*\*  
 \*\*\*choline\*\*\* \*\*\*transporters\*\*\* , useful in diagnosis of  
 Alzheimer's disease and screening promoters as drugs for treating  
 Alzheimer's disease -  
 IN Haga T; Okuda T  
 PA (NISC-N) JAPAN SCI & TECHNOLOGY CORP.  
 PI WO 2001016315 A1 20010308 90p  
 AI WO 2000-JP5545 20000818  
 PRAI JP 1999-240642 19990827  
 JP 1999-368991 19991227  
 DT Patent  
 LA Japanese  
 OS 2001-226688 [23]  
 CR P-PSDB: AAB74665  
 DESC \*\*\*Human\*\*\* \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* protein encoding cDNA.

L3 ANSWER 80 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN AAF81711 cDNA DGENE  
 TI New rat and \*\*\*human\*\*\* spinal cord \*\*\*high\*\*\* \*\*\*affinity\*\*\*  
 \*\*\*choline\*\*\* \*\*\*transporters\*\*\* , useful in diagnosis of  
 Alzheimer's disease and screening promoters as drugs for treating  
 Alzheimer's disease -  
 IN Haga T; Okuda T  
 PA (NISC-N) JAPAN SCI & TECHNOLOGY CORP.  
 PI WO 2001016315 A1 20010308 90p  
 AI WO 2000-JP5545 20000818  
 PRAI JP 1999-240642 19990827  
 JP 1999-368991 19991227  
 DT Patent  
 LA Japanese  
 OS 2001-226688 [23]  
 CR P-PSDB: AAB74664  
 DESC Rat \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* protein encoding cDNA.

L3 ANSWER 81 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN AAF81710 cDNA DGENE  
 TI New rat and \*\*\*human\*\*\* spinal cord \*\*\*high\*\*\* \*\*\*affinity\*\*\*  
 \*\*\*choline\*\*\* \*\*\*transporters\*\*\* , useful in diagnosis of  
 Alzheimer's disease and screening promoters as drugs for treating  
 Alzheimer's disease -  
 IN Haga T; Okuda T  
 PA (NISC-N) JAPAN SCI & TECHNOLOGY CORP.  
 PI WO 2001016315 A1 20010308 90p  
 AI WO 2000-JP5545 20000818  
 PRAI JP 1999-240642 19990827  
 JP 1999-368991 19991227  
 DT Patent  
 LA Japanese  
 OS 2001-226688 [23]  
 CR P-PSDB: AAB74663  
 DESC C. elegans \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* protein encoding cDNA.

L3 ANSWER 82 OF 111 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS  
 RESERVED. on STN  
 AN 96156006 EMBASE  
 DN 1996156006  
 TI \*\*\*High\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 status in Alzheimer's disease tissue from rapid autopsy.  
 AU Bisette G.; Seidler F.J.; Nemeroff C.B.; Slotkin T.A.  
 CS Duke University Medical Center, Durham, NC 27710, United States  
 SO Annals of the New York Academy of Sciences, (1996) 777/- (197-204).  
 ISSN: 0077-8923 CODEN: ANYAA  
 CY United States  
 DT Journal; Conference Article  
 FS 005 General Pathology and Pathological Anatomy  
 008 Neurology and Neurosurgery  
 LA English  
 SL English

LOCUS (LOC): BX294147 GenBank (R)  
GenBank ACC. NO. (GBN): BX294147 BX119912  
GenBank VERSION (VER): BX294147.1 GI:32445670  
CAS REGISTRY NO. (RN): 543672-06-6  
SEQUENCE LENGTH (SQL): 314450  
MOLECULE TYPE (CI): DNA; linear  
DIVISION CODE (CI): Bacteria  
DATE (DATE): 11 Jul 2003  
DEFINITION (DEF): *Pirellula* sp. strain 1 complete genome; segment 15/24.  
KEYWORDS (ST): complete genome  
SOURCE: *Pirellula* sp.  
ORGANISM (ORGN): *Pirellula* sp.  
Bacteria; Planctomycetes; Planctomycetacia;  
Planctomycetales; Planctomycetaceae; *Pirellula*  
NUCLEIC ACID COUNT (NA): 72076 a 92563 c 83065 g 66746 t  
COMMENT:

This project was carried out by  
\*Max Planck Institute for Molecular Genetics, Berlin, Germany; \*Max  
Planck Institute for Marine Microbiology, Bremen, Germany; in the  
framework of the REGX-project, <http://www.regx.de> -----  
Genome Center  
Center: Max Planck Institute for Molecular Genetics  
Center code: MPIMG

----- Summary Statistics  
Sequencing vector: pUC19; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 7142841 bases at least Q40  
Consensus quality: 7145138 bases at least Q30  
Consensus quality: 7145484 bases at least Q20  
Quality coverage: 8.03

-----  
This sequence was finished as follows unless otherwise noted: all  
regions were double stranded, sequenced with an alternate  
chemistry, or covered by high quality data (i.e., phred quality >=  
30); an attempt was made to resolve all sequencing problems, such  
as compressions and repeats; all regions were covered by at least  
one plasmid Sequence; assembly was additionally confirmed by long  
range pcr and cosmid end sequences.

-----  
See <http://www.micro-genomes.mpg.de/pirellula/> for more information  
including minimal tiling path from a set of 220 cosmids out of  
908. See the misc feature tag below for the boundaries of the MTP  
cosmids. ----- Annotation

Center: Max Planck Institute for Marine Microbiology  
Celsiusstrasse 1, D-28359 Bremen, Germany.  
Center Code: MPIMM  
Email: [fog@mpi-bremen.de](mailto:fog@mpi-bremen.de)  
Phone: +49 (0)421 2028 938 Fax: +49 (0)421 2028 580

-----  
Three different programs (Glimmer, Critica and Orpheus) were used  
for ORF-prediction. A nonredundant list of ORFs was generated by  
suitable parsing of the results.  
Automated annotation was done with the software package Pedant Pro  
(<http://www.biomax.de>). All ORF predictions and annotations were  
manually corrected by considering all results of the different  
tools applied. See <http://www.regx.de> for more information and  
access to supplementary information.

-----  
REFERENCE: 1 (bases 1 to 314450)  
AUTHOR (AU): Gloeckner, F.O.; Kube, M.; Bauer, M.; Teeling, H.;  
Lombardot, T.; Ludwig, W.; Gade, D.; Beck, A.; Borzym, K.;  
Heitmann, K.; Rabus, R.; Schlesner, H.; Amann, R.;  
Reinhardt, R.  
TITLE (TI): Complete genome sequence of the marine planctomycete  
*Pirellula* sp. strain 1  
JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 100 (14), 8298-8303  
(2003)  
OTHER SOURCE (OS): CA 139:96134  
REFERENCE: 2 (bases 1 to 314450)  
AUTHOR (AU): Kube, M.; Borzym, K.; Heitmann, K.; Klages, S.;  
Marquardt, I.; Lehrack, S.; Beck, A.; Pawlik, R.;  
Reinhardt, R.; Gloeckner, F.O.; Bauer, M.; Teeling, H.;

TITLE (TI): Schlesner, H.; Amann, R.  
 JOURNAL (SO): Direct Submission  
 Submitted (21-JAN-2003) Max Planck Institute for  
 Molecular Genetics, proScience Ihnestrass 73, D-14195  
 Berlin, Germany Max Planck Institute for Marine  
 Microbiology Celsiusstrasse 1, D-28359 Bremen, Germany

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..314450	/organism="Pirellula sp." /mol-type="genomic DNA" /strain="1" /db-xref="taxon:117"
gene	complement(285..4451)	/gene="cycA" /locus-tag="RB7973"
CDS	complement(285..4451)	/gene="cycA" /locus-tag="RB7973" /function="electron transport and membrane-associated energy conservation" /note="PMID: 97428333 PMID: 2986626 PMID: 9281430 PMID: 11152119 best DB hits: BLAST: pir:A83363; probable cytochrome c precursor PA2266 [imported] -; E=5e-09 pir:E83075; probable cytochrome c PA4571 [imported] - Pseudomonas; E=7e-07 pir:CCTW5T; cytochrome c552 [validated] - Thermus aquaticus; E=9e-07 COG: PA2266; COG2010 Cytochrome c, mono- and diheme variants; E=5e-10 PFAM: PF00034; Cytochrome c; E=0.042" /codon-start=1 /transl-table=11 /product="probable cytochrome c precursor" /protein-id="CAD78402.1" /db-xref="GI:32445671" /translation="MNSLRRLMLLSVLVEVTV VRDTPAENVCTFRHSTLGCFCVCSQ FRWPAEQKLKLSKIRQLRKRTMPQRITTVLQWS LFFLCAGVIPGIAQRADAQDAFEF QSNDDVVAIYGNGLADRMQHPVWETFLQHQKGL DVSFRNMSFSGDRVNQRPRNQGT NDTEYLKHVAPNVVFTFYGFNESAAGPEKAGEHR DELIKLVQRYTQVQKDDGKDLRFV LFSPIAYENTGDASLPDGAELNVNLAAYTEATRE AAEITGAKFVDLFSPTYQLFQSSS ERLTLNGVHLNEAGYKQLAGIISQALLGEKPSD AELQDLYEAIEDKNWHWHNRYRAT DGNDIWGSRSTLTFVDGQSNADVLKHELVMMLDVM TANRDKVIWAAADGRTLQADDSNV PPPVKVTSNIGGGSASSNAMKEGSAVYLSPEESL AKINVPEGYELNVFASEVQFPDLA NPVQMQVDAHGRLWVASWNTYPKWEPEGKEMNSL MILEDTDNDGKADVRKIFAHVHNP LGFEFWNGGVVVTSGPDLLFLKDTGDGDKADVRY PILQGLGTS DTHHAANNLVYGPDG GIYWQSGIFLVHNHETPWKQNLNIGASGMYRFDP LTFAITPHAGNSPNPHGTSFDYWG YCYASDGTGGRCYQVRPEGNGFKMHKLEKEFRP VAANAILSSEHFPEELQNDILICN TIGFLGVKQYKLDREGDVEEEAAAEKTLKEETGP VKITRNGGLITVDHPALKDAKITG FKLSVNGRQQMNLSEVEVISGGRNIAKTAKLAQS SEYNNGTFPVQRLVDGDKGNFAHT SQQNNPWMRGDFPSPVQISEFKVWNRKGFEDRFN NGKIEFFDGDDEVVAVDIKIVSAD QEEQHREFGEVWGTPGLELLNSDDRNFRPTDAV GEDGALYVSDWHNAIIGHMQHNIR DPNRDHAHGRIFRITVKNRPLQKPVKIAQOSIEA LLENLKHPVNGVRHRTVELTKHD

gene	4473..4817	RNGVKNEALLNQLLES DVRHAVVA
CDS	4473..4817	AKTVRHFVENVDTKGGSEFAAPAELEFVKFDPK HLSGADRKTYELGATIIYQRESHCA TCHMTHGKGT PNVYPPLV GSPWVNGSEDRLIKMA LHGVWGKMTVAGKTYDPARGVPPM TAFRSLLKDDMAAVLTFVRNTWGN EASVVSPEA VSRVREETKGR TTFYKPEEILELH PLEKELMDES VTPETE VFSNEELEKELLAASPAK LAQVALAKGNFQRGKRLFHESSAA CFACHSP PAGTVRMGPDLEKATTKRSREELVDAL LRPSKLIDKDYAQVSVLTADGQIF TGIRVSENDD EIVLRNLAQPEPITISQYDVEDVI ESEVSLMPENLMRQMKNRREFNDL LKYIIIEVRKK"
		/locus-tag="RB7978"
		/locus-tag="RB7978"
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		/protein-id="CAD78403.1"
		/db-xref="GI:32445672"
		/translation="MRQPTNTLRRLNWGVKHRT TVWTSRGLSFQLGTLPRVFKPWLN LSCNGLVAFRVSGFLSIPYPAVPHNRSRSNAWPS AQGVSSLLPLTLVLRPIVGAKVSS GSEWMAVVGPFLL"
gene	4869..5462	/locus-tag="RB7980"
CDS	4869..5462	/locus-tag="RB7980"
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		/transl-table=11
		/product="hypothetical protein"
		/protein-id="CAD78404.1"
		/db-xref="GI:32445673"
		/translation="MDHLKNDLALNQIIIESCNSI QTTVHKAQMLPVSRGETGPLRWRE SCDKKIAIAGDILQFQLTEMPQV TDEC DVVQLA LSRSYGP NLMFDQIVSTHIDGKPA RPTNHSMHRS LDLHFNAIQSGSTV VIRYQVRVDR TADPSIVALDNIDVRWAFRSQSKR DAARKAHTASPGVSAPHVTGLVPAARAKASALTS SVV"
gene	complement(5520..6023)	/locus-tag="RB7983"
CDS	complement(5520..6023)	/locus-tag="RB7983"
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		/transl-table=11
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		/protein-id="CAD78405.1"
		/db-xref="GI:32445674"
		/translation="MEYTMNFGTNDFGAKDFRRG VLVATATLLSVAFFGGEAFGQCRS RGGGPPSGSPTSFTSGSQY AQNPHYQNALVSSYP QNNLIASQYQQQLLASQRQIASSA YRNTQQQRLALMQSEADVQAYRLARAESKRAARA ERIAARLREQGRSE DAYTLASVNV DKSPPRR"
gene	6183..6290	/locus-tag="RB7984"
CDS	6183..6290	/locus-tag="RB7984"
		/codon-start=1
		/transl-table=11
		/product="hypothetical protein"
		/protein-id="CAD78406.1"
		/db-xref="GI:32445675"
		/translation="MSDVSPFGCSLTGGKWIRCP SPNLSVTLKSSCHEF"
gene	6280..7695	/gene="ansA"
CDS	6280..7695	/locus-tag="RB7985"
		/gene="ansA"
		/locus-tag="RB7985"
		/EC-number="3.5.1.1"
		/function="degradation of amino-acids of the aspartate-group"
		/note="PMID: 1391778 best DB hits: BLAST: swissprot:P30364; ASPG-LUPAN L-ASPARAGINASE"

swissprot:Q9ZSD6; ASPG-LUPLU  
 L-ASPARAGINASE (L-ASPARAGINE;  
 E=3e-62 swissprot:P50288;  
 ASPG-LUPAL L-ASPARAGINASE  
 (L-ASPARAGINE; E=5e-62 COG: ybiK;  
 COG1446 Asparaginase; E=2e-56  
 PFAM: PF02530; Porin subfamily;  
 E=0.047 PF01112; Asparaginase;  
 E=1.9e-57"  
 /codon-start=1  
 /transl-table=11  
 /product="L-asparaginase"  
 /protein-id="CAD78407.1"  
 /db-xref="GI:32445676"  
 /translation="MNFKTTILAAVAFAFVAPR  
 TIQSKEPAMKTKWAIVIHGGAGSS  
 PAQLGDASSKQRTKGLQHALQTRDMLADGATAM  
 DTVEAVIRLTLEDDPIFNAGRGSVV  
 TNEGRVEMDSSVMDGKTLACGAVAGVTRVKNPIS  
 LARRVMTETKHVLLVGPGEFAE  
 TQQVPLVDPKYFLSQRDGDDASSIASATQDEDES  
 HLGTVGCVVLD SHGNLAAGTSTGG  
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gene  
CDS

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CDS

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gene product [Drosophila; E=2e-37  
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CDS

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CDS

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ref:XP-009649.1; sodium calcium
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gb:AAG60049.1; AF314821-1
(AF314821) K+-dependent NaCa
exchanger; E=4e-08 COG: MTH1155;
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gene product [Drosophila; E=5e-19  
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gene 34792..36138  
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protein trkA [imported] -
Methanosarcina; E=2e-38
pir:E83643; potassium uptake
protein TrkA PA0016 [imported] -;
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Mycobacterium tuberculosis;  
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Streptomyces; E=1e-57 COG:  
PA4960-2; COG0560 Phosphoserine  
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COG2716 ACT domain-containing  
protein; E=3e-31 jhp0597; COG0560  
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slr0697-2; COG0146  
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CDS

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complement (41446..46233

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CDS complement(46428..47630)

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 (AJ003195) membrane spanning  
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		DESTLPRLPKPVQIKTPSEMMVQQQRHLPVKIDS
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		QCDANDVTSLTVDGVIEAVRVEDDSIARVIGSTS
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gene	complement(53080..53925)	
CDS	complement(53080..53925)	<pre> /locus-tag="RB8060" /gene="spoU"  /locus-tag="RB8060" /EC-number="2.1.1.-" /EC-number="2.1.1.66" /function="rRNA processing" /note="PMID: 7590303 PMID: 2987648 best DB hits: BLAST: gb:AAF73591.1; (AE002337) spoU rRNA methylase family protein; E=2e-27 pir:C72066; rRNA methylase - Chlamydomonada pneumoniae (strain; E=5e-27 pir:A75448; rRNA methylase - Deinococcus radiodurans (strain R1); E=2e-26 COG: CPn0530; COG0566 rRNA methylases; E=5e-28 PFAM: PF00588; SpoU rRNA Methylase family; E=4.7e-24" /codon-start=1 /transl-table=11 /product="spoU rRNA methylase family protein" /protein-id="CAD78444.1" /db-xref="GI:32445713" /translation="MQKCCPMETIRSLQNAAVRR IVSLRRSRKRRAAGVVLVDGPRES LRAIEAGLKLTAIFYEIEPKLSEAGPPDMPEQAV ARQHAIDSGVHRWVTSEVERKIAAY TASTDRCVAEFVAPDDSLQLLERSSSWNDGLILV LDRVEKPGNLGAVFRSADAAGVSA VLLSDCPSDRFNPNAIRGSLGAVFTVPSASGSES QMEAFCLKTHGYRVAAMRVEGSRPL FSDSLRGKVAVVLGSEADGLADRWAGDSIDPVAL PMAGHVDSLNVSVSAAIVAFEAVR QRSNG" /locus-tag="RB8061" /locus-tag="RB8061" /note="PMID: 97426617 best DB hits: BLAST: pir:C65084; hypothetical protein b2981 - Escherichia coli (strain; E=9e-35" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAD78445.1" /db-xref="GI:32445714" /translation="MVSMGQHFCTFASMGEPTRV CYLLTFAKQLLCYQPLNARMSENV LCQPVSGRQDQKAFLDLEKRLYSDDPNWVPPLWS ERVKLVGFKHHPFYDNAEGQTFLV RRGDRVVGRLVAVVNHAHNRYHDETRGFFGFEEC EDDEEAAIELLDTAGDWLQKRGMT CVRGPVHPSLNYEVGLLDGFDTPPTFLIPYNHP YYERLIQAAGFEKSQDLYSYEASI DILETLDPKLLFVIEESTRRFNAVCRSIDPKNFN ADVRFVFLDIYNQSLQRTWGYVPMS EAEVDDQSNGLKNLLLPKLTSLAEIDGKPVGAGF GLLDYNPLIKKINGKLLPFGWLKL LMGRKKLKRRLVLSANVLPYQKWGLGLVTLYKI LPEAIKFGIEMGEFSWVLESNQLS RGTIERGGATRSKTHRIYDRSLTPESQAST" </pre>
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CDS

55165..57267

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HELICASE YOOA; E=2e-84
gb:AAG56797.1; AE005403-8
(AE005403) putative enzyme
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gene

complement(57222..57440)

CDS

complement(57222..57440)

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gene

complement(57424..57540)

CDS

complement(57424..57540)

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gene 61176..62276  
CDS 61176..62276

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PPVKDKDAERLIETEVKTRIPIST  
EDLALITWVAPLQKGSTVGRPVVMAAATKLTVSR  
RVDLLGIGGLKLDGLVPSPIALAN  
FAAHEFSELLAPPADKS AKKSKTVEETSDESSE  
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Y330-RICPR HYPOTHETICAL PROTEIN  
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gene 62454..62975  
CDS 62454..62975



gene 63046..64737  
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gene 64750..66261  
CDS 64750..66261

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E=4e-55 gb:AAB03341.1; (U62317)  
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E=4e-55 COG: aslA; COG3119  
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gene complement (66230..66388

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gene     complement(66385..67146 /gene="hisA"
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CDS      complement(66385..67146 /gene="hisA"
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HIS4-SYNY3; E=3e-56 pir:A83003;
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dazole carboxamide; E=5e-49
gb:AAF05093.1; AF150930-2
(AF150930) phosphoribosyl; E=2e-46
COG: slr0652; COG0106
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conserved hypothetical protein
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slr1343; COG3046
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CDS	complement (68890..69006)	/locus-tag="RB8084"  /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="CAD78461.1" /db-xref="GI:32445730" /translation="MSRRLAASFSSPHKVVSE WSFRPRIEAAAFYRVNPV" /locus-tag="RB8085" /locus-tag="RB8085" /note="PMID: 11705915 best DB hits: BLAST: gb:AAG31169.1; (AF314961) unknown [Salmonella typhimurium]; E=0.70 PFAM: PF01011; PQQ enzyme repeat; E=0.017" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein-putative PQQ-repeat containing protein" /protein-id="CAD78462.1" /db-xref="GI:32445731" /translation="MDFILCTAWVIARLCERTEA NAKRRTSPMTPAWLLTINMKRIFL QSSILLALGLAGCTPAASERTFDVPLEEPTRADR PSEMIVADYQQSKRRDDLQTMQDW PVLFGPHRTGATQASIPAVWPEQGPALRWDVEVG TGYGSPVTAENRVVFSHRVDDLEW IQCHDAQDGAVRWKHSLETDACDFEYSDGPYST PLIDQERRAVYHFSGSGTLVSLDF DTGEEVWRRDLHGEFQVEPELFP SGATPLLHGEH LILSLGGANNDAGIIAIHVRDGKT IWSCTDHKAAYTTPVVAQLFGQEFVMTAEGLV CLDPANGEVDWEIPHRSRAPMSYN SVSPLVWNDHVLMTGPGPGAVCLQILPDRSYEE RWKNRRLDSQYTNLLLSGDGHVFG FTSAGQGGAEELRCIEFVTGELKWKYHSLRRSQG LIAGDAMFFLGERGHLASLQRSIE EPRVLSFTQQPLMKADCYCSPAILKNGIVLKDED RIAVFDLPPSP"
gene	69030..70517	
CDS	69030..70517	
gene	complement (70518..71285)	/locus-tag="RB8089"
CDS	complement (70518..71285)	/locus-tag="RB8089"  /codon-start=1 /transl-table=11 /product="hypothetical protein-signal peptide and transmembrane prediction"

gene

complement (71254..73476 )

CDS

complement (71254..73476 )

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QSTSLGSQAAGTGPIQFTLALNAPAPGQTFDMES  
ITLLGYSELSTTIEQTVRVNFTGT  
KIVNGTMSSVTLLSGEFEADELTPLVVTFGDEFH  
GLTSLTWSQGGTARAHQFDNITFS  
TVTAVPEPGTFLAMIALATMGFVTRGRRWIGKRL  
QVV"

/locus-tag="RB8091"

/note="PMID: 20039618 best DB  
hits: BLAST: ddbj:BAA86452.1;  
(AB032964) KIAA1138 protein [Homo  
sapiens]; E=0.74"  
/codon-start=1  
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protein"

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/db-xref="GI:32445733"

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TSAVQKAAKDRDANSPEETIGDWKPVSDRKPANP  
LGEPERHAKAVENLNRLTEALMAY  
KEDKGHYPPSAQAKAGIKTLSWRVLILPYLGHQD  
LFEKFDLNPWNRSNPKELIEFIP  
DELVSPERFDSKTNWMLPAHRNYMFGDNRYPRDR  
NIEDGIENTLMLVEVNDDLAVEWT  
RPVDFEPADLGALKGSLGELRSGGTLVAWANGWP  
SYVANSVSTKQWTNAFTYESGDGQ  
RAGAIHKEPDALLAAHKPSRSETKVEAKVSGRVE  
ASKIVENTEVEAESWGENRLPVPP  
SPDLATSNQRIEQLFGEQLVRAKQNTQAELSND  
FLKKSLVMSDDAAGAYALQNAID  
LAIDSGDFMLFQAVLDQHASTFEVDLYQVNRDGL  
LEFSRRNDVDEDTASQMAFVRRAL  
VAIQEGLERNDFEGVGRIASALPRVEEERRGFRR  
ANVRGGKRDASAELVRLLOTLQLS  
SANKQYEQAAEKVAEYRKNPDDAELASALGRFYC  
FLKGDWAMGLPLVINGTSEKLSRV  
AKRDLEGANDAEDFLAIGDMWELSEGLPAGIYR  
QGTRDRAGYWYEQSLEVMPESLDR  
LHVQARVKEWQSQDPGSPLATIRTINRQLGLAEN  
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gene

complement (73451..74641 )

CDS

complement (73451..74641 )

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transmembrane prediction"  
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GLSTGLATIVTYAPYGVSKTERAE  
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TIDVAETTCKCTVGSQAQKGTLPAGEKTSVTLTWN  
TGQKSEQYEQAAARVITNDPTREVI  
DLTVSGVVRTELFVPAKGVFHS GDAGEVVESTLL  
IYSQQHDDIAVVGAESDLVGFDFWE  
SNVVPSSDSQPSLSEQQPTVINQVKLRCAQKPGR  
FQGEVKLHLLVNGESDVIEKSVEL  
TGRVHAPISFHS PMLHSRDGLDLGTLGNDQEHEF  
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DVSIEPTSRFGDYRLTIRIPKGIPSTIFNLDQKR

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CDS      complement (74638..74838 /locus-tag="RB8095"
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                                                /db-xref="GI:32445735"
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GQRWRAFGFHRWFSFSLKNRV"

gene      complement (74851..76122 /locus-tag="RB8096"
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CDS      complement (74851..76122 /locus-tag="RB8096"
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PF00114; Pilin (bacterial
filament); E=0.86"
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transmembrane prediction"
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GQCGKADWQGVSGDGSSTTFGGTA
PETAVRAELIARYFLTNGYNTNYAASWHLVRGMV
KTEADPSTGELTTWSGGGFKGLGG
STGPMSVADLERSRISSSNVGFICCAAPGDVDEA
ILGATLGFDTGTGVWGTALNQTAV
EYIASGSLLTEAFNDGPAYWNATAGNLDLIGSNE
TLAQIGCERGEPTTAGCAAPTGP
GGNGIYMQDTRDWYAVHAGSCNILMGDGHVEVFA
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CDS      complement (76119..76334 /locus-tag="RB8098"
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misc-feature  76358 763 /note="cosmid pircos-d1d02/ cosmid
pircos-d3d05 joining point"
gene      76464..76715 /locus-tag="RB8100"
CDS      76464..76715 /locus-tag="RB8100"
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TFHNPYSFASHSHSCEGSFLDEFS
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CRFSR"

gene      76684..76875 /locus-tag="RB8101"
CDS      76684..76875 /locus-tag="RB8101"
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CDS      complement(76885..78048 /locus-tag="RB8102"
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                                           systems"
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                                           general secretion pathway protein
                                           G PA3101 [imported]; E=0.063
                                           gb:AAC83358.1; (AF092918) outer
                                           membrane secretion protein T;
                                           E=0.069 gb:AAC79845.1; (AF089753)
                                           cellulose-binding protein CbpC;
                                           E=0.24 COG: PA3101; COG2165
                                           General secretory pathway proteins
                                           G and H and; E=0.006 PFAM:
                                           PF02361; Cobalt transport protein;
                                           E=0.11 PF00114; Pilin (bacterial
                                           filament); E=0.011"
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                                           DLVRRGVLVSEMRCTSTSAQASSAIEHLLSDNEA
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                                           KNVARLIEASPADRVEYIERKMLEDGYNTNYAAS
                                           WFLVRSEVILDESGQPQPKDSACT
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                                           GEPILYKETDPNYLKEPVIAASTPREGVSGWLRI
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CDS      77942..78313
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gene      78329..79276
CDS      78329..79276
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gene      complement(79324..82143 /locus-tag="RB8108"
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CDS      complement(79324..82143 /locus-tag="RB8108"
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CDS

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complement (82127..83044)
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protein"
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VTWQVLLSKLLIGFAAWVLAVL VASVCFALSWL
VLRGGWDWSAIGRISGSEIFELM
VYGVGLLICGWIAALIVRNPVGSVMLVIPLIVGL
TLLWNYSVAGLVSTHFHYGVTFLE
ATAAQRVSMLCLATVYLAALGGVVAGLARHRLAG
ASDHRWQAPAVASTSAWQPSVVQV
AWHAKPRPFRALLWQQVRQTLR VIGAAFSFALFA
LLSIWTDGNHGFDLLLVLGW PAA
HLMLGVAAFHGDRRGMRQGGFADRGWPPNLIWVT
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YLGMYGTGTLWQAFGFSVVVQ TLLFLIGVLTGQ
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GLLAFYGGYTGLLWLAAGVLLFASRRLTPFVMEG
VSSAAVWGRGLAYCLLALGVMCLC
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SWAGQRMNYAFENEAARYRDVELR
LDAELKSSEVMGEHVSQSELYGLCVDTPIAAKG Y
ASVPNWNGLPYGVSPYQHFWHPF
RRKALEVAAKWSKLSREQSFVFGALGELLNNAES
NEWIVINGLRQIAYEQNLF SDEAL
PQSEEDQLDREAFIRVVDQLVNKDLRRESRQRSL
IAEWQRFQTGEWSGWFDEDELGNEK
SFLDAPLSEPFYRFEQTRFERILDVAVRNTLD
QLEDGLPEWDDPELTKQRL LWTKL
LKDRRSGVGHQEVASPPRAPVFYREQDLLIDELR
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/note="PMID: 1924314 PMID: 8088782
best DB hits: BLAST: pir:T36523;
probable ABC-type transport system
ATP-binding protein -; E=4e-37
pir:C72303; ABC transporter,
ATP-binding protein - Thermotoga;
E=6e-34 gb:AAF81232.1; (AF263012)
ABC transporter ATP binding
protein; E=9e-33 COG: TM1028;
COG1131 ABC-type multidrug
transport system, ATPase; E=5e-35
PFAM: PF00005; ABC transporter;
E=5e-43"
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transport system ATP-binding
protein"
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LYEWMTPPEIGWVFSAFYDDGFIA
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AHDPELLILDEPTSGLDPMVRRQF
LESMVDRAAAGRTVLLSSHINEVERVADMVAMI
HGGQVKLVQSMNDLKQHTRIVTAT
MDDAHVESPDLPGRVLSETSNGRQRRWVITDWND
AGDLHWGPNDGVRQFHVSVPTLEE
VFIAVCGQPIRDEPSSFDRROEVNDGHFA"

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CDS

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complement (83172..83669)

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pir:G69999; transcription  
regulator GntR related protein  
ytrA -; E=4e-13 pir:D72336;  
transcription regulator, GntR  
family - Thermotoga; E=9e-13  
gb:AAC62421.1; (AF084104)  
hypothetical protein [Bacillus  
firmus]; E=1e-08 COG: BS-ytrA;  
COG1725 Predicted transcriptional  
regulators; E=4e-14 BH1940;  
COG1167 Transcriptional regulators  
containing a; E=3e-06 BH1164;  
COG1725 Predicted transcriptional  
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gene  
CDS

83626..85503  
83626..85503

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/function="biogenesis of outer  
membrane"  
/note="best DB hits: BLAST:  
ddbj: BAB06996.1; (AP001518) spore  
cortex protein [Bacillus; E=0.022  
COG: BH3277; COG2244 Membrane  
protein involved in the export of  
O-antigen; E=0.002 PFAM: PF01943;  
Polysaccharide biosynthesis pro;  
E=0.05"  
/codon-start=1  
/transl-table=11  
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RGIGFIRGMAFCRLMDDTDVGRWS  
MAFGFITLITPVMLLGIPGVLPFTEHFRLKRSL  
TPFVRRRIAIGTILSCTVIFVTTMLW  
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GNLFELSDRYMILHFIPATETLSA  
EIAGQAAVGQYHSGRIIPMLLSLGMTMIGGVMLP  
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MPMALCFCTWAALVTVGQNYLWTV



gene 85427..85855  
CDS 85427..85855

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RPKNGV"

gene 85827..86360  
CDS 85827..86360

/gene="fabZ"  
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biosynthesis"  
/note="PMID: 7806516 best DB hits:  
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E=2e-14 gb:AAK04875.1; AE006311-6  
(AE006311); E=3e-14 pir:C82731;  
(3r)-hydroxymyristoyl ACP  
dehydrase XF1044 [imported] -;  
E=6e-14 COG: XF1044; COG0764  
3-hydroxymyristoyl/3-hydroxydecano  
yl-(acyl carrier; E=6e-15 PFAM:  
PF01377; Thioester dehydrase;  
E=2.1e-18 PF01575; MaoC like  
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EFVPVATRMDSVKFKNMVVRPGDTVDIHVTLEQL  
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gene 86357..87190  
CDS 86357..87190

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AF197058-1 (AF197058)  
trans-2-enoyl-ACP reductase;  
E=6e-31 ddbj: BAB06562.1;  
(AP001516) enoyl-[acyl-carrier  
protein]; E=5e-29 gb:AAD04184.1;  
(L10036) unknown [Nostoc sp. PCC  
7120]; E=2e-28 COG: BH2843;  
COG0623  
Enoyl-[acyl-carrier-protein]  
reductase (NADH); E=5e-30 TM0441;  
COG1028 Dehydrogenases with  
different specificities (related;  
E=1e-09 BS-yfhR; COG1028  
Dehydrogenases with different  
specificities; E=1e-06 PFAM:  
PF00678; Short chain  
dehydrogenase/redu; E=7.1e-05"

gene 87269..88126  
CDS 87269..88126

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DYSDBGIRPFHETTRRQFLQAIDISAFSLVAVCNA
IKDQLANDASVVTIGISTTRMASE
SYGFMAPIKAALESSLAFLTKSFSRFSQVRFNAV
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KVIIPRGEAVSTNEVASTAAFLSSRSSGITAQSI
VVDAGMSINYFDADVVGAVTNASV D"
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/note="PMID: 85289113 best DB
hits: BLAST: swissprot:Q58414;
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AMINO ACID; E=4e-69 gb:AAB90305.1;
(AE001039) branched-chain amino
acid; E=4e-65 pir:F69057;
branched-chain amino-acid
aminotransferase -; E=2e-46 COG:
MJ1008; COG0115 Branched-chain
amino acid; E=4e-70 PFAM: PF01063;
Aminotransferase class IV;
E=1.9e-91"
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gene 88191..88979  
CDS 88191..88979

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amino acid aminotransferase"
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VAKNGLTEGYIRLVVTRGGNQLGL
NPFSCEDPQVIIIADTISLYPEKFYTEGLELITA
STIRNHPAALSPRVKSLNYLNNIM
AKIEAIRAGCIEAVMLNTKGEVAECTGDNIFIVR
GGRLITPPIDAGILEGITRNTVID
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gene 88972..89505  
CDS 88972..89505

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RLPNTRILIRAAHDRKAAAETGNR
FASSKSSNPFEPSSRDVGQYFHLIRTTTDGRGL
ASSRKWGTPTGNETLHGRGLHGTC
TRNAGPTNLFDDLQSPSSSGPKQARDRTPDQAVS
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TLLKTRRGDA"
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gene	90960..91187	
CDS	90960..91187	
gene	complement (91189..92931	

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/ note="best DB hits: BLAST:
pir:T47011; hypothetical protein
[imported] - Yersinia pestis;
E=0.020 embl:CAB58305.1;
(AL121854) hypothetical protein
SCJ33.06c; E=0.11 pir:E69891;
cytochrome c biogenesis protein
CycX homolog homolog; E=0.28"
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protein"
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SEADIEMRMITSGQSGIEDSATAF
SELKRIATWKREASRLIEHADATEKEKAIGRRG
ELQSLSHLASLGLKAAESLQLLA
ESLQEDSDPEVRSDSQLVLIGFAIEDLRNGKSDA
PSRVVSQIDRLLQASSSPDAATLM
VMGOAKDALLQFEHVEEASRVRAMILEEFVESGE
AIAGESDAMGGLVDMARQIAGPSF
QISEATARVQNLMEFITEANENTDPSDSAVSIN
DWKAAIESLADEQPDLLTTQFLAG
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EARTALQARDNREKIIGKTFDPDL
PSTKGDELSMDDYRGKVVLMPFWSAAFADSLLVV
DNLQKIARQYPEKVAIVGMNLDVQ
STDVPAFESRNKISFPSFRSVSDPEASVANSVAY
RFGVVSLLFVAVIDQEGKVAAIEF
SGRDLTPVVENLLR"
gene      complement(92961..93179 /locus-tag="RB8143"
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CDS      complement(92961..93179 /locus-tag="RB8143"
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/ codon-start=1
/ transl-table=11
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/ db-xref="GI:32445757"
/ translation="MQVRQGVCTEPVLRITRQS
VPDSIGGVYFERLPSRINGRDRKC
LCQISECRSSNPTRIERTVFELARWPVE"
gene      complement(93191..93622 /locus-tag="RB8144"
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CDS      complement(93191..93622 /locus-tag="RB8144"
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TVGTFFLVFGVLAPWLHYHQSRQ
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PSLENVSMISTASQNETAPSDAEI
TRRVMKIRSSWSVAERLRRRREADDRFADLLDAL
SAEHTAA"
gene      complement(93667..94122 /locus-tag="RB8146"
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CDS      complement(93667..94122 /locus-tag="RB8146"
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/ transl-table=11
/ product="hypothetical protein"
/ protein-id="CAD78490.1"
/ db-xref="GI:32445759"
/ translation="MLANTKCRVLDPFPTQLAIF
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METVAGRFEALEGLFFWDG SFTWANQSQGWQID

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gene	94339..94551	RQLLMERLRTLFSAFGEPAVSLSMRIPDRTWQDL OGFEKDV CSTNASDR"
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tRNA	94716..94788	/product="tRNA-Glu" /note="Glu, tRNAscan-SE-score 56.70%" /evidence=not-experimental
gene	complement(95002..96339)	/locus-tag="RB8150"
CDS	complement(95002..96339)	/locus-tag="RB8150" /codon-start=1 /transl-table=11 /product="hypothetical protein-signal peptide and transmembrane prediction" /protein-id="CAD78492.1" /db-xref="GI:32445761" /translation="MVSLHSNGAAPS FHERCVFA VKSRVISGGLFCLVVMMASSASAQ PDFERPPIDYLNAEVNDPVAKLAKRIEAGEVALN SDPKFGYLPVLEALDVPLSSQTL VFSKTSLQLHRISPRRPRALYFNDDVYVGYCQHG DVLEFASTDAKQGAIFYTLSQSEE KEPEFVRDRGGCLSCHASSRTQNVPGFLIRSVFA DAAGRPKLGS GTFTTDHTSPFDER WGGWYVTGSHGSMRHMGNVICTDEAQELDRESGA NQDDLGEYFR TDSHLTPHSDIVAL MVLEHQTQMHNATAANFETRQALHQSYQMNE LL EREPDI FESATRRIESSADRVLK YLLMCDEFTLTDSVAGTSTFAKEFASMGPRDPEQ RSLRDFDLETRLFRYPCSYLIYSD SFMELPAEVKSRVLEKLKHILSGEDQSEAYQH LT GKMRSEILEILRATHPDFQ"
gene	96496..96870	/locus-tag="RB8152"
CDS	96496..96870	/locus-tag="RB8152" /function="transcriptional control" /note="best DB hits: BLAST: pir:C75577; conserved hypothetical protein - Deinococcus radiodurans; E=1e-13 pir:E70324; conserved hypothetical protein aq-268 - Aquifex aeolicus; E=3e-07 swissprot:P44675; YFHP-HAEIN HYPOTHETICAL PROTEIN HI0379 -----;

Predicted transcriptional  
 regulator; E=1e-14 PFAM: PF02082;  
 Uncharacterized protein family  
 UPF00; E=6.3e-10"  
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 regulator"  
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 /locus-tag="RB8153"

gene complement(96932..98392

CDS complement(96932..98392

/note="PMID: 8168477 PMID:  
 10360571 best DB hits: BLAST:  
 swissprot:P56727; Y929-THEMA  
 HYPOTHETICAL PROTEIN TM0929 -----;  
 E=1e-09 embl:CAA57668.1; (X82178)  
 orf1 [Thermotoga maritima]; E=0.34  
 gb:AAA65436.1; (U24145) orf1;  
 upstream of ferredoxin; Method:;  
 E=0.34"  
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 SYSASNLTVQECRLSKLPMRPREVLGSETHDQ  
 YFEYYYRQLAEREQDQPDSEDST  
 PEPDQSDDSKPGEGTSHPEETLGDDSSDAGDSGN  
 DAVAEQRDETGDSSVEEDDGSSA  
 ESNEPTPDSPSLEQAADSSVGNLSESYVDPSQTG  
 AENADQWDADDLLHEEIKSAVADA  
 AENGWGWTLPGHAQERLLATLRPPLDYRSILRQF  
 RQSVLSVDRRLTRMRPSRRYGFAQ  
 MGSRYDFTTRLLFAVDVSGSMHRDLQNGFSIIN  
 RFFQYGIRSIDVVWFDTQIRCEPL  
 TFRSARRDVSITGRGGTDLGCVTEFIDEHRGYDG  
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 AS"

gene complement(98389..99483

CDS complement(98389..99483

/locus-tag="RB8157"  
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 hits: BLAST: pir:B72315; conserved  
 hypothetical protein - Thermotoga  
 maritima; E=1e-25 pir:T35221;  
 probable ATPGTP binding protein -  
 Streptomyces; E=5e-15 pir:A75429;  
 conserved hypothetical protein -  
 Deinococcus radiodurans; E=1e-07  
 COG: TM0930; COG0714 MoxR-like  
 ATPases; E=1e-26"  
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 DDWLLWADQHKVDDRVTFVQQQPQYLDGEGISP  
 SAEDANSMSGVLVKTTPDRRGWARVS  
 SMLQGVETIQPVHVKLIAGVVGSPAAMAFRRSLA  
 SRLQVSPDQVLLQFTKHKRAIEKM  
 ALGELLMLNEQLLVHLVGDYDDADRTKALKGML  
 SYLKLLRKRKLDEAVAHLVSMTDQ  
 PKYEPAMEFFAESMELTTLLTEYVDGIRIQ"

gene complement(99522..10022 /locus-tag="RB8158"  
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 CDS complement(99522..10022 /locus-tag="RB8158"  
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 /db-xref="GI:32445765"  
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 SDELRLENEQGELECVFGKFDRE  
 IAGPISDFGEVESLVAEVLRRYVKRHAGEAKRAK  
 VRSMKSKAIVARVKALAKEEQFDF  
 ATSMDTQKLRLFVKLSSQHMIEIHIPFTRFEKVL  
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 FMQADWRTEWIRYEE"

gene complement(100220..1009 /gene="exoA"  
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 /locus-tag="RB8161"  
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 repair, base excision repair and  
 nucleotide excision repair)"  
 /note="PMID: 1708495 best DB hits:  
 BLAST: swissprot:P37454;  
 EXOA-BACSU EXODEOXYRIBONUCLEASE  
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 exodeoxyribonuclease -  
 Helicobacter pylori (strain;  
 E=3e-72 pir:C71809;  
 exodeoxyribonuclease -  
 Helicobacter pylori (strain J99);  
 E=2e-71 COG: BS-exoA; COG0708  
 Exonuclease III; E=7e-79 PFAM:  
 PF01181; Deoxyribonuclease I  
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 FDDFHLVNVYTPNSQRGLARLDYRMQWDEAFLDY  
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 LANPKANRKNAGFSDQERAGLDAVTEAGFIDSFR  
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 LTLT"

gene complement(100987..1016 /locus-tag="RB8163"  
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 pir:F75496; conserved hypothetical  
 protein - Deinococcus radiodurans;

Vng0533h<sup>-</sup> [Halobacterium sp.  
 NRC-1]; E=5e-34 embl:CAB93731.1;  
 (AL357613) hypothetical protein  
 SC5F8.03c.; E=9e-30 COG: DR0625;  
 COG2013 Uncharacterized ACR;  
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 GTALT KVSGKGSVFCADSGKKITI  
 LELQNEAICVNGNDLLAFEMSLN YNIKMMKKMTA  
 MLAGGLEFNIRLEGTGMVAITSHYD  
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 CDS complement(101702..1018 /locus-tag="RB8165"  
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 pir:G71299; conserved hypothetical  
 protein TP0648 - syphilis; E=0.027  
 pir:S49376; hypothetical protein 3  
 - Pseudomonas aeruginosa ----;  
 E=0.11 pir:F69210; conserved  
 hypothetical protein MTH83 -  
 Methanobacterium; E=0.20 COG:  
 TP0648; COG0457  
 TPR-repeat-containing proteins;  
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 NGLHDEVGTAEADLFAQMQR AFAGYITRDNLIAA  
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 RDPDYLDAYLATAELAIRKGDFQVAANTLQQA LK  
 LEEETPDLHLLAKAMESSDGQAA  
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 VVAYNLMTLRDR TAKFTVLKQDGI  
 QVRMDATEAKLYGDAVMELLLDAKQVLCEKYDEM  
 PDKPILVEIFPHQNDFAIRTFGLP  
 GGAGYLGVCFGRVITANSPASQGERPSNWKSVLW  
 HEFCHVV TLEKTNNRMPRWLSEGI  
 SVYEERQRNPSWGEKMS PQYRSMLLSDDLTPVSD  
 LSA AFLSPPSAIALQFAYYESSLV



gene	104647..105831	GSLRRLDAQFDEYAKKRANQFGAL
CDS	104647..105831	VDWSRDTLPESGDLATWKGWTRANPTNYWGLREL AKSAIEGEQWEQALIPLSRMQQLG VLTGERGGPLEWLAHRELQDRQEIRAIQDNL SQSSDALPALRRWINIGQSEEQWE NVLDAQQALAIQPLLPEFHLASAVAAEKLRHE LAVEALSALLALDPVDPAAALHFRL ANAYDEQNESFPAKHHALMALELAPRYRDAHRL WKLHHAVSEENPADAEQND AENVSAVEEEAL"
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gene	105881..106900	/gene="moxR"
CDS	105881..106900	/locus-tag="RB8173" /gene="moxR" /locus-tag="RB8173" /function="C-compound, carbohydrate catabolism; transcriptional control" /note="best DB hits: BLAST: pir:C83106; conserved hypothetical protein PA4322 [imported] -; E=2e-61 pir:G71146; hypothetical protein PH0385 - Pyrococcus horikoshii; E=1e-60 pir:H82493; MoxR-related protein VCA0175 [imported] - Vibrio; E=2e-60 COG: PA4322; COG0714 MoxR-like ATPases; E=2e-62 PFAM: PF00004; ATPase family associated with; E=0.0029 PF01078; Magnesium chelatase, subunit; E=1.7e-06" /codon-start=1 /transl-table=11 /product="probable MoxR-related protein" /protein-id="CAD78502.1" /db-xref="GI:32445771" /translation="MHFMTTDTMTHEDEAQVVEQ IRDGRERIVQELSKVIIIGQEEVIE QLLICLFAGGHCLITGAPGLAKTLLVSSVAKIFH LNFQRIQFTPDLM PADITGTEILE QSADGHRQLQFVKGP I FANVILADEINRTPPKTQ AALLEAMQEHQV TAGGQRFEELEP FFVLATQNPIEMEGTYPLPEAQLDRFLFNVLIDY LPPKDELAVVLQTTSTKPEPIQPI FTGEDVARFHAAVRRVP I AESIAAYAVRLVAATR PGRDGTDFVNQYASWGAGLRAAQ TLVLGAKARALLNGHAHVRTEDIQALAHPTLRHR VLLSYRAEAEGFNVENLVTRL LQE IPTEV"
gene	106851..107960	/locus-tag="RB8174"
CDS	106851..107960	/locus-tag="RB8174" /note="best DB hits: BLAST: swissprot:P71761; YE80-MYCTU HYPOTHETICAL 34.3 KDA PROTEIN"

conserved hypothetical protein  
VCA0174 [imported] -; E=1e-12  
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48)
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pir:S76926; hypothetical protein -
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E=1e-06 gb:AAC36156.1; (AF003632)
Pili [Myxococcus xanthus]; E=0.016
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component of an ABC-transporter;
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hits: BLAST: pir:H72201; conserved

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CDS	132980..134161	
gene	134234..135553	
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gene 135604..137475  
CDS 135604..137475

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(thiol)-lyase (EC 4.2.99.10) -;
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O-acetylhomoserine sulfhydrylase;
E=1e-124 DR0921; COG0626
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beta-lyases/cystathionine; E=7e-63
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swissprot:P94891; METX-LEPME
HOMOSERINE O-ACETYLTRANSFERASE;
E=7e-78 swissprot:Q9JZQ5;
METX-NEIMB HOMOSERINE
O-ACETYLTRANSFERASE; E=1e-77 COG:
PA0390; COG2021 Homoserine
acetyltransferase; E=1e-84 PA0389;
COG0500 SAM-dependent
methyltransferases; E=2e-26
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pir:D69083; hypothetical protein  
MTH162 - Methanobacterium; E=4e-09  
gb:AAB89585.1; (AE000988)  
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PROBABLE FERROCHELATASE  
(PROTOHEME; E=5e-82  
swissprot:P71765; HEMZ-MYCTU  
FERROCHELATASE (PROTOHEME; E=2e-62  
swissprot:P72183; HEMZ-PROFR  
FERROCHELATASE (PROTOHEME; E=3e-42  
COG: Rv1485; COG0276 Protoheme  
ferro-lyase (ferrochelata-  
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gene  
CDS

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protein; E=4e-30 swissprot:P25714;  
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PROTEIN -----; E=4e-30 COG:  
HI1001; COG0706 Preprotein  
translocase subunit YidC; E=6e-32  
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 E=6e-08 pir:G83504; hypothetical  
 protein PA1139 [imported] -  
 Pseudomonas; E=6e-06 pir:T35659;  
 probable transmembrane protein -  
 Streptomyces coelicolor; E=2e-05  
 COG: PA1139; COG2340  
 Uncharacterized protein with  
 SCP/PR1 domains; E=6e-07"  
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CDS

148395..149156

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89125597 best DB hits: BLAST:  
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gb:AAC69477.1; (AF087482)  
dienelactone hydrolase  
[Pseudomonas; E=3e-09  
ddbj:BAA74533.1; (AB019032)  
dienelactone hydrolase [Ralstonia;  
E=1e-08 COG: YDL086w; COG0412  
Dienelactone hydrolase and related  
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gene

149353..151131

CDS

149353..151131

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SYNTHETASE; E=1e-165  
ddbj:BAB04971.1; (AP001511)  
aspartyl-tRNA synthetase  
[Bacillus; E=1e-161  
swissprot:O67589; SYD-AQUAE  
ASPARTYL-TRNA SYNTHETASE; E=1e-157  
COG: BS-aspS; COG0173  
Aspartyl-tRNA synthetase; E=1e-166  
PFAM: PF01336; OB-fold nucleic  
acid binding dom; E=2.2e-11  
PF00152; tRNA synthetases class II  
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EILSASETPPFTPGQSDLPGEDLRLKYRFLDLRR  
KEMQQALIRRSEIIKCMRDYFAEH  
DFIDVETPILGRSTPEGARDYLVPSRVHPSNFYA  
LPQSPQLYKQILMVAGFDYVQVA  
KCFRDEDLRADRQPEFTQLDLEMSFVDSEDIIGL  
IDGLVAKTAKQVLGKDITLPLPRM  
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misc-feature 150511 1505

gene 151322..153511  
CDS 151322..153511

gene complement(153523..1536  
90)  
CDS complement(153523..1536  
90)

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SEAGGGTIRIHDSKVQSQVFELLG  
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(AE005155) cationic amino acid  
transporter; Cat2; E=1e-29  
gb:AAG18789.1; (AE004983) cationic  
amino acid transporter; Cat1;  
E=6e-21 COG: AF1612-1; COG0531  
Amino acid transporters; E=2e-32  
PA5097; COG1113  
Gamma-aminobutyrate and related  
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COG0531 Amino acid transporters;  
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LATTVG  
IGGLMTFRTSGGGAWINVAKVAVF  
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REPTKNIPRAMLLSLVIALLIYLP  
LLFVLTTVGT  
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SALQANLFAASRIAL  
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FLVTF  
AIAHWLAILVRQRSVLT  
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FQGIAPPEAGIIAVMW  
IAIGGVFLSLFARRARLT  
DVSNI  
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LVPIANPNNARAMIALAD  
TLVPAALGRVLVQTVV  
VAPHDWD  
P  
LVNHRPSAQLHSVMNEIL  
HASASLGVRCE  
TLTTV  
SAEPMMEIARVAKLHQC  
QSVLLGL  
SEITPEARDTPLEGL  
LQQLSSDVVVL  
RAPKDWQL  
DQSQQILVPVGGRG  
GHDYLLTRLL  
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RVIPTDTLRADQ  
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gene	complement(154068..154394)	/locus-tag="RB8260"
CDS	complement(154068..154394)	/locus-tag="RB8260"
		/note="PMID: 20150255 best DB hits: BLAST: pir:H72072; conserved hypothetical protein CP0257 [imported] -; E=2e-10 pir:F81677; conserved hypothetical protein TC0667 [imported] -; E=4e-10 pir:B71520; hypothetical protein CT388 - Chlamydia trachomatis; E=6e-10 COG: CPn0497; COG1872 Uncharacterized ACR; E=2e-11 PFAM: PF02594; Uncharacterized ACR, YggU family COG; E=4.7e-22"
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		/transl-table=11
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gene	complement(154391..158104)	/gene="putA"
		/locus-tag="RB8262"
		/note="synonym: poaA"
CDS	complement(154391..158104)	/gene="putA"
		/locus-tag="RB8262"
		/EC-number="1.5.99.8"
		/EC-number="1.5.1.12"
		/function="degradation of amino-acids of the glutamate-group"
		/note="PMID: 96062224 best DB hits: BLAST: pir:H64526; proline dehydrogenase (EC 1.5.99.8); E=0.0 pir:B71980; proline dehydrogenase (EC 1.5.99.8); E=0.0 pir:C81297; proline dehydrogenase (EC 1.5.99.8); E=1e-180 COG: jhp0048-2; COG1012 NAD-dependent aldehyde dehydrogenases; E=1e-123 Cj1503c-1; COG0506 Proline dehydrogenase; E=2e-56 sll1561-2; COG1012 NAD-dependent aldehyde dehydrogenases; E=1e-51 PFAM: PF01619; Proline dehydrogenase; E=2e-36 PF00171; Aldehyde dehydrogenase family; E=0.0014"
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		/transl-table=11
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YELLRMPEVRCISVKLTTLTLYSQVS  
PLAREHTIRMVADRRLERLYRNANHMDDGSKAKDK  
FVYLDMEEYS DLYLTADVLRATTLE  
RGDLDSVQAGIALQAYVPD SCLVMRDLIEWSTKR  
VAGGGAPLTIRLVKGANLEMERVH  
ASVGGWPLAPYTNKHDT DANFKRMLRELISAAAD  
GNIRVG VASHNLF DVALAMIWTQR  
SGASDSVQFEMLEGMANHQRRALTERDAAMLLYA  
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TQFVNEPDTDWSLPHNSKWAQETLDRWKPLCDEQ  
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swissprot:O67466; YE94-AQUAE  
HYPOTHETICAL PROTEIN AQ-1494  
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conserved hypothetical protein -  
Deinococcus radiodurans; E=4e-10  
pir:I39564; hypothetical protein 6  
gbd-region [imported] -; E=1e-08  
COG: aq-1494; COG0824 Predicted  
thioesterase; E=3e-13"  
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gb:AAK03329.1; (AE006164) unknown  
[Pasteurella multocida]; E=1e-04  
swissprot:Q58707; YD11-METJA  
HYPOTHETICAL PROTEIN MJ1311 -----;  
E=2e-04 pir:S47803; hypothetical

gene 158178..158603  
CDS 158178..158603

gene 158639..159688  
CDS 158639..159688

		intergenic region); E=0.002 COG: MJ1311; COG1082 Predicted endonucleases; E=2e-05" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAD78550.1" /db-xref="GI:32445819" /translation="MRPDQPTRSLSNRRQFLRRI GVTSAVGYAAYLAHQVSPSPLSVN GLPGQGRALWAEELSESKTETSTGYLKQSLKAGM IRAGKSDAANPWIERFRIAKDAGF EGVEPNTSPGMDVEAMVAASAETGLTIDGTVGGY HWGTTHTSSDAATRKAQQLLLEES LQQTADLGANTFLIVPGHKGDTAEVVRQRAFEA LDRAVPLAEKLGVKILIENVVNHF LYDHGGDEKQSAQPLADFVDSFNTSSIGVQFDLG NHWKYGDVAEWVKTLGHRIGKLDI KGFSREQGRFTDVTEGDIDWASVRKALAEIKFEG WVAAEVGGGDAERLKKIHGQIETA LHCSKSLSQIKAETA" /locus-tag="RB8268" /locus-tag="RB8268" /note="best DB hits: BLAST: swissprot:P73460; YB44-SYNY3 HYPOTHETICAL 34.4 KDA PROTEIN SLL1144; E=2e-40 swissprot:Q9WZX6; Y872-THEMA HYPOTHETICAL PROTEIN TM0872 -----; E=7e-40 qb:AAK02218.1; (AE006048) unknown [Pasteurella multocida]; E=4e-38 COG: sll1144; COG0275 Predicted S-adenosylmethionine-dependent; E=2e-41 PFAM: PF01795; Mraw methylase family; E=2e-100" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein-putative methyltransferase" /protein-id="CAD78551.1" /db-xref="GI:32445820" /translation="MTASQPLDQADQDSESSSAG SSAAETEHVSVMPNEIVQVREIN PTTIIDGTYGGGGHTRLLAEVLADAGSDSDTPRV IAIDRDPVAVRRDEQKSWIKDDPR IELFLGSYESSPKALDALDLTHADALVLDLGLSS DQLADRNRGFTFTIDDAELDLRFD PENGVPAPHRWLQQHSEKEIADAIYRFGEERFSRR IAKQIFLRARERNPVTKVGEI CRRCVPRSRNHDHPATRTFQALRIAVNDELGGL TRTLQSA PDWIA PGGRVAVISFHS LEDRIVKNAFREDHRWEILTKKPLRPTDEEVQAN PRRS AKLRVAKRVE" /locus-tag="RB8271" /locus-tag="RB8271" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="CAD78552.1" /db-xref="GI:32445821" /translation="MGRERSRTVSKSSSHKITC RETLCLATVRFGSISAGIRFVFER KLIFCMLGSAIPIERRWPSWPVSRGAWIGVCACW ILLTGCKTTAPVHVWQPPQLAVEP AGVAFMGISGPDEWAEPIEDALLTDQPSRWRLIA AEQLESPANIRLVSGFEEEPNDMA VSAAARREGLRYLLHGEILQATGHEDRDDKVSLS WRLTGLOADAESAGMPVSVDEALI SQRYPHLLNIPDVAERTRRAVVLETKRLLAASVD RQQVTLASPRLSPGSRAIRRGNEL ARSGNWPAAEHRWQQVLESHPRNAAALINASIAA
gene	159685..160662	
CDS	159685..160662	
gene	complement (160746..161867)	
CDS	complement (160746..161867)	

gene	161882..163753	ANKSLAEETLFWIEMRQRDYHNAFDLPPPPEGWL
CDS	161882..163753	ISRGE" /locus-tag="RB8274" /locus-tag="RB8274" /function="two-component signal transduction" /note="PMID: 8346225 PMID: 9097040 best DB hits: BLAST: swissprot:Q06067; ATOS-ECOLI SENSOR PROTEIN ATOS ---- pir;; E=2e-17 gb:AAD47419.1; AF100457-2 (AF100457) histidine kinase [Myxococcus; E=2e-16 ddbj:BAB04255.1; (AP001508) two-component sensor histidine kinase; E=3e-14 COG: atoS-3; COG0642 Sensory transduction histidine kinases; E=2e-18 Rv1827; COG1716 FHA-domain-containing proteins; E=1e-08 PA2882; COG0642 Sensory transduction histidine kinases; E=2e-08 PFAM: PF00498; FHA domain; E=3.2e-19 PF01590; GAF domain; E=4.8e-18 PF00512; His Kinase A (phosphoacceptor) doma; E=6.6e-07" /codon-start=1 /transl-table=11 /product="sensor protein atoS" /protein-id="CAD78553.1" /db-xref="GI:32445822" /translation="MASLFVIRGRDQGKHFQLAP TVTRLGRESSNNVQLLDNEASRSH AEIRGDGTGRRYELVDLGSSNGTLVNNRKITRHV LTSGDRVEIGSTLLIFTGTGNVSA LDAAHGVDIVRQVRGGDASNIVSSLSREGVVSPY TPGGSSSNGPSTDKPATSP TTLPP PIPPPVENPPTPSEDERVDSSASGSDPPGQFHGP PVIGRLDADRSLV MYLTAIAVGR TDDLDEVLDRLV LKLVFDWVEADRG CIMLRDPESK RLTPAARCDRESATGGTKQNPSSK PQDRIQISHTILDYVLQHKQGVRTNDALDDERFD SAASIVQGGVREALCVPLQGRYEI VGMLYVD TYTTPGELVRKGGATRFHDEHLRLITA VGHQAALAI EDTFYYSALLQGERL AAMGQTIATLSHHIKNILQGV RGGSYLIESGLQK DDTDAIRGWSIVDRNQERISNLV LDMLTFSKEREPDLQEGNLNEVSDVVELMQSRA GQSEIELVSDLDATLPIATFDSEA IHRAVLNLVTNAIDAATKTVLVKTFYDAAQGWIV DVEDDGEVPEEDREQIFSLFESK KGARGTGLGLPVSAKVLREHGGTLTVDDAASGGA RFRMILPATGTDINELSRSETQA" /locus-tag="RB8275"
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CDS	97) complement (163760..1638	/locus-tag="RB8275"  /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="CAD78554.1" /db-xref="GI:32445823" /translation="MHHPRVAFGSKERKSFSQFP DEKARPGVDNRIGGIISLRMSFTP F"
gene	complement (163907..1642	/locus-tag="RB8278"
CDS	57) complement (163907..1642	/locus-tag="RB8278"  /codon-start=1 /transl-table=11 /product="hypothetical protein-transmembrane prediction" /protein-id="CAD78555.1" /db-xref="GI:32445824" /translation="MDRNDAGATVFQQHELHPPL

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gene	complement(164696..164938)	/locus-tag="RB8281"
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CDS	complement(165169..166014)	/locus-tag="RB8282" /codon-start=1 /transl-table=11 /product="hypothetical protein-transmembrane prediction" /protein-id="CAD78559.1" /db-xref="GI:32445828" /translation="MAGRRIVCPQCKTTLQIPAT MGAGKVKCPKCELMMLAVRAPVTVH VPEENLFDNLPSLGSSAAAPPSSVFRPSGPVTVY QPPKPAKKRGGGSKAAVKIISTIA GLGLLCVLLCAGGIFAVGYLGSRHSGWTSVTYKG YTVSMPAGEDRRDKSQQFPGTTVH ELTGRRKETGSQYSLVVADLPAVIDPNIPIAELL RDMRIRLSNPRPVTRSGVEGMAGT MQSGVGAIEGSDCEIYVHNRLVVAVYSPYSEIK DLVGGQQRKPRSNESELDKPSEFFD SLEFK"
gene	complement(166175..167167)	/locus-tag="RB8284"
CDS	complement(166175..167167)	/locus-tag="RB8284"  /note="PMID: 98196666 best DB hits: BLAST: pir:F70440; conserved hypothetical protein aq-1630 - Aquifex; E=3e-18 pir:D71323; conserved hypothetical protein TP0436 - syphilis; E=3e-18 pir:F69999; conserved hypothetical protein ytgI - Bacillus subtilis; E=1e-16 COG: aq-1630; COG0618 Exopolyphosphatase-related proteins; E=3e-19 PFAM: PF01368; DHH family; E=2.4e-12 PF02272;

		/codon-start=1 /transl-table=11 /product="conserved hypothetical protein-putative a phosphoesterase or an exonuclease" /protein-id="CAD78560.1" /db-xref="GI:32445829" /translation="MGVNWKAFVDQIQHYQSFLV VSHIRPDCDALGSELGMAEVLRAV GKDVRIINAHRTTPPALSFLDPAGNIEVLGDSVEA EDVKADCIMILDTSAWAQLGDMGD VIRASRADKMVLDDHHVGEDELGARMYKDYQSEAT GHLVVQAADALNVPLTRTMATPLF AAIATDTGWFRFSPVTSPTYRTIARLIDAGVVPS EVYGDLYERDTLGRLLKRLGLILSR TTTEMDGALVYTSVNKEDFELCGAQPNDTEDAIN LTLAIRGTQAGVIFVGQVRGGFKL SFRSRCSLDCNEVARQFGGGGHKAAAGAFLEGTL DEVQDRVLPPIVREALAVALG" /gene="ribF"
gene	complement (167183..168154)	
CDS	complement (167183..168154)	/locus-tag="RB8286" /gene="ribF" /locus-tag="RB8286" /EC-number="2.7.1.26" /function="central metabolism" /note="PMID: 7772835 PMID: 3023344 best DB hits: BLAST: pir:T35984; probable riboflavin kinase (FAD synthetase) -; E=3e-46 pir:C83077; riboflavin kinaseFAD synthase PA4561 [imported] -; E=4e-42 pir:C82293; riboflavin kinaseFMN adenylyltransferase VC0681; E=2e-41 COG: PA4561; COG0196 FAD synthase; E=4e-43 PFAM: PF01687; Riboflavin kinase / FAD synthetase; E=3.3e-32" /codon-start=1 /transl-table=11 /product="probable riboflavin kinase (FAD synthetase)" /protein-id="CAD78561.1" /db-xref="GI:32445830" /translation="MTSLIHLSDLAGDSDLHL LSL QGGAVSIGNFDGVHLGHRALLERV RWHAQRVGGKAIIVMDPHPASVLRPHGAPPSLT SLSRRAELMSGSGIDHLLVCEATR DFLNQTAEEFFQRLIVEQLSAKAIIEGPNFFFGR DRAGNTTRLKELAAERQIDVEIVV PSVRDERMVSSSRIREAIIASGDIVLANQMLGSRY RLTGVVTTGEQRGRTLGFPTANLG GVTLLPEHGVYAALACGDECDGPTNHPAAVHIG PNPTFNERQETKIEAHLDDYDGD YGKSLSLTLVSQVRGVKIFADASALKQQLQIDLO TVRETVSSLQSRP"
gene	complement (168273..169187)	/locus-tag="RB8287"
CDS	complement (168273..169187)	/locus-tag="RB8287" /function="unspecified kinase or ATP dependent regulatory protein" /note="PMID: 20406833 best DB hits: BLAST: pir:H82489; conserved hypothetical protein VCA0191 [imported] -; E=2e-23 pir:G81111; conserved hypothetical protein NMB1197; NMB1159; E=4e-21 pir:C72317; conserved hypothetical protein - Thermotoga maritima; E=9e-21 COG: VCA0191-2; COG0063 Predicted sugar kinase; E=8e-24 PFAM: PF01256; Uncharacterized



gene  
CDS

169350..170591  
169350..170591

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/codon-start=1
/transl-table=11
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protein-putative sugar kinase"
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MTIGLGDDGEKFADPAWQSLKDRL
SAQAAIGCGPGMTTGS GGATIVEGLLAKKDLPLV
LDADALNIIAQNDWLS DGRFERSK
ADAACVLTTPHPGELQRLTGASAKDVDAQVEAAAE
LACRLGLTIVVKGGPSHVAYQNGD
GGKQVWQNTTGNPGMATAGCGDVLGTGIVTSLLGQ
GLSGPDAAKLGVIHGRCGDEAAA
RWSHAGMTSLHALDALALVADEMTQPAD"
/locus-tag="RB8290"
/locus-tag="RB8290"
/function="other cation
transporters (Na(+) ,K(+) ,Ca(2+)
,NH4(+) ,etc.)"
/note="PMID: 8170937 best DB hits:
BLAST: pir:S76018; hypothetical
protein - Synechocystis sp.
(strain PCC; E=2e-61
swissprot:Q58752; YD57-METJA
PUTATIVE POTASSIUM CHANNEL
PROTEIN; E=1e-36 swissprot:Q57604;
Y13B-METJA PUTATIVE POTASSIUM
CHANNEL PROTEIN; E=2e-34 COG:
sll0536; COG1226 Kef-type K+
transport systems, predicted;
E=1e-62 MJ1357; COG1226 Kef-type
K+ transport systems, predicted
NAD-binding; E=1e-37 MJ0138.1;
COG1226 Kef-type K+ transport
systems, predicted; E=2e-35 PFAM:
PF00520; Ion transport protein;
E=0.45 PF02254; KTN NAD-binding
domain; E=5.2e-39 PF02080;
Potassium channel; E=2.2e-09"
/codon-start=1
/transl-table=11
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channel"
/protein-id="CAD78563.1"
/db-xref="GI:32445832"
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ICAIAlIAYIQMGWSVSDAIYMVV
ITIFGVGYGEVKPVDTPALRTLTIAlIVLGYGAA
IYTVGGFIQFLVDGELQSLLRNRK
MSQGIASLRAHTIVCGFGRMGVRVAEELQELGQP
FVVIDENAAARVEEAQQAGMLAMVG
NATDEDILMAAGIDHARGLATLLPDDAANAFICV
TARDLAEKVEIVSRAENHSAQKKL
IRCGANYVVMATIGAMRVLTQLLVRPTASAVLES
HGLSHGISEELSAIGLNLEELRLT
SSSPLVSKPLAEIQVRGNRGFLIVGVKRGEDPIQ
MNPSGTLILEVNDIVIVVGHQNDI
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/locus-tag="RB8291"
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/EC-number="4.1.1.21"
/function="purine-ribonucleotide
metabolism"
/note="PMID: 98049343 PMID:
8809759 best DB hits: BLAST:
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gene

complement(170605..1714  
53)

CDS

complement(170605..1714  
53)

gene	171457..172791	conserved hypothetical protein; E=4e-29 pir:S76797; hypothetical protein - Synechocystis sp. (strain PCC; E=7e-28 gb:AAD29318.1; AF117208-1 (AF117208) circadian phase modifier; E=2e-24 COG: AF1275; COG1691 NCAIR mutase (PurE)-related proteins; E=4e-30" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein-putative phosphoribosylcarboxyaminoimidazol e mutase (purE)" /protein-id="CAD78564.1" /db-xref="GI:32445833" /translation="MNLPSNQPPSPALLQILQDL ASGQTDVEAAAEISIQASSIGSAAD MQTVPGATVDLGRRLARCGFGEVIYGEKSTDLMT QIVQTQVAVGQGCLITRIDATAAA QLRRVFENTRYNPSARTLRIGCGDENLDPIGVEG HSTHVAVVTAGSTDAHVAEEAAET LAWMGVACERIDDIGVAGPQRLLAAVPRLRAAAA IVVVAGMEGALPAALAGHVATPVI AVPASTGYGANFAGLTPLMGMLTSCAANVAVVNI DAGFKGGYFAGLIASGIANAKSEA ASAEAA" /gene="argG" /locus-tag="RB8293" /gene="argG" /locus-tag="RB8293" /EC-number="6.3.4.5" /function="urea cycle, biosynthesis of polyamines and creatine; assimilation of ammonia, biosynthesis of the glutamate family" /note="PMID: 20158877 PMID: 90046714 PMID: 3174461 best DB hits: BLAST: pir:H72210; argininosuccinate synthase - Thermotoga maritima (strain; E=2e-97 pir:D75490; arginosuccinate synthase - Deinococcus radiodurans; E=3e-96 pir:C83204; argininosuccinate synthase PA3525 [imported] -; E=2e-87 COG: TM1780; COG0137 Argininosuccinate synthase; E=2e-98 PFAM: PF00764; Arginosuccinate synthase; E=2e-190" /codon-start=1 /transl-table=11 /product="argininosuccinate synthase" /protein-id="CAD78565.1" /db-xref="GI:32445834" /translation="MLLDFPARILLTVLACFAPD NLNARPSNIADSPAFGCRSEMKSC VLAYSGGLDTSVILGWLQDQGYEVHCVYVDLGQP CEDRDAIMEKARTCGAKSSRLVDV REELCRDFAFPVLAWQAKYEQIYLLGTSIARPLI SKVCLEVAREVGATAYAHGATGKG NDQCRFQLAAEALDPNIEMIAPWRIKSFRDAFPG RTELIEYCDVKRIPVKASTAKPYS SDENVLHISYEAGKLEELDVNGVELVEFGMGVSP QDAPDKPEEVTIGFESGVPKTLNG KAVNALEMVEQLNDIAGRNGVGRIDMVENRFVGM KSRGVYESPGMTVLYDALMYVEQL TMDRDLMHRLRDRMAPEVAEMVYGFWYTPKMDAL MSFIETAQRPVGTGEVTLQLYKGN MVSSRTSPNSLYDEEIATMEGGGSYNQDDAEGFL RIQGLPSRVQGRVSPRKF" /locus-tag="RB8295"
CDS	171457..172791	
gene	complement (172907..1738	

CDS	complement(172907..1738 30)	/locus-tag="RB8295"  /codon-start=1 /transl-table=11 /product="hypothetical protein-transmembrane prediction" /protein-id="CAD78566.1" /db-xref="GI:32445835" /translation="MTFLFTCPHCQSQTETEVEDEY SGRTGDCVVCGREITMPEFAGSRR MGNRPGKRKNSAIWFVAAGLALLLIGAGLIAAVQ VGSRTAKKIRTGRQRLSSIKNLEK IASALNAYAADHGVYPAPYTVDAAGRKLHWSRV ILPYLDEDGLYNQIDKDVWNEGE NQMLLYSQTPAVYRHPESSSWGTGTVYHLVTGAG TLFPSTGPLGPRQVTDGATKTILL AEGQMNTMTESWMEPYDLDIGSVGGLINPPSGNG LGGATDGGVCVATVEGSGYFLPDT TPPLTVQALITPTGGEPLSDDVLDDEWASTQP"
gene	173814..174359	/gene="dtd"
CDS	173814..174359	/locus-tag="RB8300" /gene="dtd" /locus-tag="RB8300" /EC-number="3.1.-.-" /function="other detoxification" /note="PMID: 20459059 PMID: 10383414 PMID: 10918062 PMID: 11568181 best DB hits: BLAST: gb:AAF82117.1; AF276071-1 (AF276071) conserved hypothetical; E=3e-37 ddbj:BAB04962.1; (AP001511) BH1243~unknown conserved protein; E=3e-36 pir:E72338; conserved hypothetical protein - Thermotoga maritima; E=9e-36 COG: BH1243; COG1490 D-Tyr-tRNA <sup>tyr</sup> deacylase; E=3e-37 PFAM: PF02580; Uncharacterized ACR, COG1490; E=3.8e-5 /codon-start=1 /transl-table=11 /product="D-tyrosyl-tRNA(Tyr) deacylase" /protein-id="CAD78567.1" /db-xref="GI:32445836" /translation="MNRNVIRSFHLISDAPRV ATNLAHLATTWIANHPMKIVLQRS QHASVSVGDKIVGQIERGLVALIGIGHEDTEATA SALADKTAGLRIFSDDNGKMERNV IDAGGDVLAISQFTLLADCRKGRRPAFTDAAPPD RANELYEHYVSELKKTGLSVPCGI FAADMAVSLTNDGPVTIILEL"
gene	complement(174384..1754 12)	/locus-tag="RB8301"
CDS	complement(174384..1754 12)	/locus-tag="RB8301"  /codon-start=1 /transl-table=11 /product="hypothetical protein-transmembrane prediction" /protein-id="CAD78568.1" /db-xref="GI:32445837" /translation="MRDRPAPPSWLGG LAVGVSG NLVGPPFPARRLLSVRVSLAGFKT HISTSTVVGCA YGYWGVFDQGMSE SALLAGGLC SVSGMLPDLSDSGVPLRETSFL AAVVPMLMIDRWDLGLSHEAMALAAMIVYIAIR FVAVEGFRKFTVHRGMWHSIPAAL VAGLIA YMAMPCASEAVRVYKSCAVLVGFLTHLI LDEIWSLDFSRGSMRVKKSFGTAL KFFGSSPLANIFVWGQLGLFIYLA WGDHEILDRL RQVRMRDRYAVPSQDEINPDYT NPSLFAPWESREPPQWQPRVTSPQESPSNFGWPS PAQPGATQPGVVQPGMGQ RVARPN WPPALPQR"
gene	175602..176399	/locus-tag="RB8306"

		/function="biosynthesis of peptide antibiotics" /note="PMID: 2542219 best DB hits: PFAM: PF02674; Colicin V production protein; E=8.4e-14" /codon-start=1 /transl-table=11 /product="hypothetical protein-putative a gene in the purF operon involved in colicin V biosynthesis" /protein-id="CAD78569.1" /db-xref="GI:32445838" /translation="MQTYDILMTVILVGATLLGAIRGFAWQLASIASIVVSYCVAYHYREPFSQNIHAAPPWNQFLAMFILFVGTSFVIWVALRMVSGMIDRMRLKEFDRQIGALFGLAKGALLCTIITLFAVTLFGERTQRAIVASESGRLIARVLAESNSIMPPELDSVVRPYLDQFSDEELGEPSASEGSWLSQTPPIAPNIDPNWSHSNAPTANNFAPQNGFQQAQNDPRSQSPFGGFGGSSTPTPNADFNSAAGSQQPAPTWQOSATPLWQTPRR"
gene	176354..176554	/locus-tag="RB8309"
CDS	176354..176554	/locus-tag="RB8309" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="CAD78570.1" /db-xref="GI:32445839" /translation="MASIRDAAVANATTMIARHLGIAMTANDRGGAYSRSPGHSDLQRHQAKAQTRKTPETRVLRSTSNTT"
gene	complement (176695..177654)	/gene="accA"
CDS	complement (176695..177654)	/locus-tag="RB8310" /gene="accA" /locus-tag="RB8310" /EC-number="6.4.1.2" /function="fatty acid biosynthesis" /note="best DB hits: BLAST: gb:AAK02376.1; (AE006064) Acca [Pasteurella multocida]; E=4e-72 swissprot:P43872; ACCA-HAEIN ACETYL-COENZYME A CARBOXYLASE; E=6e-72 ddbj:BAA77860.1; (D83536) Acetyl-CoA carboxylase (EC 6.4.1.2); E=1e-68 COG: HI0406; COG0825 Acetyl-CoA carboxylase alpha subunit; E=5e-73" /codon-start=1 /transl-table=11 /product="AcetylCoA-Carboxylase" /protein-id="CAD78571.1" /db-xref="GI:32445840" /translation="MAGPGLEFENEIADLEEQIASLERNTDRSEEIDSAIRSLRLARVAKLKETYSSLDPWQTVQVARHKNRPYTRDYLNLA FDEFVELHGDKHFGDDRAMLSGFAKLDRFKVMVIGHQKGRITYKERAACHFGCAHPEGYRKAMVKMKMAEKYRLPVICFIDTPGAYPGIGAEERGQAQVIAESMFMSDLKTPVICV VIGEGGSGGALGIGVGDRVAVLQHAAYYSVISPEGCAGILWKSHEHAPKAAAALRFTSDHLLRLGVVDDVLEEPLGGAHRDHHQMATRMKTYLSRQLSELEEMPVDLMLEQRYEKFRKLGVFLEES"
gene	complement (177658..178752)	/locus-tag="RB8311"
CDS	complement (177658..178752)	/locus-tag="RB8311" /EC-number="2.7.1.-" /function="unspecified kinase or

/note="PMID: 7774814 best DB hits:  
BLAST: pir:H69878; probable  
protein kinase (EC 2.7.1.-) yloP -  
Bacillus; E=2e-27 pir:T36717;  
probable serinethreonine protein  
kinase - Streptomyces; E=1e-26  
pir:T36501; probable  
serinethreonine protein kinase -  
Streptomyces; E=2e-26 COG:  
BS-yloP-1; COG0515  
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E=1e-28 PFAM: PF00069; Protein  
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yloP"  
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IDEGDQKRYALKILRQSMSNDKAE  
LASLKHEYNVGKALNSPRIIKMIDHRVENGRPFL  
VLELFSEMNMKQALRKGPESLAYM  
LDKIIEQAAEGLYYMHTKNWIHRDIKPDNYLVSH  
TGETKLIDFTITEPKRTGLSKMFY  
KAKNIQGTRSYMAPEQIRGKLCDSIDIYSFGCV  
LFEACTGKPPYTGTPTNDLLSKHL  
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/locus-tag="RB8313"

gene

complement(178844..1800  
88)

CDS

complement(178844..1800  
88)

/locus-tag="RB8313"  
/function="glycolipid  
biosynthesis; protein modification  
(glycosylation, acylation,  
myristylation, palmitylation,  
farnesylation and processing)"  
/note="PMID: 10531250 best DB  
hits: BLAST: gb:AAD50490.1;  
AF172324-8 (AF172324) WbnE  
[Escherichia coli]; E=7e-21  
pir:C70036; capsular  
polysaccharide biosynthesis  
homolog yveN -; E=2e-19  
pir:T35514; probable glycosyl  
transferase - Streptomyces  
coelicolor; E=2e-17 COG: BS-yveN;  
COG0438 Predicted  
glycosyltransferases; E=2e-20  
PFAM: PF00534; Glycosyl  
transferases group 1; E=9.5e-43"  
/codon-start=1  
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/product="putative glycosyl  
transferase (WbnE)"  
/protein-id="CAD78573.1"  
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LPIELIDSLRRAIHPLHDWNATRD  
LRRTLDFDPDVVHTHSAGKGLLGRHVWGWLKRA  
STGKRPPVVHTVHGAPFHEYQSKL  
AHDFFVRCERWAASRCHKLISVADAMTDLMEAG  
VAPREKFVTIHSGMNVDPFVHAVD  
HREAVRQRYGLRDEHVVGKIARLFHLKGHADLV  
PAAKLVA DRHPNVRFLLVGDGILR  
GELEQQIESLGLKEHFIFTGLVPPSEVPAMIGAM  
DILVHAS YREGLARALPQALIAGR  
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gene	complement (180097..1809 15)	/gene="whiG"
CDS	complement (180097..1809 15)	/locus-tag="RB8316" /gene="whiG" /locus-tag="RB8316" /function="transcriptional control" /note="PMID: 2507166 PMID: 94259284 best DB hits: BLAST: pir:S29615; whiG protein - Streptovorticillium griseocarneum -----; E=5e-44 gb:AAB41960.1; (U58281) sporulation sigma factor [Streptomyces; E=9e-44 prf:2013252A; RNA polymerase:SUBUNIT=sigma factor [Streptomyces; E=1e-43 COG: TP0709; COG1191 DNA-directed RNA polymerase specialized sigma; E=8e-41 fliA; COG1191 DNA-directed RNA polymerase specialized sigma subunit; E=2e-38 BS-sigD; COG1191 DNA-directed RNA polymerase specialized sigma; E=7e-34 PFAM: PF01399; PCI domain; E=0.026 PF00140; Sigma-70 factor; E=1.3e-59" /codon-start=1 /transl-table=11 /product="RNA polymerase sigma factor whiG" /protein-id="CAD78574.1" /db-xref="GI:32445843" /translation="MIITEDSMPATATADDPILK VWTSEFKSTTKDAPDYEPLRNQLVE RYMQLVRYNGERIWQRLPDGVELDDLISAGMFGL MDAIDAYDTERGVKFETFCVPRIR GAMLDELRLKMDWVPRLVRSKASKLATATKTLEAR FGRAPTVOELSAHMEIDVKEVEKM QSEANAVGVVSLNKKWYETDSYKDVREIDILEDK KGEDPTRRVQKNDLMRLVTKGLNR NERLIIILYEEELTMKEIGATLDLSESRVSQMH TAIVNRLQQQLGVRRLFEFGA" /note="cosmid pircos-clg10/ cosmid. pircos-c4e02 joining point" /locus-tag="RB8318"
misc-feature	180953 1809	
gene	complement (181037..1813 18)	/locus-tag="RB8318"
CDS	complement (181037..1813 18)	/locus-tag="RB8318" /codon-start=1 /transl-table=11 /product="hypothetical protein-transmembrane prediction" /protein-id="CAD78575.1" /db-xref="GI:32445844" /translation="MDGDVTRSLALSLGSFAMGL VVLRGIIWHGEMAGDVASEAIGTLI VFMGIGGLAGAIADQLIRDGVEDLYRKRVKWFQE GVAETASEETENQTK"
gene	complement (181308..1814 21)	/locus-tag="RB8319"
CDS	complement (181308..1814 21)	/locus-tag="RB8319" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="CAD78576.1" /db-xref="GI:32445845" /translation="MIDESHLRLFLKCPFNEFGI EEFDPFLEFSGLPPLFGR"
gene	complement (181485..1828 79)	/gene="flhF"
CDS	complement (181485..1828)	/locus-tag="RB8320" /gene="flhF"

		<pre> /locus-tag="RB8320" /function="biogenesis of flagellae" /note="PMID: 1447978 best DB hits: BLAST: pir:B72319; flagellar biosynthesis protein FlhF - Thermotoga; E=9e-32 ddbj:BAB06156.1; (AP001515) flagella-associated protein [Bacillus; E=3e-22 swissprot:Q01960; FLHF-BACSU FLAGELLAR BIOSYNTHESIS PROTEIN FLHF; E=2e-21 COG: TM0907; COG1419 Flagellar GTP-binding protein; E=8e-33 AF0622; COG0541 Signal recognition particle GTPase; E=3e-09 PFAM: PF00005; ABC transporter; E=0.018 PF00931; NB-ARC domain; E=0.2 PF00004; ATPase family associated with va; E=0.13" /codon-start=1 /transl-table=11 /product="flagellar biosynthesis protein FlhF" /protein-id="CAD78577.1" /db-xref="GI:32445846" /translation="MMHIRTFRANLQAALADIR DQMGPEASVLHTRQVRNGWMGWLG RTHVEVTAGLHSGPEDGTSHDASGSRVSANYADE PLQPADVRSVNSVAASSGYGTSPT GTPNINAGTINPGAAPVSSGQNPMDAAYQNYDAS HQHSSSTGIQGFNAGNGAGQGGF YGAGYASGELSPADSLSLRLLQAGVEESTARRWM ASASSFAAGIANSES AVQSDQRWM EHLQRAVARELNLCGPRTQPGDRHVVALVGPTG VGKTTTVAKLAAGFRIEARRRVGL LTIDTYRIA AVQQLKAYAEIMDLPMQVVEKPEQM ETALSALGDVDLVLIDTAGRSPRS DARIEQLSEFLRAAHPDETHLVLSATSSGENIRT TLEGFAPVRANAVTLTKLDETPCM ASVLAALTGRDRV VAPPLSYLTNGQQVPDDIAVA DASGLVAQLLPHMPTAGLGEMGFE TMDGYESLHYGEAA" </pre>
gene	complement (182876..184939)	/gene="flhA"
CDS	complement (182876..184939)	<pre> /locus-tag="RB8323" /gene="flhA"  /locus-tag="RB8323" /function="flagellar organization; type III protein secretion system" /note="PMID: 8097015 best DB hits: BLAST: ddbj:BAB06157.1; (AP001515) flagella-associated protein [Bacillus; E=1e-119 pir:C72319; flagellar biosynthesis protein FlhA - Thermotoga; E=1e-115 swissprot:P35620; FLHA-BACSU FLAGELLAR BIOSYNTHESIS PROTEIN FLHA; E=1e-114 COG: BH2438; COG1298 Flagellar biosynthesis/type III secretory pathway; E=1e-120 PFAM: PF00771; FHIPEP family; E=1.6e-261" /codon-start=1 /transl-table=11 /product="flagella-associated protein" /protein-id="CAD78578.1" /db-xref="GI:32445847" /translation="MQLLMRYRDLVLPIGIIACL VVILVPLPPFLMDLLLATNITVGV IVLLTTVYVSTPLEFSIFPSLLLATTLARLVLVN ATTRLILTSTESGSGGAAGGVIQG </pre>

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                        (AP001511) CMP-binding protein
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SUBUNIT B; E=0.0 pdb:1D9Z; A Chain  
A, Crystal Structure Of The Dna  
Repair Protein; E=0.0 pdb:1D9X; A  
Chain A, Crystal Structure Of The  
Dna Repair Protein; E=0.0 COG:  
BS-uvrB; COG0556 Helicase subunit  
of the DNA excision repair  
complex; E=0.0 VNG2390G; COG0556  
Helicase subunit of the DNA  
excision repair; E=1e-179 TP0116;  
COG0556 Helicase subunit of the  
DNA excision repair complex;  
E=1e-176 PFAM: PF00271; Helicase  
conserved C-terminal doma;  
E=2.3e-19 PF02151; UvrB/uvrC  
motif; E=1.2e-12"  
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B"  
/protein-id="CAD78620.1"

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gene	228679..229314	/gene="tdk"
CDS	228679..229314	/locus-tag="RB8399" /gene="tdk" /locus-tag="RB8399" /EC-number="2.7.1.21" /function="nucleotide metabolism; pyrimidine-ribonucleotide metabolism" /note="PMID: 2060797 PMID: 2041474 best DB hits: BLAST: gb:AAK03320.1; (AE006163) Tdk [Pasteurella multocida]; E=2e-66 swissprot:P44309; KITH-HAEIN THYMIDINE KINASE ----- pir;; E=3e-65 swissprot:P23331; KITH-ECOLI THYMIDINE KINASE ----- pir;; E=2e-64 COG: HI0529; COG1435 Thymidine kinase; E=3e-66 PFAM: PF00265; Thymidine kinase; E=4.9e-88" /codon-start=1 /transl-table=11 /product="thymidine kinase Tdk" /protein-id="CAD78621.1" /db-xref="GI:32445890" /translation="MAKLYFYYSTMNAGKSTVLL QSSYNYRERGMNTLILSPEIDTRF GSGKVASRIGIESESVFNTSDNLLNLVRNETRI NPLHCVLVDEAQFLTRTQVRQLSD VCDDLIDIPVLAYGLRTDFQGNLFEGSEHLLAWAD TLTELKTICHCGRKATMVLRVSES GOVIRDGEQVQIGGNERYQTVCRLLHFKEAIYQRA EDELPLLDNSNEPRQSER"
gene	229393..231687	/gene="rnr"
CDS	229393..231687	/locus-tag="RB8402" /note="synonym: VvacB" /gene="rnr" /locus-tag="RB8402" /EC-number="3.1.-.-" /function="rRNA processing; mRNA processing (5'-, 3'-end processing, mRNA degradation)" /note="PMID: 9603904 best DB hits: BLAST: ddbj:BAB07272.1; (AP001519) ribonuclease R [Bacillus halodurans]; E=6e-88 swissprot:O32231; RNR-BACSU RIBONUCLEASE R (RNASE R) (VACB PROTEIN; E=8e-84 gb:AAK05040.1; AE006328-8 (AE006328) ribonuclease

BH3553-1; COG0557  
 Exoribonucleases; E=1e-76 PFAM:  
 PF00773; RNB-like protein; E=2e-87  
 PF00575; S1 RNA binding domain;  
 E=3.2e-08"  
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 DVPEDVFVPTGMTAGALEGDLVAVTIEPSRRGGI  
 EGKVVEVLQARRRQFTGTFFSSPQ  
 PDQPGSDTIEGPVVYLDGVHYEAPVSVGDVRGLP  
 LQDGDKIFVEIVDFPDEESGGGEA  
 VILERLGSSKNPAIDTLTIMRQYALPDEFSEDVL  
 DEAREQADAFDDDDVPTDRKDLTD  
 MLTITIDPFDARDFDDAISLQREDGRWRLWVHIA  
 DVSHFVPPGGKLDVEARRRGTSVY  
 LPDRVIPMIPEIISNHLASLQPERMRLVKTVEIE  
 MLDDLITITHSEVHNAAIRSDKRFN  
 YEQIDQFIASPAAFQKDWGDSICELLTHMHTLAM  
 QIRKRRFKDGALSMDMPDIKLELD  
 RTGKVKGAYQTENTESHQIIIEEFMLLGNEAVATW  
 LDDQELNFLHRIHAPPERRKLRQL  
 TSFVKDLGLGFDNVESRFEIQAVLDKVAGTTLEN  
 AVNFAVLKSMKAVYGPREGHYA  
 LDKEHYCHFTSPIRRYPDLVHRLVQRLIEQKST  
 PDESFAELVKLGHECSDAERNAAQ  
 AERELIQLKLLHFLKKKQGETLEAVISRVFADGI  
 HARCLKLPVDGFIPVTELPDQYR  
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 /EC-number="2.4.2.21"  
 /note="best DB hits: BLAST:  
 pir:E64856; hypothetical protein  
 b1120 - Escherichia coli -----;  
 E=2e-60 gb:AAG55866.1; AE005321-9  
 (AE005321) putative nicotinic  
 acid; E=2e-60 gb:AAC78722.1;  
 (U89687) putative nicotinic acid  
 mononucleotide:5;; E=4e-60 COG:  
 ycfY; COG0846 NAD-dependent  
 protein deacetylases, SIR2 family;  
 E=2e-61 PFAM: PF02146; Sir2  
 family; E=3.1e-57"  
 /codon-start=1  
 /transl-table=11  
 /product="probable nicotinic acid  
 mononucleotide:5,6-dimethylbenzimi  
 dazole phosphoribosyltransferase"  
 /protein-id="CAD78623.1"  
 /db-xref="GI:32445892"  
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 PHPEAPDDDSMRGCLRPNVVWFGE  
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 /locus-tag="RB8406"  
 /codon-start=1

gene 231899..232618  
 CDS 231899..232618

gene complement(232600..233673)  
 CDS complement(232600..233673)  
 /locus-tag="RB8406"  
 /codon-start=1



		/product="hypothetical protein" /protein-id="CAD78624.1" /db-xref="GI:32445893" /translation="MLACVCEKVKTSIVMLLLGE FARISASVRQSPCRDEFTMPAFHI QRSQTIDADTRDVYDAVRDYSTWTRWSPWLQVDP DAEVTVSDPSNELGATYHWKGELV GEGSMTHRQLQAPKSLSANASVQADLAFVKPFKS QSKVEFEIEPVMTDGRPGSKITWH MRGKLPWFLEFWMRSMMETFVGMDYERGLLMFKQF VETGEVLKLEIKGVVSEPDRLII GQRGGCTMDDIGCHMAATLERVKSHYNADDERVH EWASLYHTTSDLRKRWFDYTAGYL ADAGTPVPDGCVADTVPAGKFLLRHIGEYAHLG NAWSGGIQYIRYKKLKMAKAIGCE VYRNDPETTETKDLITDVYIALK" /locus-tag="RB8407"
gene	complement (233700..2345	
	45)	
CDS	complement (233700..2345	/locus-tag="RB8407"
	45)	
		/note="best DB hits: BLAST: pir:T37061; probable secreted protein - Streptomyces coelicolor; E=2e-27 pir:T35483; hypothetical protein SC6C5.12c SC6C5.12c - Streptomyces; E=2e-16 pir:T35506; hypothetical protein SC6E10.19c - Streptomyces; E=9e-11 COG: DR2293; COG3021 Uncharacterized BCR; E=7e-04 PFAM: PF01260; AP endonuclease family 1; E=0.88" /codon-start=1 /transl-table=11 /product="probable secreted protein" /protein-id="CAD78625.1" /db-xref="GI:32445894" /translation="MHWMLILFVRKMLFLAIAFA SFAFMLRSPLVLAQEQTNSTIRL RVLSYNIHHGRGTDGKIDLDRLANVIRSVDPDLV AVQEVQDQNTTRNGMVNQVETLAVQ TSLHGKFAKQIDYDGGEGYQAVLSKYPIESLEVH WLPGDPIRERRIVGVAEILIHKTR LRFATTHLHHSRADLREKQATELNRLILACGSTPV ILAGDFNAKPASLAMQTLQAKWRI ATTESMHTFPARSPNRQLDYVAMYVANSWRIVES EVLDEPVASDHRPLLVEIELETHS GSLPK" /locus-tag="RB8409" /locus-tag="RB8409" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="CAD78626.1" /db-xref="GI:32445895" /translation="MFDSKSKPSETAATVRRPVW THQDFSGGGYFGTIPKSTDRCGVF TAGVLTADVDLRCIGLKRSTNEDDALFSTEQSRC SIQNWRSQKIPHQPENWDR" /locus-tag="RB8410" /locus-tag="RB8410" /note="best DB hits: BLAST: embl:CAB57873.1; (AJ132579) coat protein readthrough [Oat golden; E=0.10 embl:CAB57874.1; (AJ132579) coat protein [Oat golden stripe; E=0.10" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="CAD78627.1" /db-xref="GI:32445896" /translation="MTLCSLQSSRDAQSKIGDRR KSRTSPKIGTGERSIGALKTREQL NRLRFAGQPSYTEGSTRRPLPPSAGQLAGSSESQ SLTCETMPRNRIANDDSPMERLA IKR"
gene	234547..234840	
CDS	234547..234840	
gene	234746..235063	
CDS	234746..235063	

CDS

235092..236180

/locus-tag="RB8411"

/function="transcriptional control"

/note="best DB hits: BLAST: pir:H83475; probable transcription regulator PA1359 [imported] -; E=0.067 embl:CAA64677.1; (X95394) aldehyde dehydrogenase-like protein; E=0.52 COG: PA1359; COG1396 Predicted transcriptional regulators; E=0.006 PFAM: PF01381; Helix-turn-helix; E=7.3e-11"

/codon-start=1

/transl-table=11

/product="similar to transcription regulator"

/protein-id="CAD78628.1"

/db-xref="GI:32445897"

/translation="MAQTASFLTRKIGFGMAQAN AQLKQARQSLGLSQLQLAMRAGVS SRTVQFAESGQNVSIGTMRRIAGALGMQADQLVR IDPGTGQDGFaelPWSVADKFRSN RGFDEGSMCRNEADVIEVVRQLRENFSVQIQKWG TSHDQQQALQKNSAIDEVYFRYEQ RYVDLWRRNPECIRLDRFEDTVGGVSIVLPLTAE SFHAFRDGKLAWLDISADDLADQS QYLLLDsvTEFTKQCRRPWYQVTKSLSLITFNQV ASLAQSPNQSDfEMVSFSASPLNE RRLGTIGFIPEPTKEPEFSYPIYWFGEDPRILAK EEYSNWATFKHFAMLIKSVDKAGL RRRMIRNLLSMVKRLQRPASISRQAA"

gene

complement (236128..237204)

/locus-tag="RB8414"

CDS

complement (236128..237204)

/codon-start=1

/transl-table=11

/product="hypothetical protein"

/protein-id="CAD78629.1"

/db-xref="GI:32445898"

/translation="MLRFVWRNRLATTGRLTWIG GGSMNGKILSYSAGSTSLDPFKFR VIDSQKPTDKMKRLATIFPDLPFFVDPSQSLVV DAYPAALGGMEAMTRVITYLHPPT CIRALRLAAAENRRVVFIAQPLAGADLLLQAMET QMDWPTELLWATGGYPLPASLERS VEAWLANRGCRLTVLQAYGVAELDHTLMASMRG SDSHPIYQLIDPRLELDSFEDGCS LNKHVRFQGIrtanQDRIESCGSGYRIHGNPSLY GDGALRWLEKWQPNdWWNCTGYLS DRDGAIALQORRGRTTNAEVSINCLSLPAMASLP RGVACLPVEHFDFMSDDGMSWMEK PKWNPAAFKQLDAKSIARRAAAVA"

gene

complement (237132..237758)

/locus-tag="RB8415"

CDS

complement (237132..237758)

/note="best DB hits: PFAM: PF00583; Acetyltransferase (GNAT) family; E=0.72"

/codon-start=1

/transl-table=11

/product="hypothetical protein"

/protein-id="CAD78630.1"

/db-xref="GI:32445899"

/translation="MDVLHCFGTADPLFDVVQEIRRDGSEQTLyHYDEYSNHYILKWQ GQPLGTLTMLAAANGRLDCEDHYPTVLLDQHGDE LFASCKLRIRRGpSTPIAALRTLVRGSWAHQLANGKRISIANADVrmKAFYRRMGFTY LpgFDFIHPELKTQsIVLLMAADA RGRSYCQDMFAELAKQSDQPALVEMCCGSFGETG SRPRVGSGLAAVA"

gene

237883..237999

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CDS

237883..237999

/locus-tag="RB8417"

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gene	complement (237986..240421)	
CDS	complement (237986..240421)	/locus-tag="RB8418" /gene="priA"  /locus-tag="RB8418" /function="DNA synthesis and replication" /note="PMID: 9086272 best DB hits: BLAST: swissprot:P94461; PRIA-BACSU PRIMOSOMAL PROTEIN N' (REPLICATION; E=1e-130 embl:CAA71348.1; (Y10304) priA [Bacillus subtilis]; E=1e-123 swissprot:P74397; PRIA-SYNY3 PRIMOSOMAL PROTEIN N' (REPLICATION; E=1e-112 COG: BS-priA; COG1198 Primosomal protein N' (replication factor Y) -; E=1e-131 PFAM: PF00005; ABC transporter; E=0.66 PF01443; Viral (Superfamily 1) RNA hel; E=0.33 PF00271; Helicase conserved C-terminal; E=7.8e-09" /codon-start=1 /transl-table=11 /product="primosomal protein N" /protein-id="CAD78632.1" /db-xref="GI:32445901" /translation="MGYLAPAGKKRSSHVMLSDS SLSNLGDPDTLNFPPFAAAPVPADS SSSEPTQNELFETDPPPWELTVGEDVQLASIVFA RSPHGPYDYRIPDDLDDVLRPGMR VGVPLGHRKKPTPGWCVSIKTGNAAQKKLRDVSE VIDDEPLCDAALVRLVMFIAHYQ VPAGQVFDTLIPASVRDNAGTRKTTYFRPAPGLT EEQIAKLPSKQQSAMRFLIAQDRP MTAAEIAIMAECTEDPIRRLRKKELLVPEVRREL SQNIRIRAQANDGETRKTHTDLTAQ QENALSRINSAVDSGRGRTLHLHGVTGSGKTEVY IQAIEHVVKQAGSAIVLVPEISLT PQTRGRFEDRFQNVAVLHSQMSASERHFHWQRIR RGEVQVVIGPRSAVFAPLPNLGLI VIDEEDHDTSEFKQDKQPRYHARKVAHARAMALGIP LVLGSATPSMEAWHATQTGHAEV TMSERVGNRPMPPDVQLVDLRVKEERGKGGAISRP LHAAVLETLKEKGQAILLNRRGY ATTIQCPACGTVCACPDCLMPLTHHRDGGKAMCH YCDYTIPTPPWCPACRFDGMRYGG LGTQRLEMEAKARFPDARIARMDSDTMKRAGSHQ RVLSEFRAGEIDVLLGTQMIAGL DFPNVLLVGVINADSALHFPDFRAAERTFQLVTQ VAGRTGRGDRGGRVIVQTFTEHP AIQAAARHDYLFVEDEMVNRRKKFNYPPLGSVAR IIRGPLEDKTESVADAIVDRLEK ARDLLKAEVRILGPAPPPIVKISGKYRFHLLLQA TEAAVVGEVIRRLADFKVDPKEE IEFLVDIDPVNLM" /locus-tag="RB8420" /locus-tag="RB8420" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="CAD78633.1" /db-xref="GI:32445902" /translation="MSSFSSRAQDNPSIIAHPV TRLVTRLNCPALPRPESPSLSRSF HPELLTQTPPEPLVPIRLGRGRLGSHRGAADG NRGSRNAHPERRRPHQTAPHRVKE"
gene	240382..240843	
CDS	240382..240843	

gene	240840..241310	AIRIPSSSHYTGSLKAMR"
CDS	240840..241310	/locus-tag="RB8421"
		/locus-tag="RB8421"
		/codon-start=1
		/transl-table=11
		/product="hypothetical
		protein-signal peptide and
		transmembrane prediction"
		/protein-id="CAD78634.1"
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		/translation="MTEHRPSPMHPRSRSVPTIL
		RNILAVVAGLFLGSVLNMAIVTIG
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		LAHAFGTLVGAFVAAKIAASHKMK
		FALGIGVFFLLGGITMAMTFGGPLWFIVLDLVGA
		YLPMGYLGGLTARATRPQPT"
gene	241270..241428	/locus-tag="RB8422"
CDS	241270..241428	/locus-tag="RB8422"
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		/transl-table=11
		/product="hypothetical protein"
		/protein-id="CAD78635.1"
		/db-xref="GI:32445904"
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gene	complement (241421..2433	/gene="atsG"
	76)	
CDS	complement (241421..2433	/locus-tag="RB8423"
	76)	/gene="atsG"
		/locus-tag="RB8423"
		/EC-number="3.1.6.-"
		/function="sulfatase"
		/note="PMID: 9634230 best DB hits:
		BLAST: pir:F70837; probable
		sulfatase (EC 3.1.6.-) atsG -
		Mycobacterium; E=1e-40
		gb:AAF55607.1; (AE003724) CG14291
		gene product [Drosophila; E=1e-20
		gb:AAF29467.1; (AF156255)
		N-sulfoglucosamine sulfohydrolase
		[Mus; E=3e-20 COG: Rv0296c;
		COG3119 Arylsulfatase A and
		related enzymes; E=1e-41 BH1718;
		COG1413 Phycocyanin alpha-subunit
		phycocyanobilin lyase and; E=0.010
		PFAM: PF00884; Sulfatase;
		E=5.2e-22"
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		/transl-table=11
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		TTAGVCAPCRSGIITGMYQTTLGT
		QHMRCQAKLPESIRPFSTYLRESGYFCTNNSKQD
		YQFETPKGSWDQSSSKAHWRDRPD
		QDTPFFSVFNFTGCHESGIENDAKYKSVTKGLSE
		RERQDASKLSTFPYPYPTPAARE
		DWKRNYELITALDHWVGGLLDQLNADGLD EDTIV
		FFWSDHGVGLPRAKRWLYDSGTHI
		PLVIRMPAQFRSTDNVAGVVDDRLVSSIDFGPTV
		LNLAGLDVPEPMQGKPFLLTSPLSK
		LAAADR DYVYGARDRMDERYDIIRMVRDQRYKYI
		RNYEPLKPYFQYMNTPEKGQTMRS
		IREAEQAGTLPEAAMPFFRGTKPTEELYDLEND
		HEIHNLASSSDHTEVLHRMRAAHE
		QWVTRTKDLGLIPEPILAERASELGSQYAVLRQS
		DDSELANRVAAAALAASEGPRALP
		EMRSALDDIDSAVRYWGATGIGNVFARGEIDKLP
		YLMDLQERLADES VTVRVAAARAL
		CHSGDPEATSKALSVLAEALADGAQWERLQAAIV
		LDEIDEKALPVIDSMQDALEPRQE

gene	complement (243479..244753)	/gene="mntH"
CDS	complement (243479..244753)	/locus-tag="RB8430" /gene="mntH" /locus-tag="RB8430" /function="metal ion transporters (Cu(2+), Fe(2+), etc.)" /note="PMID: 10844693 PMID: 10712688 best DB hits: BLAST: pir:T44945; hypothetical protein 6 [imported] - Natronobacterium; E=1e-48 swissprot:Q9RPF3; MNT1-PSEAE MANGANESE TRANSPORT PROTEIN MNTH1; E=1e-18 pir:B83105; probable transport protein PA4334 [imported] -; E=1e-18 COG: PA4334; COG1914 Mn2+ and Fe2+ transporters of the NRAMP family; E=1e-19 PFAM: PF01566; Natural resistance-associated macrop; E=0.00026" /codon-start=1 /transl-table=11 /product="Manganese transport protein mntH1" /protein-id="CAD78637.1" /db-xref="GI:32445906" /translation="MSFATLAGMKLPKFFRRFGP GLLVTAAFIGPGTVTKATTAGANF GHTLLWAIGFSVIATIVFQEMASRLGIVTGRGLG EAIRPTIPNALARGLAIVLVVSAI IVGNAAAYQAGNIAGAAVGVAATGMQHQTLVSIV IGLTAWCILMIGHYRSLQRILVAL VVTMSCVFLLTALSVPIDWRSIALGWIQPTIPDG GLKEVLAIIGTTVVPYNLFLHATA SAEKWSSDKKEPVSDENIRDAIQHSRGDTILSVG LGGLVTAAVMATATAAFFQSNTGF TNLADAARQLEPLLGNHARWLFGVGLFAAGLTST ITAPLAAAYAAAGCFGWPIDLDKW RLRTVFTTVIVFGTSFAASGSKPTDIITFAQIAN GLLLPLLAIFLLAVMNNALLGKH RNHWIANTLGVLTVVVSVLGLRSLVSVSFAG"
gene	244767..245624	/locus-tag="RB8432"
CDS	244767..245624	/locus-tag="RB8432" /note="best DB hits: BLAST: pir:F70844; probable fusion protein - Mycobacterium tuberculosis; E=1e-07 embl:CAC04235.1; (AL391515) conserved hypothetical protein; E=2e-04 pir:E83611; conserved hypothetical protein PA0269 [imported] -; E=0.020 COG: Rv3327-2; COG2128 Uncharacterized ACR; E=1e-08" /codon-start=1 /transl-table=11 /product="probable fusion protein" /protein-id="CAD78638.1" /db-xref="GI:32445907" /translation="MNSHHSSSGYPVMPRSSELV HTSATTIANNDSDNANQRVWNFCA AALILRPPITHPSEVLMTTGLKPLTDAEAREVEL VFRLTKSHLGFVPNSMRTMARQPA ILSSFTLMVGNILGQPSDAKSPIWLGIRLVIKNV IWSLRNMRSKDRPLALKNLVAHV TSGAAGCRYCQAHTIGEARDQGVPIEKLEAVWEF DRSDLFDEAEKSALRFALAAGSHP NGVTADHFADLRKHYTEDQIVELGATIALFGFLN RWNDTFATTLPEESAFAFANQHLSA SGWEIGKHG"
misc-feature	245160 2451	/locus-tag="RB8432" /note="cosmid pircos-a3c02/ cosmid pircos-cle07 joining point"

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gene	245842..248907	/gene="cti"
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gene	255833..256477	
CDS	255833..256477	



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gene	complement (257117..257458)	
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gene	257496..257663	
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		Bacillus subtilis; E=1e-08 pir:R3BS18; ribosomal protein S18 - Bacillus stearothermophilus; E=1e-08 COG: BS-rpsR; COG0238 Ribosomal protein S18; E=1e-09 PFAM: PF01084; Ribosomal protein S18; E=2e-16" /codon-start=1 /transl-table=11 /product="30S ribosomal protein S18" /protein-id="CAD78649.1" /db-xref="GI:32445918" /translation="MYVDYKDLELLSKMVNRQGR IMGRRKSGCTAASQHAVTAAIKRA RFMALLPYVGE" /locus-tag="RB8462" /locus-tag="RB8462" /EC-number="3.1.2.23" /note="PMID: 9837940 best DB hits: BLAST: ddbj:BAB05718.1; (AP001514) 4-hydroxybenzoyl-CoA thioesterase; E=3e-07 swissprot:O67466; YE94-AQUAE HYPOTHETICAL PROTEIN AQ-1494 -----; E=6e-06 pir:B83525; conserved hypothetical protein PA0968 [imported] -; E=7e-06 COG: BH1999; COG0824 Predicted thioesterase; E=3e-08" /codon-start=1 /transl-table=11 /product="probable 4-hydroxybenzoyl-CoA thioesterase" /protein-id="CAD78650.1" /db-xref="GI:32445919" /translation="MNDSASDGAPTQRAPVYQTQ RRVEFRDQDAAGIVHFSAFFPMME AAEHEFLRSVGIPVMPHHESEERLTWPRVAASSD FHGPARFEDILQIDLHVDRIGQSS ISYRFELTCEGRRIATGKITAVCCDLKAGGKLVK TNVPDDLQRQLSGPQND" /locus-tag="RB8463" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="CAD78651.1" /db-xref="GI:32445920" /translation="MRRLDWPRSRSPSFRLRRLS FFGKFGHSNLLQDRVEDLFGGFEI RHFGLELSQDASRDGHLFASRGRGVQQHHARHHD EVQVVEPEVNGAFAFRGTRQCDVV TFQVFVLASEHLVDFTEDDFVFSGDRQRFQRHKS AAGQIERGSLVAFVFGSFDQLPVV RVQQFQAEAFESCGHVFVQSF" /locus-tag="RB8464" /locus-tag="RB8464" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="CAD78652.1" /db-xref="GI:32445921" /translation="MPATFEGFGLKLLYPDNNWL VERAEDGEQDQATFDLPGGGFVSL ETLPTREDEVVLGEIDQMLRGQYEDLERDNNVL PGATEGERAVDLRFYYLDLVVMSR VVLLDAPAPTREQMPIAGRILAQLQAEMSDFEAA EQVFNAIILQQIRMAELPEEA" /gene="fur" /locus-tag="RB8465" /gene="fur"
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ornithine decarboxylase (EC
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Diaminopimelate decarboxylase;
E=8e-44 PFAM: PF02784;
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gene 265206..266162  
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(EC 4.1.1.65) precursor; E=9e-61  
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CDS

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radiodurans (strain; E=1e-49. COG:  
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299165..300271

gene

300336..300863

CDS

300336..300863

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carboxyl carrier protein  
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swissprot:P49786; BCCP-BACSU  
BIOTIN CARBOXYL CARRIER PROTEIN  
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300867..302219

CDS

300867..302219

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E=1e-138 pir:S74380; biotin  
carboxylase accC - Synechocystis  
sp. (strain PCC; E=1e-136 COG:  
sll0053; COG0439 Biotin  
carboxylase; E=1e-137 PFAM:  
PF00289; Carbamoyl-phosphate  
synthase L; E=5.1e-48 PF02786;  
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T; E=1e-118 COG: PA5131; COG0696
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BH0592; COG1015
Phosphopentomutase/predicted
phosphoglycerate mutase; E=3e-06
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misc-feature

310485 3104

gene

complement(311043..3114  
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CDS

complement(311043..3114  
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hemoglobin major component
[Paramecium; E=3e-09
swissprot:P15160; GLB-PARCA
MYOGLOBIN (HEMOGLOBIN) ----- pir::
E=2e-08 COG: Rv1542c; COG2346
Hemoglobin-like proteins; E=2e-19
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Protozoan/cyanobacterial globin;
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2641	gcgaacgtca	gcgggtcaaa	tcggtacatc	cccgcgccc	caatgttcag	gttctgcttc
2701	cacggagtct	cgtggttgtg	aacgaggaaa	atcccgcttt	gccaatagat	cccaccgtct
2761	ggtccgtaaa	ccaaattggt	ggcgcggtgg	tgagtgtcgg	aggtaccaag	cccttgcaaa
2821	atgggggtatc	gcacgtccgc	cttgctcatcg	ccatcggtgt	ccttcaagaa	caacaggtca
2881	ggtccggacg	tgacaaccac	accgccgttc	caaaattcaa	acccgagagg	gttgtgaacg
2941	tgtgcgaaaa	tcttgccggac	atcagctttg	ccatcgttgt	cagtgtcctc	caatatcatc
3001	aaggagtcat	tcattctcct	gccaggttcc	cactttgggt	aagtgttcca	actggccacc
3061	cacaatcgtc	catgagcatc	aacttgcatt	tggacggggg	tggctaatac	gggaacatga
3121	acttccgacg	caaagacgtt	gagctcgtaa	ccttccggga	cgttgatctt	cgccagagat
3181	tcctctggac	ttaaagtaggc	gacgtgccc	tctttcatag	cattggaact	ggcactccca
3241	ccaccgatat	ttgaggtcac	tttgaccggc	ggtggaacat	tgctgtcgtc	agcctgcaag
3301	gttcgcccac	ctgcggctgc	ccaaatcact	ttgtcgcgat	tggcggtcat	cacgtcgagc
3361	atcaccaatt	catgcttcag	cacatctgcg	ttgctttgcc	catccacgaa	cgtcaacgtg
3421	gaacgactgc	cccaaagtgc	attgccgtcg	gtcgtctgat	accggttgtg	ccagtgccag
3481	tttttgcct	caatcgcttc	gtacaaatcc	tgaagctctg	catcagacgc	tggcttttcg
3541	cctagcaatg	cctgtgaaat	gataccagcg	agttgcttgt	aaccagcctc	attgaggtga
3601	actccgttga	gcgtgagtcg	ctcggaactc	gactgaaaca	actggtaagt	cggcgagaac
3661	aagtcaacaa	acttcgcgcc	cgtgatttcg	gctgcctcac	gagtcgcctc	ggtgtaagcg
3721	gccaaagtta	cattcagttc	cgccccatcg	ggcagactcg	cgtcgcctgt	gttctcgtag
3781	gcgatcggac	tgaacaggac	gaaacgcaga	tcctttccgt	catctttttg	cacctgcgtg
3841	taacgctgaa	cgagcttgat	caattcatcg	cgatgctcgc	cggctttttc	cggctccggca
3901	aacgactcgt	tgaaccata	aaaggtgaaa	acaacatttg	gcgcgacgtg	cttcaaatat
3961	tcggtgtcat	tgggtgaacc	ctggtttctc	gggcgttgat	taacacgatc	ccccgaaaaa
4021	ctcatgtttc	gaaaactgac	gtcgagccct	ttcaactgat	gctgaagaaa	ggtttcgacc
4081	caaggatcat	gctgcatccg	atcggccagg	ccgttgccat	agatggcgac	gacatcgttc
4141	gattggaact	caaaaagcgtc	ctgtgcatca	gctcgttgcg	cgatgcccgg	aatgaccccg
4201	gcacatagaa	agaaaaggct	ccattggagg	acagtcgtga	tcctttgctg	cattgttcgc
4261	tttctcagtt	gtcgaatctt	ggagtgcagt	ttcagctttt	gttctgcagg	ccagcgaaac
4321	tggctgcaaa	cgaagcatcc	taacgtggag	tgacggaacg	tgacacagtt	ttccgctggg
4381	gtatcgcgga	ctggtactgt	aacttcgtaa	agaacagaca	acagcatcaa	agaacgacgt
4441	aagctgttca	cgaaagcgaa	tccctgtcgc	atatcgacga	gccaacgaac	actttgcgac
4501	gttctactgaa	ctggggcggt	aaacaccgta	ccaccgtctg	gacaagtctc	gattaagct
4561	ttcagctcgg	aacgctcccc	cgagtcttca	agccgtggct	caatttatca	tgcaacggat
4621	tggctcgttt	tcgtgtctct	ggtttcctca	gcattcccta	tcggcggttc	cctcataacc
4681	gttctaggtc	gaacgcgtgg	ccttcggcac	aaggagtttc	ttcgcttctc	ccattgacgc
4741	tcgtgctccg	tccgatttgt	ggtgcaaaa	tctcttcagg	cagcgaatgg	atggcggtcg
4801	tcggaccggt	tctttgaaaa	ccagcgccga	gcagtgccac	aggagcgga	cgatggaaga
4861	cgaccaacgt	ggaccatttg	aagaatgatt	tggcactgaa	ccagatcatc	aatcgtgca
4921	gactcgattca	gacaaccgtc	cacaaggctc	aaatgcttcc	agtctcgcgt	ggagaaaccg
4981	gacctctccg	atggcgtgaa	tctgttgaca	agaaaatcgc	gatcgcgtga	gacatccttc
5041	agttccaact	cacggttgag	atgccacagg	tcactgacga	gtgcgacgtt	gtgcaactag
5101	cactttcgcg	aagctacggt	cccaacttga	tgttcgatca	aattgtatcg	accacatcg

5221	atgċgatċca	aāgtggċtċg	accgtttgtca	ttcggtaccā	āgċccgċgtc	gaccgcaccg
5281	cggatccatc	aatcgċtċgċt	ctcgacaaca	tcgatgtccg	ctgggċgttc	cgctcacaaa
5341	gcaaacgcga	tgctgcccgc	aaggcacaca	cggcttcacc	aggcgtctcc	gccccacacg
5401	tcaccggcct	cgċtċcggċt	gcccgtgcaa	aagcgtcggc	tttgacttca	agcgttgċtt
5461	gaaacgtċtt	cċgaacagaa	acċgaagatc	tggcaatcċg	cgċgtċccat	gċcagatgċt
5521	cagcgtċtċg	gggggċtttt	atcgacgttg	actgacċgca	gagtgtacċg	atċċtċtgaa
5581	cgċċttgtt	caċgaagtċg	ggcggcaatg	cgċtċtgccc	gagċċgċgċg	tttagattċg
5641	gċtċgtgċga	gtċgatacċg	ctgaacatċċ	gċċtċacttt	gċatċaatgċ	tagċċgċtċg
5701	tgċtgagtċt	tċċgatacċg	cgagċtċgċg	atċtgacċgt	ggċttgċcaa	caċgttgċtg
5761	tgataċtċg	acċgċgatċag	gttċgttttċt	ggatagċtċg	tgacċaatgċ	gttċtgċcca
5821	tatggatttt	gggċataċtċg	cgagċċgċtċ	gtgaatgaag	tgggactċgċ	tgatggċggt
5881	ċċtċcacċtċ	gagaacċgaca	ctggċcaaāt	gċttċaccċg	caaagaacċg	aacċgataac
5941	aaagtċgċtċg	tagċgactaa	aacċċcacċgt	cggaaatċtt	tċgċacċaaa	atċatttgta
6001	ċċgaaaċtċa	ttgtgtactċ	catċgċgtċg	tċgaagaatċ	aaaggċaacc	gacċċgċċa
6061	acċgċacċgac	tċgtċċtċta	ċċtaacċaag	gacatċttċg	ċgaaaaaacċg	tċacċtgaaċg
6121	tċgatċċaac	gċgggċagag	ċttattgaaċ	ċgagċċggaa	atċgaatgag	attgaacċgg
6181	ggatgagċga	cgċtċċċċt	ttċggċtċgtt	ċċċtċaccċg	tggaaaatċg	atċċgatċtċ
6241	ċċtċċċtaā	tttċtċagċt	acċgtgaaga	gċtċgtgċċa	tgaatċttāa	gacaacċgatċ
6301	ċttċgtgċgċg	ċċgttgċgtt	tċgċtttċtċ	gċċċċċgaa	ċaatċċaaag	tāaagagċċt
6361	gċċatgaaga	ċċaaatgggċ	ċattgtgatt	ċatggtggag	ċċggċagċtċ	acċggċtċaa
6421	ċttggċgacċg	ċatċgagċtaā	gċaacċgċċċ	aaaggtċtċg	aacacċgċgtt	gċaaacċggċt
6481	ċċgċatātċg	tggċggacċg	ċċgċacċggċċ	atggacacċg	ttgaagċċgt	gattċgaacċ
6541	ttggaagacċ	atċċaatċtt	ċaacċgtċgga	ċgaggtċċag	ttgtgacċga	ċgagggacċg
6601	gtċgagatċg	atċċatċċgt	gatggatċgg	aagacactċg	cgċgtċggċg	agċtċgtċgg
6661	gtgacacċgg	tċaagaacċċ	gatċtċactċ	gċacċċċggg	tgatgacaga	gacċgaacac
6721	gtċgtċgtċg	ttggtċċċg	tċċċgacċgag	ttċċgċgaaā	ċtċagċaagt	gċċtċtċgtċ
6781	gatċċgaaāt	acċttċtċgtċ	ċċaacċgċgat	ggċgatgacċg	ċatċċagċat	tċgttċgċċa
6841	actċaggatċg	aagacċgaatċ	gċatċttgga	acċgtċggċt	gċgtċgtċgt	ggattċċċac
6901	ggċaacċtċg	ċggċtċgaaċ	ċagcacċgga	ggcacagċaa	acaaactċgċ	aggċċagċtċ
6961	ggċgatċtċac	ċċatċgttċg	ggċċggċċċċ	tacċgċgċċa	atggattċgtċg	ċgċċgttċċa
7021	ggaaċċggċg	ttggċgaaċga	gtacatċċċċ	aacagċtċtċg	ċgtatgacat	ċgċċċgċċaa
7081	atċċggċtāċg	ċgaatċagċtċ	gċtċgagċtċa	gċagċċacċg	acatċatċgtċ	gaatċgactċ
7141	gatċċggċgtċg	ttggċgċgatt	gattċgtċgtċ	tċtċagċaaċg	gċgagatċgt	gatċgacċac
7201	aacacċċċtċg	gċatgagċtċg	ċċgacċagċċ	gacagċacċg	gacċgttċċga	aacċgacttċg
7261	atċtċċgaca	acċgtċggagċ	acċggċgċgaa	gċgacaċċa	aatċaaacċċ	atċċgċatċċ
7321	gacċgaatċaa	agatċaggċga	acċgtċċag	ċċacagċċa	gċgattċggaa	tċgċggċaac
7381	attgacċgtt	tċatgaagċt	ċtattċgaaċg	agċgatċaaċ	tċacċgttċtċ	ċtċċggċtċgt
7441	gacċgtgacac	gċgċattċga	ċċgċacattċg	ċagċgatāċa	aagaacċgċta	ċċċacttċċg
7501	gaaaagatċg	gaaagċtċac	tttċacagac	ċtggaatċċċ	ttċċċgtċgg	tāactċċgċċ
7561	atċċaaċgtċċ	tċggċgċtttċg	gaaactċgtat	ċgaatċggagċ	ċgatċggagċg	ċaagttċacċg
7621	ċtċgttċtċċ	gacċgttċċċ	ċgaaggttċg	aagatċgtċċ	acċgacċac	ċtċaaagċtċċ
7681	ċċċgactċċg	aataggagċtċg	aacċgacċċċ	gatċtċtċaaā	gċcagaaagċg	aactċċgtċga
7741	ttċgttċtċċa	ċċċggċtċċg	gtċgtċagact	ċttċċgtċac	ggatċagċtċg	ċacttċaatt
7801	ċċċtċtċgat	ċgtċacċagċ	atċgttċtċtċ	gċtttċgaaā	ggċtċtċċċa	acċgċgċtċg
7861	gactċgtċgac	gċtċggċatċg	gtċgatċtċga	tċtċaaċċaa	ċċċattċċgt	atċċatttċa
7921	atċċgagċċt	gċggċċċatt	ċtċtċagaga	actċgttċċa	ttgtċacċgg	ċċgaatċċgċg
7981	aatċacċgċga	ggċċgacċtċg	ċgactċgċa	ċtċaaacċċg	ċtċċċċċaa	gagċtċċċg
8041	gaagċċċċg	ggċtċgtċċċa	aatċgagċċg	acċaaagċtċg	actċgatċgag	ċggatttċtċt
8101	ċċgacċacċċ	tċgatāgttċg	atċċċċċċċ	ċċgagċtċgaa	acċgaaċgtċg	tċggċtċatċ
8161	aaaagċtċat	tċtċaaatċa	tċgatċċċċg	aagċċggċtċga	ttacċgaacaa	ċactċggċċt
8221	tċatċċċacċ	gactċagċċa	agċgttċċtċg	agattċgatċa	agċċċċgagċt	tċtċtċċatċ
8281	ċggċtgċacċg	ċttċatttċg	aacċgattċg	atċaaċgagċg	tċttċagċċt	tċċaaacċċg
8341	ctċatċgacċg	ċacactċgatt	gċċċgagċtċ	ċactċgacċt	gacċggactċ	ċċċċgacċg
8401	ċċgaacaaċgt	ċaatċċtċtċ	gtċaatċgagċt	ċtċgtċtċgaa	tgċċtatċgag	ċggċtċggċtċg
8461	atċċggċtċgt	tċgttċċgaa	ċagċtċċggċg	aacċgttċggċ	gagacċttċg	ttċgacttċg
8521	ċtċgċtatċg	ggactċċaat	gggttċtċaaċg	ċtgacċaat	gċgagacagċt	tċggċċtatċ
8581	gggattċggċt	ċatċaaċċgċg	ttgaatċgatċg	acatċċċgtt	tgatċagċttċ	acċgattċgaac
8641	aactċċċċg	tċgactċgttċg	ċċgaatċċga	ċgatċgatċa	aaaatċċgaa	ċaggċtċtċċa
8701	tċgċacċgtċg	ċċgtċċaatċg	tċgaagċċċg	ċgtacacċċa	gaagaaaacċ	gggtċaacċa
8761	agċċatċgac	ċċgtċċaatċg	ċċgacċċgac	agċatċggċtċg	ggaatċgacċa	tċgaatċċċċ
8821	gċagċtċċac	gatċacaaat	acċacċċċgt	ċagċċaaāāg	gaatattāċa	agċtċtċtċg
8881	gttċtċtċaac	aacacacċaa	tċggaagtċga	aaacċċaaċg	ggċaaagċċg	tċgtċgttċga
8941	ċttċtċggċgt	ċċċaaatċg	acċtċċċact	acċtċċagat	ċaagċgagċa	atċgaagċċg
9001	ċċtgċaaċċg	gaaatċċgtt	ċgtċċgaagċ	ċaaagaaāac	gċggċgtċtċg	aagċagċtċga
9061	tttċgagaac	tċgacacagċ	aactċtċċaat	ċgċgtċċgac	aacċaacċtċg	aattċċaaac
9121	gċtttċċaatċ	ċċċċċgtċa	gttċċgacċċg	tċgacċgaag	atċgaagattċ	tċgatċgacċa
9181	gtċggċtċtċg	ttċacagċgċa	agċtċċċċga	ċaagactċgtċ	tacċgagatċċ	actċgtċatċga
9241	gattċċċċgċa	gatċgtċatċg	gatċgaaāat	ċgaagċgtċg	actċatċċċga	gtċtċtċċċg
9301	aacagċċċċg	ggċċċċgċg	atċċċgtċċċg	gtċċaacċtċ	atċttċgagċtċg	aattċċgagċtċg
9361	agagattċgtt	tċgaagċgaag	gċagċċċċac	ċċaacċgtċtċg	gacċtċgactt	ċagċatċċċċg
9421	ċgactattċċ	ċagċċċċċat	ggaaċċċċċg	ċaacċċċatċ	gacċgtċatċ	tċaaacċċgg
9481	ttggċċgatt	gċatċgaaat	tċċaaċaatċ	gċactċggċċa	ċagċttċtċac	ttċaaacċċċ
9541	actċċċċaa	agċtċgaagact	ċaacċgttċgċg	atċċċċgttċg	gaacaaċċċgt	acċgaagagċg
9601	ċċgaacċgatt	ggċtċċċgtċg	gtċtċtċċagċ	gċtċgtċċggċ	aatċċactċċg	ċaatċaaċċgt
9661	ċċċċgaacaa	gtċċċgaaag	ċggċċaaċgaā	acċtċċgaaā	gatċgatċċċ	ċċagċgactt

9781	gāttcaāaaa	ċtgaċgaagc	aaċtġgaatc	aacccaġccċ	ġcċaċċācgc	ttgtcatġgt
9841	ggagatggaa	gagccacgcg	aaacċtttgt	gatgcaacgt	ggcaactact	tgtcacctgg
9901	ggaccgagtt	tcaccgggga	cgccgatggc	tċttcatcaa	atgaacgagg	acċttccaaa
9961	gaatcgċctg	gggċtagcac	gttġgttġgt	cgatċċcgcg	aatċċgttga	ċgċċċgtgt
10021	gacġgtċaat	cgċtġgtġgg	ċtcaattġtt	tġgtcagggā	atċgtagaca	cgċtġgaaga
10081	ċtttġgaacg	cagċcatċgc	caccgacgca	ċċċgatttġ	ċtċgactġgg	tġċċċttġga
10141	attġgtċgaa	tċagġttġgt	cgatgaaaca	tġtċċtġaaa	acġatċġtga	tġtċġgaaac
10201	ċtatċaacag	gactċċaaag	tċċġġċaga	tċtġatċġag	ġċġacċċġġ	ċgaataaatġ
10261	ġtacġċgagġ	ġġacċġtġtt	tċċġatġtċ	agċġgagatġ	attċġċġaca	atġċtttġġċ
10321	ġġtċagċġga	tġġtċtċċġ	ċaaaaatġca	ċġġtċċtċċā	atċatġċċġċ	atċagċċġac
10381	ġġgaatttġġ	ċġtċaagtag	ġġċġgaacġā	acċgaagtġġ	atċġċġġċāā	ċġġatċaaga
10441	ċġatāċċga	ċġċġċġttt	acġtġġtttġ	ġġġacġġċċ	ġċacċttacc	ċġġċtttġt
10501	gaatttċġat	ġġtċċċġatċ	gaagtċtċtġ	ċġtġġtġġġt	ċġġċġagaaā	ċċaacacġċċ
10561	ġċtġċagġċā	ċtġacattġċ	tċaacġatċċ	ġġċttacġtċ	ġaaatġġtċċ	tċġtċtġġċ
10621	aaatċġċatċ	tġatġtġaac	acċċtġacġġ	ġagċġactċċ	ġatċġactttt	ċġġġġġċatt
10681	ċġaaatċġtt	tġtġtċġagac	ġaccagċċċċ	ċċaagaatċċ	ġċtċġġttġā	tġacġttċċt
10741	tġatġagċġā	aagġagċacc	tċċattċċāā	tċċċġagċtt	ġċċaagtċġċ	ċġttċġgaga
10801	ġċaatċġttt	ċġgaāċaāċā	ċtġtttatċċ	atċċacagaaā	gaattġġġġġ	atġġttċtā
10861	ċġtċġġgaac	ġtċċtġttġā	atttġġacġā	ġacaatċacġ	aagġactġāā	acċtċċċġċ
10921	aaatċċċtċġ	actċattġag	atġatċġtċġ	aagatġāāāā	ċċtatċġatċ	ċāāāāāāāā
10981	atċaatġtġt	ċġġtġġġġġ	agċaatġtċā	ġġgaāċġaga	ċġġtċġāċā	actċtttċag
11041	ċġtġċċġġċā	tġġġċċtċġġ	aggattċġċt	ċtġacatċġċ	tġttċċagġtċ	tġāāāāāāāā
11101	ġġagċġttċġ	ġacagġagaaā	aattġġatċċ	ġġġttġġāā	ċacacċatċċ	agċtċġġċċ
11161	āāaagtġtġā	tċċatċtċċā	ċatġġtġġġġ	ġċċċċġtċġ	atċtġġatċt	ġttċġatċā
11221	āāāċċġttt	tġġagġagġġ	tċġġġāċāā	ċtatġċċġġ	atġagttċtt	ċāāġāāāāā
11281	ċaattġġċat	tċattċġtġā	āāāāāāāāā	tġtġttġġġā	ċċċāāāāāā	ċāāāāāāāā
11341	ċaattċċāāā	ġttġtġġāāā	atċagġāāāā	ċāāattċġā	acċtġatġċċ	ċāāāāāāāā
11401	acġġtċġċġġ	acġaatġtġt	ċttċatċāāā	acġġtġċatā	ċġġacċaatt	ċaatċāāāāā
11461	ċċġċċāāāā	tġtġtttġtġ	ċagġtġtttċ	agġġatċġġ	ġċġġċċċāā	ċatċġġttċġ
11521	tġġġtċagtt	atġġgātāāā	āāāāāāāāā	āāāāāāāāā	ċġġactttġt	ċacġtġatċ
11581	acġġtċāāā	tġtttġġāāā	ġġġāāāāāā	ġġāāāāāāā	ġġġġtttċt	ġċāāāāāāā
11641	ċatċagġġāā	tġāāāāāāā	ċagċāāāāā	ġāāāāāāāā	tġtttċttatċ	tāāāāāāāā
11701	ġġġatġġġġ	ċġtġġāāāā	tġāāāāāāā	ġtġatġġġġ	tċāāāāāāā	ċāāāāāāāā
11761	ċġġttġġatġ	atġttġġtġā	ċċċtġāāāā	tġāāāāāāā	tġāāāāāāā	ċāāāāāāāā
11821	tatċġġatġċ	āāāāāāāāā	tċċġāāāāā	atġāāāāāāā	atāāāāāāā	ġġġāāāāāā
11881	ċatċagatġt	atġġāāāāā	acġġāāāāā	acġāāāāāāā	ċāāāāāāāā	ċċġāāāāāā
11941	ċġċġtttġġ	tġāāāāāāā	agġāāāāāā	ġtāāāāāāā	tġāāāāāāā	atġāāāāāāā
12001	ċatġāāāāā	tġāāāāāāā	ċttġāāāāā	āāāāāāāāā	āāāāāāāāā	āāāāāāāāā
12061	ġġttġatċā	āāāāāāāāā	acāāāāāāā	atġġttġāāā	atāāāāāāā	āāāāāāāāā
12121	ġġtġāāāāā	ġtġāāāāāā	ġatġāāāāā	ġġāāāāāāā	ġtġāāāāāāā	āāāāāāāāā
12181	ġtġāāāāā	atāāāāāāā	āāāāāāāāā	acġāāāāāāā	tġāāāāāāā	āāāāāāāāā
12241	ċġtġāāāāā	ċċāāāāāāā	ġāāāāāāāā	ċġāāāāāāā	ġāāāāāāāā	āāāāāāāāā
12301	ċāāāāāāāā	acttāāāāā	ċāāāāāāāā	ċāāāāāāāā	ġāāāāāāāā	āāāāāāāāā
12361	acċttċġġt	acāāāāāāā	ċāāāāāāāā	ċāāāāāāāā	atāāāāāāā	āāāāāāāāā
12421	ġāāāāāāāā	ġttāāāāāā	tġāāāāāāā	ċāāāāāāāā	atāāāāāāā	āāāāāāāāā
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12541	āāāāāāāāā	tġāāāāāāā	ġāāāāāāāā	ċāāāāāāāā	atāāāāāāā	āāāāāāāāā
12601	tġāāāāāāā	ċāāāāāāāā	ġāāāāāāāā	ċāāāāāāāā	atāāāāāāā	āāāāāāāāā
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12721	āāāāāāāāā	ġāāāāāāāā	ġāāāāāāāā	ċāāāāāāāā	atāāāāāāā	āāāāāāāāā
12781	tāāāāāāāāā	ġāāāāāāāā	ġāāāāāāāā	ċāāāāāāāā	atāāāāāāā	āāāāāāāāā
12841	āāāāāāāāā	ġāāāāāāāā	ġāāāāāāāā	ċāāāāāāāā	atāāāāāāā	āāāāāāāāā
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13021	tatġġtġġt	tġġġġġġġ	tġġtġġtġā	tġtġāāāāā	ġāāāāāāāā	āāāāāāāāā
13081	tġtġāāāāā	ġtġāāāāāā	ġttġāāāāā	ċġāāāāāāā	āāāāāāāāā	āāāāāāāāā
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13201	tāāāāāāāāā	ċāāāāāāāā	ċġtġāāāāā	ġāāāāāāāā	āāāāāāāāā	āāāāāāāāā
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13321	āāāāāāāāā	tġtġāāāāā	atāāāāāāā	ġāāāāāāāā	āāāāāāāāā	āāāāāāāāā
13381	ċtttġġttċċ	tġāāāāāāā	ċġttāāāāā	ġāāāāāāāā	āāāāāāāāā	āāāāāāāāā
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13621	āāāāāāāāā	ġāāāāāāāā	ġāāāāāāāā	ġāāāāāāāā	āāāāāāāāā	āāāāāāāāā
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13741	āāāāāāāāā	ġāāāāāāāā	āāāāāāāāā	ġāāāāāāāā	āāāāāāāāā	āāāāāāāāā
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14041	āāāāāāāāā	ġāāāāāāāā	atāāāāāāā	ġāāāāāāāā	āāāāāāāāā	āāāāāāāāā
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14221	āāāāāāāāā	ġāāāāāāāā	atāāāāāāā	ġāāāāāāāā	āāāāāāāāā	āāāāāāāāā



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19441	tcacacgggtc	tacaaagatc	acaacc̄caḡg	caacgcagga	actcagagcc	cctacggact
19501	gtgggggtgt	cttggcacca	aagccaacaa	agaaacggtc	tcatttgact	cgttttgata
19561	gccggaaagg	catttgctcc	ggcaaatac̄g	aattagaagc	gttggttgcaa	tctcgcagca
19621	acgcttcctt	cctttccgat	ttcttcacgc	ttctcttcat	tcaatttgca	accagatgac
19681	caataccaaa	cactccaacc	gattgatcac	ctttctgtcc	ctgatgtgcc	tctcgttact
19741	ctgtgctgga	tgcgacaaca	acgaatcgac	tgtcatccag	caacc̄cgct̄g	atgcggcaca
19801	ggagatggaa	gactacgaat	cgatgatgaa	ctcatcggcg	aaagaagctt	acggaaagta
19861	ggccattcgc	tcacatcgcc	atcaacgctg	gatccgatca	cgggtccagc	gttttgactt
19921	gagtgatcgc	cctcggtcga	tccaatcgct	caagatcttc	aacaccatcg	attcacagaca
19981	agactgccta	gcaggctggt	gatttattga	gccgcaccgc	gttagcggcg	gttgattaga
20041	cgccaaccgg	ggctaacgcc	caacggctaa	tgattgtcat	tccgcatgcg	actatatcaa
20101	cāgcctgaac	cgttcaatcc	ttcgcaaccg	cgttgggact	ggctttcaca	tccgattggg
20161	tcaaaccgcg	tggaccgctg	agtttḡcctt	tcaaacggtg	cgatgcaaac	gtggcgttcg
20221	ccaaccgcac	attcagtttc	agatccgcgt	agggtgactc	ctcttttaac	tccgggtgaat
20281	caccttc̄cgc	tgcgggcca	tcgtaaac̄tt	ccaaacgaat	cggaaacgtg	agttcatcgt
20341	cgatgtaggc	gttggcacga	tggaaatgtga	caccgc̄cttc	tttggatgga	tgaacaatct
20401	gaatgtgagt	ggctggccgt	cccatcacc̄c	gagcattccg	aaaatagḡtc	acttcgggtg
20461	tgtcgc̄cḡgt	gggatcgttt	tccatgtcga	attcaatcag	tccgatcaat	cgactcatga
20521	tctt̄gt̄caaaa	tccaatgtcc	gtgatcggat	agttgctttg	ctctttggcc	tgacgcccgt
20581	gagggtcaat	cgaaāgcacc	aaatagctca	gcgc̄cc̄cḡcc	accttt̄tc̄ḡg	acacgḡgct̄t
20641	tgccttc̄ḡtt	ctcac̄ct̄tc̄g	atgtagagaa	ctcgtcgatc	gcgtagagta	cgtgḡḡgatt
20701	gatactgcaa	gaagacggac	agcgḡtgaaa	catcgc̄ct̄tg	ctcattggac	tgttccactc
20761	tgacgḡcḡag	gtccatgatt	tgagḡcḡttt	gcaactcacc	atcgattcgt	tcccgtttga
20821	tcaḡct̄tḡca	actgtaatcg	ctgacattct	gccgaatgtg	gtcgḡcatga	gccttgḡcaa
20881	acccaagtgc	ccaacc̄caaaa	gggtgatcat	cgatcgḡtḡg	gtgcaatcga	tgatc̄ct̄cc̄g
20941	cgttḡcc̄cḡc	cgtgc̄ct̄tt̄t	gcattccatca	acggaḡccaa	agcgt̄ct̄ct̄t	gtcgagaacg
21001	acttc̄cacc̄g	cgatgtc̄ḡct	gacactgt̄tt	ggatgac̄ḡtt	ggc̄ct̄cḡt̄cc	aaacc̄caḡtt
21061	ccgc̄ḡatt̄gc	ctḡct̄tḡḡcc	aactḡgt̄cc̄g	tctgat̄ct̄tc	tacc̄gc̄gat̄c	ttctgc̄acc̄g
21121	acact̄cḡacc	gatt̄t̄ct̄gat	tcatt̄cc̄at̄ct	tgacc̄gc̄act	ctgḡḡcc̄acc	gatgc̄ḡgt̄tt̄t
21181	cgtc̄gḡcḡca	aac̄gḡḡcaat	gaḡtt̄ḡḡtaa	gcḡacc̄cc̄caa	tac̄ḡac̄gc̄ac	gac̄aḡt̄gt̄ca
21241	aggt̄ḡgat̄gc	gac̄gt̄tḡḡcc	gaaḡtt̄cḡaa	gḡcḡḡcḡgḡt	cat̄gḡat̄ḡag	gtc̄gḡcat̄ag
21301	aagat̄gḡct̄c	caaat̄gḡcḡg	t̄cḡaātt̄t̄cc	gt̄t̄cḡtt̄t̄cc	gḡtḡgt̄ḡct̄c	gt̄t̄caḡcc̄ca
21361	atcḡgḡcḡaag	tcc̄gt̄tt̄gt̄g	cac̄ḡaāac̄gt̄	gcc̄ḡatt̄gt̄c	tḡcaaaāat̄c	caaḡtt̄tc̄ag
21421	attaḡcḡac̄g	cccc̄at̄gḡgḡ	aaac̄aāct̄ga	aaaḡḡaḡcaa	tct̄ḡct̄ct̄gḡ	aagḡaāaḡag
21481	tgḡac̄gt̄ct̄g	gacc̄acc̄ḡga	aaāacc̄cḡca	taḡc̄ct̄t̄c̄ct̄	acc̄gt̄tt̄c̄gc	ccc̄ac̄aaāac
21541	cgḡaḡcc̄ḡag	gt̄ct̄gt̄tt̄ca	cḡac̄ḡct̄acc	aac̄at̄cḡct̄c	gc̄aḡgḡcaat	caacc̄act̄cc
21601	agt̄c̄aḡtḡag	agḡt̄ḡct̄tt̄t	caatt̄tḡaca	tc̄gc̄cḡḡatt	gc̄att̄ct̄ḡag	ac̄gc̄gat̄c̄gc
21661	gaaac̄ḡcaac	gt̄ḡaāact̄cc	catt̄c̄ḡaḡcg	ac̄gḡgc̄aḡga	aaāact̄t̄c̄ct̄	cc̄gc̄cḡct̄tḡ
21721	taatt̄gt̄tac	ct̄cc̄gc̄gat̄g	tc̄at̄c̄ct̄tt̄g	gḡgt̄cḡtḡat	caat̄cc̄gt̄ga	aac̄ḡaāct̄tc̄
21781	ct̄ct̄tt̄c̄ct̄t̄	cgt̄caāagḡc	at̄cc̄at̄gḡgḡc	at̄c̄gt̄cat̄cc	cact̄cḡtt̄ct̄	gat̄ct̄t̄c̄ct̄c̄
21841	ac̄ct̄gc̄ct̄cḡ	tc̄at̄ct̄gḡcḡ	aḡc̄ct̄gc̄gat̄	gḡatt̄tḡaaa	tc̄gc̄ḡaḡtḡa	gt̄ac̄at̄cḡga
21901	cḡcaat̄ct̄ct̄	cc̄gāagḡcḡt̄	tc̄gc̄gḡcḡgḡc	ac̄gat̄caat̄g	cc̄at̄ct̄cc̄aḡ	tt̄cc̄at̄cc̄cḡ
21961	gaact̄ct̄t̄ca	caact̄ct̄gat̄	cḡcc̄ct̄gt̄tc̄	gt̄ḡct̄tt̄cc̄ḡ	acc̄ḡaḡat̄gḡ	gt̄tt̄t̄cḡat̄c̄
22021	gḡcat̄cḡḡca	cc̄acc̄gc̄cḡḡ	caḡtḡcḡtt̄ḡ	tt̄caac̄gḡca	tḡatt̄att̄t̄cc̄	cgc̄gḡtat̄gc̄
22081	att̄ct̄c̄aḡcḡ	tḡgt̄tḡḡct̄t̄	tḡt̄cḡtḡat̄ḡ	gḡcḡtt̄cḡtḡ	tc̄acc̄t̄cḡgt̄	caac̄gt̄tt̄t̄cc̄
22141	ac̄ac̄gc̄gt̄cc̄	tt̄ct̄t̄c̄ḡcḡa	tgḡaat̄ct̄cḡ	tt̄ḡatt̄ct̄tt̄t̄	gt̄ḡaḡtt̄cat̄	t̄ct̄cat̄c̄ct̄ḡ
22201	ct̄gat̄c̄aat̄ḡ	gagaac̄aāct̄	tc̄att̄gḡtḡḡ	caaḡgt̄tt̄ga	t̄ct̄tḡat̄ḡct̄	gat̄gt̄ac̄gc̄ḡ
22261	act̄t̄act̄tḡḡ	tḡtac̄at̄ḡct̄	gac̄ḡac̄gat̄ḡ	aaat̄cat̄ct̄ḡ	aḡtt̄gt̄cc̄cḡ	caac̄ḡac̄ḡaḡ
22321	caacc̄aḡaca	at̄gat̄gḡcḡa	agāaḡagḡat̄	gaḡt̄cccc̄ac̄	gc̄gḡccc̄cḡct̄	cḡcc̄aḡtt̄tḡ
22381	tt̄tt̄act̄ḡga	t̄ct̄cc̄gḡagḡ	ccc̄ḡct̄gt̄tḡ	gact̄tḡḡaac̄	gat̄gḡtt̄c̄ḡt̄	caāaḡacc̄at̄
22441	cat̄c̄gc̄gaac̄	aḡat̄ḡaāaga	aḡaāac̄ct̄gḡ	aac̄gḡct̄gḡḡ	gatt̄gt̄ct̄gt̄t̄	gacc̄aḡcac̄ḡ
22501	gḡaḡt̄cat̄cḡ	cc̄at̄gḡc̄ct̄ḡ	ct̄gḡac̄att̄ḡ	gt̄att̄gḡc̄ct̄	gc̄gaat̄gḡct̄	cgḡc̄aḡcḡgḡc̄
22561	cc̄gḡccaac̄ḡ	tt̄ḡagaat̄cc̄	at̄catac̄ḡaa	tt̄gt̄tc̄gḡac̄	aaac̄ct̄t̄c̄ga	agḡc̄ct̄gḡgḡc̄
22621	at̄ḡcc̄aḡcca	tḡtt̄c̄ḡt̄c̄ḡc̄	gḡt̄cat̄ct̄tt̄t̄	gc̄ct̄cḡat̄gḡ	caacc̄aḡcḡt̄	t̄c̄ct̄ḡac̄ac̄ḡ
22681	gt̄cat̄gt̄cca	tt̄c̄gc̄ḡac̄gc̄	tc̄gt̄gat̄gḡc̄	gact̄ac̄ḡac̄ḡ	at̄gc̄gḡtḡgḡc̄	caac̄gc̄c̄ct̄ḡ
22741	gḡcaḡcaaca	t̄ct̄tt̄ḡac̄at̄	tt̄ḡct̄t̄c̄ḡcḡ	ct̄c̄gḡgt̄t̄cc̄	ct̄tt̄gt̄t̄c̄ct̄	gt̄ac̄ac̄ḡct̄c̄
22801	at̄caac̄gḡcc̄	cc̄at̄t̄gc̄aat̄	gḡaḡccc̄ḡaḡ	at̄c̄gc̄gḡct̄c̄	aḡaḡcḡḡaga	act̄gc̄gt̄tt̄ḡ
22861	tt̄t̄ct̄ct̄t̄ca	t̄c̄ct̄ḡac̄gat̄	cat̄cḡgt̄tt̄t̄c̄	tt̄ḡatt̄t̄act̄	ac̄at̄cḡḡcaa	ac̄ḡaḡgc̄gt̄t̄
22921	gc̄gḡct̄gat̄ḡ	gaac̄caaḡta	cgt̄cḡaaat̄ḡ	aaac̄ḡagḡca	aaḡcḡtt̄tḡc̄	tt̄tḡct̄ḡac̄ḡ
22981	at̄gt̄ac̄gḡtc̄	tḡtt̄t̄gt̄gat̄	ct̄ac̄at̄c̄ct̄ḡ	ḡct̄cac̄ḡaaa	ac̄gat̄gt̄c̄ga	aḡtḡgt̄cc̄ac̄
23041	caḡat̄ct̄cc̄ḡ	at̄cac̄ct̄ḡca	aāc̄ct̄t̄c̄ct̄a	aaāat̄ḡct̄gc̄	caḡcḡat̄c̄gḡ	aḡcc̄att̄gt̄t̄
23101	taḡc̄aḡc̄ct̄ḡ	tt̄gat̄tt̄aḡt̄	c̄gt̄atac̄c̄ga	gt̄ḡacaac̄aa	tt̄aḡcc̄gat̄ḡ	gḡcḡtt̄aḡcc̄
23161	cc̄gḡtt̄gḡcḡ	t̄t̄ḡc̄ct̄aāc̄	gc̄cḡct̄taac̄	gc̄gḡtac̄gḡc̄	t̄c̄att̄aāat̄c̄	aāacc̄cc̄cḡt̄
23221	taḡccc̄ḡct̄c̄	gḡact̄gḡac̄ḡ	at̄cccc̄aāac̄	ct̄ḡaat̄cat̄c̄	aact̄cact̄tḡ	tt̄gt̄aḡact̄ḡ
23281	att̄gḡt̄cat̄ḡ	tt̄tt̄t̄c̄ḡcc̄ḡ	cgt̄tt̄ḡct̄t̄c̄	c̄ct̄gḡaat̄cḡ	tgḡcḡac̄gt̄ḡ	ac̄ḡaāat̄ḡga
23341	tc̄ac̄ct̄ac̄aḡ	aāaḡt̄cḡtt̄c̄	gaḡtt̄ḡact̄a	ct̄tḡḡaaḡcc̄	ac̄gt̄cc̄gt̄t̄c̄	tt̄ct̄t̄c̄ḡc̄ga

23461	ccgacgtgct	cgcgtcgctg	acaacgcact	gcattgattg	ccacggtccc	gaatcagctg
23521	aagcaaactc	gaggattgat	caactgacca	gcgatctcgc	cgatcgcgaa	aacgcactga
23581	aatggatcga	gattcgcaac	gcgatcaatc	tcggcgagat	gcctcccgc	ggcgaaccgc
23641	cacttcccgt	cgacatcatc	tcacaaacgt	ccgagtgggt	ttcaggcgag	ttgagagaag
23701	tggatcgatt	cgcgaactga	gcggacaac	aagtctgtct	gcgtcgattg	aaccgcatg
23761	agtacacgca	cacggtttcc	gactgtttgt	cgatgaagtt	cccaaccggc	gaaagtcac
23821	tcgatacatt	gccacccgat	ggaaccgcag	aaggtttcga	caaagtcagc	tcggcactga
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23941	cgattgtgga	cggfccaccg	gaatacccga	cggaaacaat	gcggctggag	tttgaggaaa
24001	tcgctgacag	tcatgcgatc	ggatatctcg	tcacacgtcg	gggcatgaat	ccggtccccg
24061	gtggactgca	attgatcgaa	ggcagcacgc	gatcttttgg	gatgcttcgt	taccgggtc
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24361	acacaaagct	gtccatgggt	cagcgtcccc	gcgaaaactt	catgagacga	atcaatgaag
24421	tgggtgaagc	cggcgacttc	accgagtcgc	ttcgctggc	cggctcgcaag	ctgcgcgagg
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24601	gtcacacgac	ggtcttggtc	cgcggcgaag	caggaaaccga	tgtcctggct	tacgctcgcg
24661	agatcctttt	gcgacttttg	ccgaccgcct	ggcgacgccc	ggtcgaagag	agcgaaatcg
24721	aaccgatctt	gggagtcatt	caatcggaac	tcgcaaacgg	cgaaacattc	cacgaagcca
24781	ttcgcgctcg	attggccgcc	acattgacgt	caccgaactt	cctctacctt	gcggaaggca
24841	ctgggaattg	cgccgacact	tccgtgctga	ccaaccacga	aatcgcgctg	cgaatgtcgt
24901	acttcccttg	gtcttccatg	ccagaccaag	agctctttcg	cgctgcccga	gacggcgaac
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25621	gtcgcaatct	gccggagatc	gacgccagcg	gccgactccc	caacggcaac	gaattcacag
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25921	caagacgctc	aaccgcggga	tgcttctgcg	tggtgccagc	acctgtttgg	cgctgccttg
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26161	caccgtgttg	tcgggaacct	cgctcagcca	cggcgggtgg	cacgatgggt	cctaccgctt
26221	tgcgacatcg	attgctcgcg	gcgaaaaaca	aaccatttcg	cctgaccaat	tcgtcccgga
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26581	caattccatt	cctaagttg	aaacgacgtt	gggcgcgaa	atggattggt	atgatcgccc
26641	caaaccacaa	cctaaccctg	atgggttttg	tgattacgaa	aaagccatcg	cgcccagggg
26701	caatgggaag	tttgtctacg	acacgtacgc	gaaattgatg	tacgacttga	tcgcccttgc
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26821	tgtgtaccca	gaatttggtg	tctccaaggg	ttatcacgaa	ctgacgcac	acggcaacga
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27121	gccgctttct	tctctatggc	aaaccatggt	ggaacggatg	ggagtgaacg	tggacgggtg
27181	gttccaagac	agcaccggaa	cgatcgggga	actcctcgca	tgattcgcc	gtgtatcaaa
27241	cgactgcacg	ccgcactcgt	gttggcggtg	acactgacag	tgcccatcca	agcacaaggaa
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27361	gaatatcgcc	gagggttttg	cggttcaggg	caacgtgac	gccaattcgc	actggctcac
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27481	aaaccattcg	agctgcaaac	aacggaagtc	accgtcgcgc	agtttcgcga	atttgtggaa
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27721	tcgagtggtg	tgcggaaca	ggaaacgacg	acgtatcgat	tgccaaccga	agccgaatgg
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27841	gcctacgttc	atgcgaacgt	cgccgatggg	gctctcgagg	ccgctcaacc	aaacacaacc
27901	cgctatcagc	gagcgggtcaa	actagaagct	gacgacggcg	atggcgtggt	cttcaccgcc



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38761	ċċggċttġct	acġggċċatġg	ċggaccattġg	acġatċaccġ	acġtċaatġt	ċċtġctġggġg
38821	ċgtċtġċgċa	tċgatċgċtt	tċċċtċċċg	tġggatttġg	aagċggċtċa	aacġgtġġctġ
38881	ċgacaacac	atċaacacċt	gċċaacċgac	agċactċttt	ċaccggaaca	ċaccġċgac
38941	ggtttċtġc	aattġgċgat	ċacġcaaatġ	gċċgaagċag	tċċgagġgt	ċacaactġċc
39001	gċċggaagtġ	atġċgagaca	aatġgċattġ	gtċggttċċg	gaggċgċċċ	gggagġtċac
39061	ċtttġċcaaa	tċġċgġactċ	gċtċgaaatġ	actċatġtga	tġgatċacċc	tġattċgġga
39121	tġgtatċtġ	ċggtċgġtat	gggtġċċgċg	tċgatċggċc	gtattġġtac	ċgaatċagtġ
39181	caaattċacċg	tċġċċċgċc	gattċċtġaa	actġċċgata	ċaacġgċatċ	acċaacġtċc
39241	ċtttċċgġgċ	agatċċċgċc	attġċaatċg	gċċgċgaagċ	ggacactċċg	ċċaatċgċaa
39301	ċaacagġttċ	gacaagaaga	aaacattċca	gġggacactġ	tċttġċacġt	ċgtġċatċag
39361	tġtgacġcca	gaccattġgg	gacġċagġcġ	acġttġċċga	tċgatċtġtt	tċċċtġagag
39421	acġċtċċċa	atċgttċtga	ċġċgaagċat	ċagġċċacġt	tġggttatġc	ċċgacatċc
39481	atġċċcattġ	aaatċgtġac	gġtċċġtġc	gaagċċacġa	tġgagċggac	gtċaaacġca
39541	aacġagtġtg	ċacġġatġaa	gtċġgċaagt	tċaacċaaga	ċgatċċġac	acċċċgċaag
39601	ċġgġagġtġ	tċtċgatġtg	ggċtċgagga	ċċtttċċgaa	aagttġacċt	attggċacċġ
39661	gattċgatċc	tċġċaggġca	ggċtċattċc	ggaccatċġg	tġgtġgċggg	tċċċtattċc
39721	gttttġgttġ	tċgaaccagġ	tġggatġgċg	acġatġtċga	gċgacġgġat	tġtgagatċ
39781	ċġcaaggagċ	ċtgċttġttċ	agċċaacaca	aactċatċġg	ċactċagċac	ggagċaactġ
39841	gacġacacċa	tċġċgatġga	gatċġċgċg	agaagagtġc	aggġċatċċg	ggagċaatġ
39901	ggċgaagtċa	tċġċċġċac	ċagċgtċagċ	gtċaacġtga	aagagċġtċg	ċgatċċagċ
39961	tġtgċċgttċ	tċċtċġċgċa	ċggttċċttġ	gttġċċaacġ	ċġċacacġt	ċċċġtġċac
40021	tġgggtġċga	tġagċċacac	ggċtċġtagġ	tġgatċġcag	actacċċgaa	gatġtċġċġ
40081	ggċgatċċt	acatċagċaa	ċgatċċġtat	gċċggtġgtt	ċġcatċtġċc	tġacatċacċ
40141	gtċgtġacċc	ċggtċtċttġ	tġatġatġac	acacċċċtċt	ċttċacġċċc	aaatċattġg
40201	ċċttġġcact	tċtttġtġċg	tċċġġatġc	ċaccatġġtġ	aaatċġgċġg	ċatġgtċċċt
40261	ggatċċatġg	ċacċċġġġg	aactġgttġg	gċagaagaag	gċgttġgtġt	gċacaacġag
40321	tġtttġgttċ	gċaacġggċa	atċtċaccac	gċġċacattċ	gċaaactġġt	ċagċagtġca
40381	acġtatċċtt	ċġġtāatġt	ċgatġagaac	atġgġtġaca	tġġġgċggċ	ggagċggċca
40441	gggċaggġtġ	gtġġgaatċg	aattċgaacc	ċttġċċgact	ċgatġacġaa	gactċġttta
40501	acġgaactġc	tāaaacagġt	actġċatġtċ	gġtġgtġaag	ċgaccġġtġc	ċtggatċgaa
40561	acċċtġgggag	ċġġacċġġg	aaacttġtġg	gatġġġtċg	acġacġgġaa	ċċġgatċċaa
40621	gtċgaactġc	aaccġgacċa	aaccacġgtġ	ċġttġġġgaa	tġgatttċtac	gggċacġġgċ
40681	ċcagttċatġ	acaacġgċtt	ċaatġċċaca	ċġgtċaatġg	tġaccġġġgċ	ċgtattġtġac
40741	gtġġtċġġt	gtġtġtġġc	gggġgaattġ	ċċtġtġtġġ	acġgagtġġt	ċaagġgaatċ
40801	gagttġatċa	tċċċaaacġg	ċttġġtġtċa	ċċtġtġġtġ	gttċaacġċc	ggagaccagċ
40861	ċċġġgġtġg	tġġġġgaaa	tġtġġagacc	agċaatċgag	tġgtġgatġt	gġtġġtagġc
40921	gġactġggġġ	tġġġġġġgċ	atċtċaaġga	acaatġgaaca	acttġttġġt	gggtġactċa
40981	acġttġġgat	actacġaaac	ċattġgtġgċ	ggggġggġtġ	ċaacġgġġata	ċġġtġggga
41041	gġgġagġġtġ	tċċataċaca	catġacċaac	acġġgaatċa	ċġacċċċga	aatċtġggag
41101	tġġġgttġc	ċggttġġċċt	tġggġgttċc	gġgatċġġcċ	gaggġagġġg	aggċċtġgggt
41161	ċtċċatġġtġ	gġggġġagġg	aatġatġtġcġ	gaaatġgġaat	tċċtċġġċċc	gttaacġġta
41221	tċactċatġc	ċċtċaaġagġ	aacġactġcġ	gġgtacġggga	tġaacġgtġg	agaaccagġc
41281	ċagċċagġgġ	gtċaaacact	ggġtġatċag	tċtċagġġga	ċggaacttċc	ċttġġġgacċ
41341	agċċaagaag	tġgatġcagġ	ċgatġġtġtġ	atċatġgaga	ċtċċġġġġg	ċggagġttac
41401	ggċaaagaac	tatġġagagġ	aacġtġġgaa	ċtċċtġgag	gċġgatċact	ċggacatċc
41461	tċtġtġttġt	tġgtġġact	ċgtġġċtċc	atċġgttċttġ	acatċġġtċt	ċagaatċċċc
41521	gttġtġatġc	gatċċtċtċt	ċtttġaacġt	gtāagtċaaa	agġtċċaat	gaatċtġġġc
41581	ċaacattġtġ	tġġġatġġg	ggatċaatċt	ċacacġactt	tġgatġacġt	tġgtġttġct

41701	āacaēccatt	tgēcgācgēc	gcacgcēgtē	gēccggāacg	gtcaggēgāg	cēcgcacgag
41761	aagtagcatc	ggcgtgaccc	aaggttgctc	cacggēgcag	ccccaggcat	catcgaatga
41821	acgactccaa	cgaattgatc	catccacggg	cgagatcgca	tgcacēcgcg	tgattggctg
41881	aaccgtcgct	ccacccgaga	cagccaccga	acgcaatgac	gcaaggētcg	gactcggctt
41941	gcgatgcctt	ggcagcacca	ccatttgatc	ctgगतagac	atcactgac	cgccatacaa
42001	gcccēttcga	gctggcacca	tcacatcagc	aatttcacgt	cccgacaaca	aatcccaaat
42061	cgētgētcgt	ccattgtgat	ccagcaacgt	aaagtaacgt	ccatcagtca	tctccgcata
42121	ggctgaggcc	tcgttgacgt	tttggctgtc	ggcaacccga	tgcagcacgg	tttctccgga
42181	actcatgtcg	accaactcaa	ccaattgagg	gtcatgcatc	tccttgggcag	cctccagggt
42241	cgctctcaac	tcttcggccg	catcagacgg	caccttggtc	tctcgattca	cctgcgtcac
42301	cgētcagcac	tgcgatccaa	gcgacgagat	cacggēttcca	atcgagcgtt	tttgattcc
42361	cāacaattcca	ccgtcgtgga	tgēcatagct	ctccacttga	ttttgcgact	tactgaccac
42421	caacacccga	ccttcggcgt	gaacgaccgc	gtttccaacg	gcttcgggtg	gtgttcgcca
42481	acgttcttcg	cccgagacgg	catccagaca	aatcagttcg	gttccttgaa	gcaagaacaa
42541	tcgatcgccc	aagacgggac	cgagaatcaa	ctgcgcttcg	ccattgtctg	cggtcgctga
42601	gaccatcatg	tttcgataga	tctggttgcc	gaacggggtc	gcggcacttc	ggcgtttagc
42661	gaccgggttg	ccgtcggctc	cgagtgttcg	cctccatcga	attgcgtctt	caccgttcgc
42721	cccgagtgtt	cggaacagg	cgattgcatc	cagttccgac	tgggttaata	acagacaaca
42781	cccaccgctg	tacgtcaact	cgētgccgag	cgatcgcat	cccgaaaaac	cttcgagggg
42841	gatcgagcga	tgaatgccat	acgggttaat	caacgccaac	gagttcatgt	tgēcactcat
42901	cgcatēccaa	ccgcgaagtt	gacgtcccat	caagtgaagtc	gactttgcgt	agcgtcgggtc
42961	attcatcatc	atgcccgtgg	accgaggcat	tctcatcgac	tgccattcca	aatcgacatc
43021	gcgaggccac	tgētcgccc	tgēcatattc	acgtcctcgg	ataggattgg	ctgcagtg
43081	gtcttcgatg	aaagtgtctg	ctccgaccgg	ttcgtatcgc	ctcaaacgtt	ggcccaaaag
43141	ctccccgacg	gccaatcgat	ctaagttcca	cgcttctttg	ctgtacagtt	tcgcaagcat
43201	caacaaacgc	tcattgtctca	atgattgcaa	tgētcgctct	gttgēcatct	tatcgcccca
43261	aatcaaacgt	tcggccaaca	gaccatcttc	catgagcaac	gcacggggcg	ccatgtcccg
43321	gcgcaaaccg	ttggētcgctg	ccacgacagg	tgaaaagtgt	tgcagcgtcc	gcactcagcg
43381	cgctccatct	atgēttcccc	gtgatgaaa	tagtgactcg	acctttccgg	tcactctaac
43441	caactcatcc	tcttgaggcag	tcgacaccaa	ttgtgccacg	cgtgcactga	tccaatcgctc
43501	aacgggtgaac	tgētcgtgccg	cattgggaaa	gaccgcgtcc	atgtcgcgat	tgagcgtcgg
43561	atgtcgcagc	accaattcgg	acaaatccag	cagcaactcc	aacgccttgg	gatgatcaat
43621	ggaatcagcc	gattgatcga	cggatccttt	gatttgcaaa	accaacaact	cggtcgcgtg
43681	ttcgggttga	tcaatcagct	tcataaaagc	ttccaaatcg	acactggagt	cgctcgggtt
43741	ttgacggaga	ctgcccagca	tcgēttccac	cgacaacatg	atcacttcat	cgttgctggg
43801	atccaaatcg	cgagcctttc	gaagcaactc	gagtgcctga	ggētcgctgtt	ctgctcgat
43861	caacaattcc	gcttttcgga	cgagagcaaa	gaagtētatcg	ggatcttgct	gcaacagagc
43921	atccacgcgt	ggētgcaaa	aacgctcgcc	ataggccacc	gcaaccatcg	tcgēggattg
43981	cgagatcaat	tcgcccgtcg	tcgēgatcaa	gttgcccaaa	gggaaacgca	cggttcgctg
44041	ctgcaaaacc	tcgcccatttt	gcaatgagat	ctcgatcagc	tcatccgtgg	tcgtgggcag
44101	atagtaacga	tccgttccaa	atacgcgcgg	gcccgagatc	cgttgccacg	gacgaaccaa
44161	agtcggtggc	tgggaccaaa	cttctgcattc	atcgtttaac	gaacacgctg	acacttcatc
44221	agcaccaacg	acgaaaaaca	agtcatcttt	gacaccggca	acgtaggcca	atcggatgcg
44281	gtttttcggg	gtgaaacgat	tgētcēcagt	caagacatcg	agaacttgca	atcgatcgca
44341	ttcaatcgga	gttaggacca	ccgaagtgc	ttttgcaatc	gccaacgaat	gtgtccagcg
44401	acgactgagt	tgattcgccg	acacgcgagt	gttgggacga	tagatgctgt	gaacaaactc
44461	ttgacttcgc	gggatttggg	ttccccaacg	aatcgttcga	tcaaccaaat	tgattgcgac
44521	cgtggcgccg	gctccggctcg	gacaaatcaa	caaccēgtca	tgataagtgtg	gcatggctcc
44581	ggcgacgcgg	ggaaccggat	cagaaccaat	cccgcgggac	tccaccgcga	ccaggacttg
44641	ttgccattga	acggagccgt	cggcgggac	caagcacaat	aaaacgactt	caccggcaat
44701	ctcggcaatc	acataaaggt	cacctcgaaa	cggaagcggc	ggcccacagga	aaaaggcttc
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44821	ttttacatcc	aacgcccaca	atgtgttcgc	caatgaagac	atgccacggc	tcgcaaaagg
44881	gctgaaccgc	tcgatctcaa	ttttgtctcaa	gtcgtcgatc	agaaagactc	ggcgtccatc
44941	gctcgaaatt	tgaccgaacg	gcacgtcgtt	ccagacacgc	tgaacgagga	tatcaaccgg
45001	gtcttcttcc	tcctccatcg	ggētcēgtcag	ttcgggēcgac	aaagcggttt	cggcggtagc
45061	aaaccatggg	tattggccaga	cgcgttttcc	ggētcēggaaa	tcaacaccca	acaaacgctg
45121	cgētgētcgc	atcaacaatt	gatcggccac	ctgcacacga	gtccaagagg	ggcggcgcaa
45181	ttgaccggta	gctttcagct	gctgtgtctt	ctcctgaatc	atccgttctt	ggcgaggcgt
45241	ggtggacgac	tccaccatcc	atcgcgggtt	gctcagtggc	atttgaccgg	agcctgaact
45301	gttgcgatcc	gcgctgccac	ccaacaaggg	ataattctcc	gccaacgctt	cagcggtgac
45361	taagtcggat	tcgctctcg	ctcggatgta	ttctttccaa	gcgacttcat	cggcttcgcc
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45481	cgcccagagca	cacgcgatgg	catgcaagat	caccacggac	tcaccaactt	gttcgacgat
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45601	ccattcacgc	accgccaaca	aaaccgaagc	cttgatccc	gcttcgggat	gaaacgtttc
45661	gcgtcgcacg	cgcētcgactg	ttttccaatc	tcgttttggc	ccggcttctt	ccagcagttt
45721	ttccgcccagg	ggaccgtagc	gaagctggta	gatttccaga	ccttggttcg	gaagctcacc
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45841	agcctccgct	tgatccgtct	cgtcctcaat	caattggcca	tcgēggēcca	acatgcctcg
45901	ttggtcactg	agaggtcgtat	cggctggtatc	atcatcatca	gccctggcaa	tcggataata
45961	atagtcctgc	atcatttcag	aggacgggtt	gtcaccggat	cgaagcaaca	ggtttcccaa
46021	gtgcacgacc	gcgtcgtctg	aacgtttctc	atcgatcgct	tcctccgcgt	cgcgaatgac
46081	ttgccgcatg	cttcgtgggtg	ggggaagaaa	ctccgcatcc	cccatctgca	tccgcgaatc
46141	aaatagccct	tgagcttgag	cgtttttcga	ttggagcgcac	atcgcgaaaa	acattgcggc



46261	attgḡcggtg	āaaḡtḡactā	ctcagaḡcāa	ttaaaaācāā	gctatḡgaac	āāacgḡactḡ
46321	cgcccgcgag	ggcacacgaa	atcgcgatct	cattgtatcg	cccccggtt	ctcaciaaacc
46381	agtgtgatct	tccgcccgaac	gggtggccga	aggaatcttt	cgccgcatta	gaaaaggctg
46441	gccggatccg	cccgaaccag	tttccgcagg	gccagcaatc	cgctgatcag	gcacatgagc
46501	gtcgtcagaa	ccagcacgga	cccggcgcg	gagaccgtca	atgccatcgg	caaacccggtc
46561	agcgattcga	gcattcgaāa	caacaacaaa	cgatcaaga	cgcggggaat	gaatcccaga
46621	accgacagat	acaccgattg	tgcaccacc	aacccgacga	agaatcgatt	ggggtatccc
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46741	tagcaaatga	tgattccaac	cgcgaatccc	atcaggggtc	caatcaagaa	gatcattcca
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47041	tcgggtcccca	atgtgaacga	accacaagt	tcgatcgatt	ggttcgacaa	ctcgattcgc
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47161	tcgaccagtg	cggtatctcg	ttgccgcagg	gcattctcgg	tttcgtccag	gccggcgata
47221	ttcaaccagg	gccgtggtga	atcgccctgc	cccgtggaat	aaagacttgc	gttggggacc
47281	gaaatcacgc	ggatcggtcg	cgatggactg	ccttcgactc	gcacccggtc	catggttcgc
47341	tcgatcaaca	acgcttgcat	gtccgtcacc	gccggatccg	ctttgactcg	gcggagcaaa
47401	gaacgcggga	acctttcgtc	cactggcaac	atgtaacgag	cagggctgat	cgcgaccaac
47461	tcgcaatcga	cgacctcgat	caatcgcacg	ggactatcga	gcaacgcgtt	gcgaaaaccg
47521	ttttgagtga	acatcagcac	ggcggcāaac	cccactccc	ccgcggccac	gcacaatctc
47581	gcgggattgc	cgatcagatt	tttccaggca	agtgggggtc	gtggactcat	cagcgaccct
47641	ctgtttcagc	gtcacgctga	aggttgāaaa	cgatctgcag	aaaatccttc	gcgtcgctca
47701	agtcacggta	aacgttgga	aaacgaatgt	aggcgacttc	gtccagcgct	gcgagtttcc
47761	gcaacacgac	ttcgccgatc	gttgcggtgg	ggatttccat	gtcaaattcg	gcgtaaattcg
47821	cttctttctat	tttctggacc	gtcttttcga	tctcgctcgt	ggtgacggca	cgtttcgaac
47881	acgctcgctc	gattccgcgt	ttgatttttt	cgcgatcaaa	cggtcgcggg	gtttcgtcac
47941	ttttgaccac	ccgaacattc	agtgcacga	tttgttccag	cggtggtāaaa	cgacgtcgac
48001	acgttttgca	cagccgcttt	cgccgaacca	cgtaaccagc	ctcggccgtc	cgcaatctt
48061	ggactttgtc	gttatcggaa	tgacagaacg	ggcaacgcac	ttgcagtcaa	attcaatgta
48121	gaaaattgac	ccgaaattca	aacgctccgc	cccgggtggac	tgggcaagca	tgattcacga
48181	gtcttttcgaa	ggtgtgctat	gatcgctccag	aacgtcttcg	gatgcgaggt	gtctggtccg
48241	acaatcacag	accgagccat	cacagtgtag	cgccccagaa	cgcggtgatt	tcggccaagt
48301	aggacaaccg	tttcggctca	gaacaattgt	ttggttctgc	gacgacttgc	caacattggc
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70021	tgagċtācaa	ċtċggtċtċġ	ċċgttġgtt	ġgaacġacca	tġttċtġatġ	gtċċċgġċċ
70081	ċgggacċgġg	ċġcagtġgt	ċtċċaaatċċ	tġċċgġatċġ	ttċċtacġgaa	gaacġtġgġa
70141	aaaacġgacġ	actċċtċgat	agċċaatāca	ċċaacċttċt	gċtċtċċgat	ggċċatġtċt
70201	ttġggttċac	gtċċgċgġgġ	ċagġgċgġtġ	ċċgaactġċġ	ċtġċatċgaa	ttċġtċacġgġ
70261	gtġaattġaa	atġgaagtāc	ċacagċġttċ	tġċġtċġċag	tċagġgactġ	atċġcagġċġ
70321	atġċaatġtt	ċtttċtċġga	gaacġċgġċċ	acttāġċċtċ	gċtġċaacġċ	agċatċgaag
70381	aacġċġgagt	gċtċtċġttċ	acċċāacāac	ċtċtċatġaa	ggċagactġċ	tactġtċġċ
70441	ċagċċatċċt	aaagaacġġg	atċġtġċttā	aagacġaaga	ċċgaatāġċġ	gtċttġtġact
70501	taccacċtċt	tċċatāatċā	aacċacttġg	agagġtttāc	ċaatċċatċġ	tċgacċġċga
70561	gtċacāaaatċ	ċċatċġtċġċ	ċagagċgatċ	attġċgagaa	acġtċċċagġ	ċtċċgġċācā
70621	gċġgtġacċġ	tġtġaatġt	gatġttġtċġ	aactġatġag	ċtċtċġċagt	tċċacċċtġā
70681	ċtċċatġtċā	gactġgtċāā	accġtġaaat	tċatċacċġā	acġtāacġac	ċaatġgġagtġ
70741	agttċġtċtġ	ċttċgaactċ	accagācāac	aatġtċacċġ	aactċatċġt	tċċġttġcācā
70801	attttġtġac	ċġgtġaaatt	ċactċġgagġ	gtċtġċtċāā	tċġttġttġā	tagċtċġċtġ
70861	taacċāagta	atġtġatġga	ċtċċatāatċā	aatġtċtġtċ	ċtġggġċagġ	agċattāagā
70921	gċċagċġtġā	attġaattġg	ċċagttċċċċ	gċċġċċtġgġ	acċċāagtġā	agtġgattġgġ
70981	tċtġactġgġċ	ċatċċċacċā	ċtċatċactġ	ċtttġttġgġ	gataċāāāāā	ċttġċċċġtġ
71041	gaaatċċċġā	ċataċattċċ	ttċāatāacā	tactġtġacġ	ċċċċagġċt	atċġtċagac
71101	gacċċtācċā	ċagtāāāācċ	atċagaattā	tġgaactġcā	ttġtċċtċġt	gacġacagġġ
71161	ċċatġaactġ	ttċgāgāāc	ċāāāacġttċ	gċāagācāāā	ċgaagācāācā	aacāāatāāā
71221	ācāāacġgtċ	gċċāāactġġ	gċtċttāġac	ttċtċāacċġ	tċttċatāġt	ċatċacċtġġ
71281	tġċattċact	tġagtācġċt	ttċgagċċac	aacċtġċtċġ	agatċagċġt	tttċċġċtāā
71341	acċtagttġt	ċġattġatċġ	ttċġgatċġt	tġċgagċġga	ċtġċċgġgat	ċċtġċġactġ
71401	ċċattċċttċ	acacġgġċċt	gċacatġcāā	gċgatċċāag	gattċċġgċā	tċacttċċāā
71461	ggactġċtċġ	taccagtāġc	ċċġtċġġtċ	acġggtċċċt	tġacġatāġā	tċċċċġtġġ
71521	ċaatċċtċċċ	gacagtċtċċċ	accacatġtċ	gċċtattġċċ	aagaagtċċt	ċagċatċġtt
71581	ggacċtċtċċ	agatċtċġċt	tġgċāacċċġ	ggāāagtċttt	tċacttġttċ	ċġttġatġac
71641	ċāacġgċāac	ċċċattġċċċ	aatċġċċttt	ċagāāagċāā	tāāāacċġġċ	ċġagagċtġā
71701	tġċċāattċċ	gċatċġtċċġ	gattċtttċġ	gtactċġġċġ	acċttċtċċag	ċġġċttġċtċ
71761	atattġċttġ	ttċġċagāag	ācāactġgtġ	ċtġāaggagċ	ċġgācāagċt	tttċagċġga
71821	ċġġtċacġġ	ttġċċacċċċ	ggacattġgċ	tġċċgāāac	ċċtċgacġċt	ċċtċċtċċac
71881	tċġtġgċāāā	gċġgaagċāā	tċċġgċāac	tċċttċāāāā	tċġtttċġtt	ċtāāacċttċ
71941	ttġaattġċġ	actāġġċtċ	ggċġgācāāā	tġċċatttġā	ċtċġċagtġt	ċċtċġtċċac
72001	atċatttċġā	ċġċgāāāact	ċċaatāġċċċ	atċtċġattġ	acċtġatāāā	gatċġacttċ
72061	aaaggtġgac	gċġtġttġat	ċċāagacċġċ	ttġāāāāagċ	atġāagtċġċ	ċġtġtċġat
72121	ċġċagatċā	atċġċagċġt	tċtġċāaggċ	gtaggċacċt	gċġġċġtċat	ċtġacatċac
72181	ċaatġatttċ	tttāġāāāat	ċġttġċtċag	ċtċġċċġtġt	gtċtġattċt	gtċtċġtċġ
72241	aactāactġċ	tċċċċgāacā	actġtċġat	tċġttġattġ	gaggtġġċtā	agtċaggāġā
72301	tġgtġggācċ	ggċaatċġat	tttċacċċċā	actċtċtġċċ	tċāacċtċċġ	tattċtċġac
72361	gatċttġgat	gċttċāactċ	ggċċgāāāc	ċttċġċtċċ	acċttċġtċt	ċġtġġġgġā
72421	tġgtttatġt	gċagċāagċā	atġċatċġgg	ċtċtttġtġg	atġgċċċċċġ	ċċċġtġċċċ
72481	atċacċtġac	tċatāċġtġā	acġċġttġgt	ċċattġtttċ	gtġgacacċġ	aatġgġcāac
72541	atācġāaggċ	ċagċċatttġ	ċċċāagācāc	ċacġġtācċt	ċċġatċġcā	attċacċġag
72601	ċġatċċtttċ	āaagċacċtā	gatċċġċċġg	ttċgaagtċġ	acċġgacġag	tċċattċġac
72661	tġċtagatċā	tċattġacċt	ċċacġagċat	ċagċġtġttċ	tċaatċċċat	ċċtċaatatt
72721	gċgatċġċġċ	ggatāacġgt	tġtċċċāāā	ċatġtāgttġ	ċġatġagċċġ	gċāacatċċā
72781	attċġtttġtġ	ċtġtċāāatċ	gċtċtġgġā	āacċāactċā	tċagġaatġā	actċaatċag
72841	ċtċtttġttt	ggġgāacġat	tċċacġġċat	gttġagatċġ	āacttċtċāā	atagatċttġ
72901	atġċċċgāġā	tāaggācāāā	tċāāāacċċt	ċcāagācāat	gtċttġatċċ	ċagċċttċġċ
72961	tġġċċġgac	ggċġggtāat	gtċċttġtġtċ	ttċċttġtat	gċċatċagġg	ċttċġgtċāā
73021	tċġattġgāġā	ttċtċġactġ	ċċtttġċatġ	acġċtċtġġċ	tċacċċāāag	gatttġċċġg
73081	tttċċġatċā	gagactġġċt	tċċagtċtċċ	gattġtttċt	tċċġgactġt	ttġċatċacġ
73141	gtċtttġġġt	gċċttċtġcā	ċġċċġatġt	tġtagċġġċġ	ttċġċċġtċt	ċċtttācċċċ
73201	tġċtttġġġġ	tċgācċacċt	ċtġatġċġat	tġċċġtġċtġ	actġġġtġag	tttġtġċċtt
73261	ċġġgāactċċ	tċtċtttċġt	ċċgāactttt	ċġgācġagċā	ċġtġġġġcāġ	ċġġġġġġat
73321	ċāactċttċt	ttġtġggāc	ċacāċċċċċ	gċagċācāac	aatġġġġatċ	ċcāāāacġag
73381	ċġacācċatċ	gtċċċġācġā	ċġtġġġatġ	acċāactġgt	ċġcāāagācġā	ttċċacttċċ
73441	tġāagtġttā	tċactċatċġ	tttġcāacċā	ċġġacċġat	tāāagġāāac	ċaatċġgāāā
73501	agtċttċġtt	ttċġggatċā	ċġgatttġgā	ċġtāacċtċġ	tttċtġatċċ	āaatġgāgā

73621	tāggfēcaāē	g̃gatacatcō	āgtgaŧtŧt̃g	gāctgačatc̃	cagāacgctg	agagčacgčē
73681	cttcgctcgaa	gtgctttcga	acaatcagat	gaaactcgtg	ctcttggtcg	tttccaagtg
73741	tgcccagatc	aaggccatct	cgcgaatgga	gcatgggtga	gtgaaaacta	atgggagcgt
73801	gcacgcgtcc	agttagctcg	acactttttt	cgatcacatc	tgactcacca	ttgaccagca
73861	agtgcagctt	cacttcgcct	tgaaaacggc	ctgggtctcg	agctcgacat	cgaagtŧtga
73921	cttggttgat	gacggtcggc	tgctgttctg	acaaagacgg	ctgtgagtcg	gaaggaaacga
73981	catttgattc	ccaatcgaat	ccgaccaaŧt	cggactcggc	accgacgact	gcaatatcgt
74041	cgtgctgttg	gctgtagatc	aaaagagtcg	actcaacgac	ctcaccgcga	tcgccggagt
74101	gaaaaacacc	cttggcaggc	acaaagagtt	cggtcctgac	cacgccggaa	accgtgagat
74161	cgatcacctc	tcgcgtttggg	tcgtttggtaa	tgacccgcgc	ggcttgttcg	tattgttcgg
74221	atttctgacc	tgtgttccac	gtcagtgŧga	cactcgŧttt	ttcgcccggt	gcgagtgttc
74281	ctttctgtgc	acttccaaca	gtgcatttgc	aggttgtctc	tgcaacgtca	atcgŧcagtg
74341	gtcccggccc	atgattccaa	atctcgaatg	cgtgcgaagc	ggttgŧgtgc	gggtcgacca
74401	gcccgaagtc	gtaccgggta	gatggcaaaa	ccgcttgccg	caatcccac	gactgggcct
74461	ctttctcgag	ggcctcttcg	cgtttgatca	acgaaacctt	cttctcgtat	tcagcgcgtt
74521	cggctcttcga	gactccatac	ggagcgtaa	tcacgatgg	cgccaatccc	gttgaaaggc
74581	cgccaaggac	agacggcagc	aggattccaa	caagcaaaaa	ctttcctgtg	atgctcatca
74641	cactctattc	ttcaaagaaa	aggagaacca	acgaaatgg	aagccaaaag	ctgcctatct
74701	ttgtccgcaa	acattcctga	actcgcgctc	attgggtggc	atgctttgcg	taaaacggcc
74761	acggcatcca	ttgaaagatg	ccgtggcttg	aatggacgga	actcgcaatg	attccacctt
74821	acgaaacgga	ttgttcaaac	ccgaaatgga	tcactcaaag	ttgcctttga	agtagccatc
74881	gttgatgaag	ataccggcga	agaatttgŧc	gcgaggcatt	tccaacttgt	cgtcggcgta
74941	gccaacacca	gagatctcag	cttcggtcaa	accggtgacg	gggaaaccag	gattcaagaa
75001	tccgtcggcg	ttgctgtcgg	cgaagacttc	aacgtgacca	tcgcccatca	gatatŧtga
75061	gctacctgcg	tgaacggcgt	accagtacacg	agtgtcttgc	atgtagatcc	cgttgccgcc
75121	tgggcccggŧt	ggagcagcac	atccagctgt	ggtgggttcg	ccacgctcac	aaccgatttg
75181	cgcgagcaga	gtttctgttg	taccaatcaa	gtccaagttt	cctgcagtcg	cattccagta
75241	ggcaggctccg	tcgttgaacg	cttcggtcaa	caacgatccg	ctggcgatgt	actcgacagc
75301	ttcggtttga	ttcaggggcag	ttccccagac	gcccgtttcca	tcgaaaccga	gagtgcgacc
75361	gagaatcgct	tcgtcgacat	cgccaggagc	tgccacagccg	atgaagccaa	cgttgctgct
75421	gctgatacgg	cttcgctcca	agtcggcgac	gctcattgga	ccagtcgata	cgcccaaacc
75481	cttgaatcca	ccgccggacc	aagtggŧcaa	ttcgccggŧg	ctcggatcag	cttcggtttt
75541	gaccattcca	cggaccaagt	gccaagaagc	ggcgtagttc	gtgttŧtaac	cgttggŧcaa
75601	aaagtacgca	gcgatcaact	cggcacgaac	agcggtttct	ggagccgttc	cgccaaaggŧt
75661	ggtggagctt	ccatcgcccg	aaacgccttg	ccaactcgct	ttgccacact	ggcagcact
75721	caggcgŧgcc	aacggtgcag	cgtccttggc	tcggtggŧg	tccttcccgt	acaagtcat
75781	gagtttttcc	gagcccttca	atgggttcga	agggŧccaac	gactcgttca	tgttgccgtc
75841	gccaacgŧtg	acgaggtcag	caacccaacc	gtattcgŧcc	atgcaaccat	cgcgtcgga
75901	gtccgacgct	ccactgcaga	acgttcccga	aggagcacga	ttgctgtatt	tgaacaggcc
75961	gatgccgatg	ttcttgaggŧ	tggcttggca	ctgagctgca	cgggcagctt	cgcgagcctt
76021	ggtgatggct	ggcaacaaca	aagŧtgcmaa	cacagcgatg	atcgcgatca	cgaccaacaa
76081	ctcgatcagg	gtgaaacctg	atŧttcgaaa	ttgcgacttc	atagtctttc	ctgagatttt
76141	agttgcogaa	agccgaacgg	cttcgacctt	gtgttaaaat	gagatgtggŧ	gagtttggŧg
76201	gcgttggaŧt	cacaagagct	gagacttgtt	ccagcaagct	tcagcttgtc	gagcgtcacc
76261	gactccttct	tcttcgggaa	gaaacctggŧ	ggagagactc	tctcccaagc	ttcaattcca
76321	ttgcgtgatt	gcaatcacgc	caatcgŧctt	ctttcagttg	ccgtgacgtg	tgccacaggc
76381	taaggcaaac	ctcctttcgg	tagagaagct	tctggttgcŧ	gtcagcctcc	gtcaacagat
76441	tcggtggctg	acaagacatt	catttgggtg	gtgttttaca	agaagccgat	agcaccaaca
76501	ggcttcacaa	cttgcatcca	caaacctttc	acaatcccta	ctcattcgct	tcgcattcac
76561	acagttgcga	aggcagcttt	cttgatgaat	tctcccgcga	taagactcac	aaaactcatc
76621	gaatcaaaac	cgaagggcccg	cgaŧcttcca	ccaagacttc	acacacattt	ctgagactga
76681	ttcatgcaaa	actgctctgt	cgaŧtcagtc	gatagcaaga	ttgcaaagcg	ggcatttcgc
76741	tggtcatcgc	ccgaacgtgc	cagŧgcgtta	gtgatagaga	ccaagcaatt	gcgggacgca
76801	tggcaaagga	gactgccgag	ccagcaaaaa	cgggactgtc	gggcgcaaca	ttcgatctat
76861	ttcgcggaŧc	gatagcgtcc	gactttagag	ttcttcaccc	ttgctattga	gcgagtagta
76921	gctcgctagt	tccaagtccg	cggcttcgac	ttcggcacŧg	gtccagaagt	tggcgŧccat
76981	tgggaatcca	ttgttaataa	aaccgtcacc	attggcgŧca	tacagtcccc	gaacacttcc
77041	gtctgccatc	aggacgtgac	aaacaccacc	atgggtgactc	gacatcccgc	ggtaatcttg
77101	tcgcgtgtcg	taattccaaa	ttcgcagcca	tctgagacg	ccttcgcgtg	gcgtgctggc
77161	ggcaatcacc	ggŧtcccttca	gataatttgg	atcggtttct	ttgtacagaa	ttggctctcc
77221	gatgatggga	gtcacatacg	gcgttccaga	tgtcaattca	ccgacgttgc	cggaaagctg
77281	gccaatcggc	gacgcatcac	acaaaagcgg	aactgtgctg	ctgggtgctt	tggcggtgtc
77341	caaaagacgc	gtcgtcaatg	gaccacgggt	cacgttgagc	gacttcagat	catttŧtgca
77401	ggcagaatct	ttgggctggg	gctgacgcgt	ttcgtccaaa	atcacttcac	tacggaccag
77461	gaaccacgac	gcggcgŧagt	tcgtgttŧga	accgtcttcc	agcattttgc	gttcgatata
77521	ttcgactcga	tccgcgggac	tcgcctcgat	caaccgagcc	acattcttga	taacggŧgcc
77581	catttcgŧtc	gtgtattcct	cggcgcccaa	ctgatcgacg	cagtcgttgg	tcgcccagtc
77641	ggcctcgŧtg	tcactgagca	ggŧgttccgat	ggcgctactc	gcctgagccg	atgtgctggŧt
77701	gcaccgcatt	tcgctgacca	acacgcgcg	tcgtaccaga	tccgccaccc	atcccacttc
77761	agtgggcaca	ccatcacgac	gaaagtcgaa	tgcacctgaa	caaaactcac	cattgggcgc
77821	gttcactgtc	cgtccagŧca	ggccgacacc	aaattgcttg	aggŧtŧttct	gacactgagc
77881	ggctcgagct	gcttcacgtg	ttctcgaaac	ggccgggagŧ	aacaacgctg	ccaacacacc
77941	gatgatcgaa	atcaccacca	acatctcaat	caacgtgaat	gcggcgŧtŧt	ttcgcggaŧc
78001	caatgggtgc	ttgagagatg	attcgaaatg	gcggcggttg	atggacatca	caatgaagac
78061	cgtggaggag	gatgagacga	gagcccaaag	agggattctc	gtgcagctcc	acttttcgca

78181	cġġctcġtċt	tċātēgcaaa	ċtaccēgacā	ccaaaacācā	aċaccatēgt	ċtēggaāgta
78241	tċccactggc	agcgaacċtē	agcatttggg	atēggēgaac	acagtēgggē	ċċtċccacc
78301	gataaaactt	tgactggagc	ccaccacgat	gttēgtēgca	atċċtēccca	cgēccēgtēg
78361	ċtēgcttēg	atēggactgg	ċtēgċtēggg	aacacagagc	gttēgtēgtac	ċtcaatēgat
78421	cēggaacēgē	aaagaacagē	cgēttēttaga	acaagēgagc	gacēgacēgg	gtēgaaacēta
78481	ċtēgctgaaa	ċactēgċtēē	agċctēggēca	aacacttēgē	tatēgaagtēca	ċccacēgttēgē
78541	caaaacēcaag	actēgēcatēca	atēggēttēcgā	agaaattēgēg	aatēgttēcaca	ċcaagagēcaā
78601	tēgagēċtēgg	acēgttēgēgē	aagēcgācaā	tēċcgāaatēg	acēgttēgātē	actēgātēgā
78661	atēċēgtēgēē	atēgacēgēgē	aaagēggēgē	cgēggātēgāā	gttēcagtēggē	atagēaccac
78721	ggēgēgaagāā	ċēgēcaāāāā	tēċtēcagēgt	tēgtēgēttēg	cagātēcgēgāā	ċtēċgttēggē
78781	aacēgtēgacēg	atēcaacāagē	agēggēcaagā	agēċēgēgēgē	gaagacēcatēg	cgēgttēccāā
78841	gtēċēctēactēg	ggāatēggēgā	ċacttēgēgtē	ggcactēgēċt	gacāāacēċēg	tēāagātēggē
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78961	aatēcaāāātē	cgēcagēċtē	acacēgtēcaā	gaagēttēcaāā	ggēggēgtēgātē	caacēgtēgag
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79141	actēgatēċgē	gacēgātēċēg	tēċtēggēċtē	ċcagēggēċēċt	ggēcagēcatēgā	tēggaatēacēg
79201	ggēcaagātēg	acagagēgāac	tactēacēcgā	agacēgēċtēċ	acāacēggēċg	cgētgāagāā
79261	gāāāagēttēcaā	cgēgtēātēgtē	cgēgtēgēcātē	ċtēggēgagac	tēcātēċtēċēē	cgētagēggēcag
79321	gtēċtēacēċtēg	gēggēggēgtēgātē	tēggacēggētac	tēgēttēgēac	tēgāgāātēca	aātēgtēgactē
79381	ċacēċtēgēċtē	tēgtēgācāāag	ċatēcgēċtēg	agēggēcagēgtē	gāāacēċtēggē	ċtēcgttēgēċtē
79441	ċtēgtēgēgēgtē	tēcagēcaāgē	ggēċtēgēcātē	ċtēgacēgāagē	tēcātēgātē	gēcaātēċtēgtē
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79621	ċcactēgēggē	aagēċcātēċtē	cgēgtēgātē	caāagēgtēgtē	cēgāacēgēgē	ċatēcgagātē
79681	ċēgttēcaāac	ċtēgēttēgtē	cēgātēttēcaā	ċēggētagāac	ggēttēcgācā	acēggagēcgēċtē
79741	tāagāacēgac	tēċtēgēttēē	ċcagēċtēcātē	atēcgāacēcag	ċēgēċēċcātē	ċtēċēgēċtēg
79801	āāāacēgttēgē	ċātēċgēgēgē	tēcagēggātēgē	ċtēggēgactēē	tēċtēgēcgāā	gātēċtēttēgtē
79861	gācācātēgtā	tēgācāācāc	caātēgātēgē	tēċgēgātēēē	aātēgtēċēċtē	tēċcggātēgē
79921	cēggaagātēg	tēgēgtēgēgē	acagēgtēttēg	ċtēgētaagēca	atēċgtēċtēca	aacēcātēgtē
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80041	cgātēgtēċgē	cēgagagēgtē	tēgācēcātē	tēggēcgāacē	tēcagagēċtē	tēgēggēgāāā
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80161	aacactēggēca	tātēċēċtēgātē	cagēcātēcgē	cgēgtēgēgacē	cācāagēċcātē	acāactēċcgā
80221	tēgēgāāacē	tēgtēċēċēēē	tēcātēċēgē	ggātēċcātē	tēċgtēcātēcā	atēcgagēċtē
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80341	agātēgātēē	ggātēgtāāac	ggacagēgtē	tēgāāāagēċtē	gāagēċtēttēcā	ċcāāātēgtēgac
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80461	atācācātēēē	gēātēttēcagātē	ggātēātēttēcgē	agēttēċēgtēgtē	aacacēċēēēcāā	cgēgtēgātēē
80521	caāagēttēcā	ggēgtēgātēggē	gēċēċtēgāac	gātēgēċcāac	atēċtēgēttēē	ggēcātēggēgē
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80641	agēċcagēcagē	caātēacēgēcā	gēċēċtēgēēē	ċcācācagēcā	ggēcgāagāāā	ċcāċtēċcātē
80701	ċacāāāagēgē	gtēcāāacēgēē	gātēttēgēgāā	cagēcāacacēē	ċēggēcgēcēcā	ggēcācagēcāā
80761	ċcēggēgtēgātē	ċēēēcgētagē	acēgēgagēcagē	ggēcāāacēgēgē	ggētagēcātēēē	agagēcagagē
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80881	ggēcgātēcāgē	aacāagagēggē	tēċtēggacēgac	ċacēgtēgāac	ċēgāāagēċēċtē	ggēcācāagēgtē
80941	tēcagēttēēēgē	tāātēgātēēē	caagātēcācāā	atēcgāggēcā	gāācācāācēg	tāācācēcagē
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81061	tēggēcātēēcā	cgēgtēgēgēgē	agāacēċēttēgē	ċēgēcātēēēēē	cgacēgātēēgē	cgētgāāāagē
81121	cgēgātēēēēē	agēcātēcagātē	gāgēggēēēgēgē	ċcātēēēgāggē	acāagēcācācā	gātēcātēgāāā
81181	acēcātēgātēttē	ċcātēēēgēēēē	āāātēgātēāā	tāgēgēgēgāac	agēggēcāāacēg	agāacēgēgēgē
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81301	tēttēggātēgē	caāgēcātēēē	gēcācēcagēēē	tēggēttēēcāā	ggēcgāagēēgē	agēggēcācēgēgē
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86821	gcggatggcc	agcgaaagct	acggcttcat	ggcgccgatc	aaagccgccc	tggaaatcgtc
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86941	ggctgggctg	ctgaaaacga	gtgcttcggc	ggggatccct	ggttacgtcg	attcctacct
87001	gtacgcagaa	aaagtcaccc	cacgcgggga	agcagtttcc	acgaacgagg	tcgcgtcaac
87061	ggcagccttt	ttactgtcgt	cacgcagcag	tggaaatcaca	gcccgaatcga	tcgtgggtcga
87121	tgcggcgatg	tccatcaact	attttgatgc	cgacgtagtc	ggagcggtca	ccaacgcate
87181	ggctcgactga	aaccgggttc	ccaagctgag	ttcgccact	caccgacaac	acacatccat

87301	cĕtĕtcacgc	gaagacġcċa	agatċāġtgt	ċtacgatċac	ggactgctgt	acġġġcġacgg
87361	cgtgttcgaa	gggatgcgga	tċtactcggg	caaagtgttc	gcactcgaag	accacatgac
87421	acggctċtac	gaaagcgċtc	gtgcgatċat	gċtggacatt	cccatcgcaa	tċgatgċttt
87481	gacgactgca	gtgaacgaaa	ccgttgcaaa	aaatggtttg	acagaaggct	acattcġtt
87541	ggtcgtcacc	cgtggtgga	accaattggg	gċtcaaccġg	ttċtċgtgtg	aagatcccca
87601	agtġatċatċ	atcgcggata	cgatċtċgtt	gtaccċtgag	aagtċtċaca	ccgaaggttt
87661	ggaactgatċ	accgcġtċga	cgatċġcġaa	ccatċċġċċ	gcġtċagċċ	ccġġġtġaa
87721	gtċgttgaaċ	tacċtċaaċa	acatċatġġċ	gaagatċġaa	ġċċatċġġġ	ccġġġtġċat
87781	tgaagcġgtg	atġċtġaaċa	ċċaaaggġga	agttġċġġag	tġċacċġġġ	acaacatttt
87841	ċatċġtċċġt	ggġġġċġġt	tġatċacċċċ	accaatċġat	ġċagġaatċċ	ttġaaggġat
87901	ċacġġġtaac	accġtġattġ	atċtċġġtċg	ċġaaaatġġġ	atċġaagtġġ	ċġagġaagċ
87961	ċatġacċċġt	ċacġacatċt	ttġtċġġġa	tġaatġċttċ	ċtaaccġġġa	gtġġġġġġa
88021	agtċatċċċċ	ġġġtċaaac	tġgatġġġġġ	agttċattġġċ	gatġġġaaac	ccġġġċċaat
88081	gactċaaaag	ċtċaacġġġ	ċċttċġtġċ	atttġtġġġt	ċġttagtġt	tġġġġġagġt
88141	ċġtagġġgaa	gtċġġġaaġa	ċtttċġġġtġ	ġagċċċaatċ	ġċġġaaactċ	ttġġġġagġt
88201	ċġġtċacatt	ttċtġtġġġt	actttġġġtċ	attġġġacġġ	aaacactċġġ	ttċġtttttaa
88261	gaacġagaga	gttċġġġaaa	ġaacċtċċċa	actatċtġġċ	tċaaacaaċtċ	ġġagġttġġġ
88321	ataacġaggġ	atċagġċatċ	ġġtatagat	ataacatġġa	aatċċatċġa	ċġġġġġaaġ
88381	ċċċtttċġt	tġġġġttġċ	ġagġgatġta	ċtċġġaaċa	tċttċġattġ	ċġaaactċtċ
88441	ġċattċtġat	tġġġġġagġa	ċatġatġġta	agġġtġġġċ	tġaaactġġa	aaccġattċġ
88501	ċttċaaġċaa	ġagttċċaat	ċċtttċġaaċ	ġġċttċatċ	ġġġagacġtt	ġġtċagġact
88561	ttċactttaat	ċġġġġġġa	acagatġġġċ	gtġġtċtġġċ	atċaaġġġa	aaatġġġġġa
88621	ġġġaaċtġġ	taacġaaċa	ttġġatġġġċ	ġagġactġġa	ġġaaċttġt	acaagaaġġ
88681	ġġġtċċaaċ	ċaacġtġttċ	ġacġatġttċ	aatġġġġatċ	gtċġagġġa	ċċġagġaaġ
88741	ċċġġġatag	gactċġġat	ċaagġġttt	ġgatġġtġt	ttċtġtċtġġ	ġtċċatċċa
88801	aaaatċċat	ċacċċġġġ	ġġagġġaaċ	gtġġttġġġċ	ġġġagġaaġ	gtagġġaaġ
88861	tġġġaaġac	tttġġġġġġ	ċċċġaaġġċ	ġġaaactċtt	ġġġagġttċċ	ġġtġġġġġġ
88921	ġagġttċġġ	tacġġġġġaa	tċċtċġġġċ	tġġtġaaġaaċ	ġġġtġġġġa	gatġġttġag
88981	gttġġġġġġ	ttttġacġġa	gatċċċttt	ġġġacġġġa	gactġacttt	ġġġactġac
89041	ġġagġtġaaa	acġtġacġġġ	agġacġaaċ	gtċċtċġġtċ	aaacġġacġt	ġġacġtġatċ
89101	ġacaaacġġċ	agġġacttġġ	tċġġġġġġt	ċaagtġaatċ	gattġġġttt	gatġġtġġġ
89161	ċaatġtġtċċ	attġġġtġag	ġġtġatġġa	ċtċaatttġġ	ċaaatġġatt	ġġtġtġġġġ
89221	ċċatġġtċċ	aaatġġġġċċ	gtacġtġacġ	gataġġttġa	tġġaatġġġa	tġġtġtġġat
89281	ttġġġġtċċ	gtġġġġġaat	ċatċċġactt	ġġġatġattġ	gtġġtċċaat	ċtġġtċċċċa
89341	atġġtġġacġ	agagġtġġġa	ċacġtġġac	aatġġġġaaċ	gttaccacċċ	ġġġacttġġ
89401	ġġtġtġtġġ	attġtġtġtċ	atġtttġttt	tġġġġacġġ	tġatċċġġt	ġġtactttġġ
89461	aatġtġtġacġ	tġġacġatġġ	atġtatttġġ	ġgatġaaġaa	ġtġacġġatt	tġtttġtġtġġ
89521	ċġacċċttġ	ġġġġġġġaa	tġġtġġġġaa	ġaagtatġġġ	ġagttġġtġġ	ġġġaaġaaġa
89581	ċatġġtagġġ	ġaagġġaaġac	tġġttġġġġġ	attġatġġġġġ	agttġtġġġġ	ttġġġtġġat
89641	ċġtġtġġġac	ġġġġġġġġġ	ġaacġġġġaa	ġaccacġġtġ	ġtġġġġġa	tġġġtġġaġa
89701	ġġaġaġacġ	ġagġtġatġa	ċtġġġaatġġ	ċatġacġacġ	ġġtġtġaaġġ	acġtġġġġa
89761	agtġtġġġġ	aaagġacġġġ	acġġġtġtġ	ġġġġġġġac	ċġaagġġġac	tġġttttġat
89821	tġatġagatt	ċatġġattġa	acaaatġtġa	ġġaagacġġa	ġtġtġġġġġ	atġtġġaatġ
89881	ġġġġatġatġ	tġtġtġatġġ	gtġġġġaaġac	ġagġaatġġa	tacttġġġġġ	tġaatġġġġġ
89941	ġtġatġagġt	ġġaagġġaat	tġttġġġġtt	agaacġtġtt	tġġtġġġaaġ	acatġġġġag
90001	ċġtġtġġaaa	ġġġġġatġa	ċġacġġġaġa	atġtġġġġtġ	ġġaaatġġaġa	atġtġacġat
90061	ġġacġaaġac	ġġatġġġatġ	atġtġtġatġ	tġtġtġġat	ġġagacġtġġ	ġġaagġtġġ
90121	ġacġġacġtġ	ġaagtġġġag	tġġacagġġa	tġġaatġġa	aaagġatġġa	tġacġġġaġa
90181	ġġatġttġġġ	ġaatġġatġa	ċġatġġġat	ġġtġġttac	gatġġġġġġ	ġġatġatġa
90241	ġtatġatttġ	ġġġġġġġac	tġatġaaġag	ġattġġagġġ	agġatġtġġ	acġġtġġtt
90301	gtactġġtġġ	ġġġġġatġġ	tġġagġġġġġ	tġaagacatt	ġġttġġttt	ġġġġġat
90361	ġgtġattttġ	ġġġġġagġġ	acattġġġaa	acġġacġġġ	ġagġġttġa	tġatġġġġt
90421	ġacġġġatġ	ġaagttġġġ	agatġatġġġ	ġġtġġġaa	ġtġġactġa	ġtġaaġġġa
90481	aaġġtġġġġ	tacġtġġġġ	ttġtġġġġaa	ġagġaaġġġġ	acġacttġġġ	ġgatġġġġġ
90541	ġġġġġtġġġ	ġacġttġġag	atġġġġġt	ġattġġġtġ	ċġġaagatġġ	ttġtġtġġġġ
90601	acactġacġġ	ġġġġġġaaġ	aaġttġġtġa	tġġġacġġt	tacaaġtġġġ	ġġġaaġac
90661	ġagġġagġġġ	gtġġġġaaġġ	tġġattactt	ġġġġtġġac	ġġġġtact	acaaacġġt
90721	ġagġġagġa	ttġġaatġaġ	aaġtġġġtġ	ġġġtġġġaa	aaaattġġġġ	atġattġagġ
90781	ġagagagacġ	ġagtġaatġa	ġatġġtġac	tġtġġagġġ	ġġaaagġacġ	gtaaġġaat
90841	gttġtattġġ	atġtġttġtġ	ġaaġacttġġ	tġagġġattġ	actacagġġa	atġġagġtġa
90901	gtġatġtġtġ	ġcagġtġġtġ	ġtġġaaattġ	ġġagġagac	ġġġactaa	aacġġattġġ
90961	tġacġatġġġ	tġagġtġġat	ttġġġġaaġ	ttġttġattġ	ġġaaatagaa	gtġacġattġ
91021	acġġġagġtt	ġatġġagġtġ	ġġġatġtġġ	atttġġġtġ	ġgttġataac	gtġġaaġacġ
91081	ġatttġġġġġ	tġagttġġat	ġaattġġatġ	gtġġġaaġtġ	agġagacġġa	ttġaaagacġ
91141	agtġtttġtġ	acġtġġġġa	ġġġġtġġtġ	ġġtġġaaġġ	agġttaaattġ	aaġġġaaġag
91201	gttttġġaġa	acġġġtġġa	aatġtġġġġġ	agaaaattġġ	atġġġġġġa	ġtttġġġtġ
91261	ttġatġġatġ	acġġġġaaġa	acagġaaġġa	aacġacġġġa	aaacġġtatġ	ġaacġġagtt
91321	ġġġaaġagac	ġtttġġġġt	ġġaaacactġ	ġġaaactġġ	ġġaaacġaaġa	ttttġtttġġ
91381	agattġaaac	ġġġġaaġġt	ġtġtġactġ	aacatġġaaġ	ttġattġġġa	ġgatġġaaġ
91441	ġttġtġġġa	tactġġġġġ	ġgatġttttġ	aagattġtġġ	acġacġaaġa	aagagtġtġġ
91501	aaaagġġġġ	ġaccġaaġġ	ġġatġġaaġ	ġactttġġġa	ġtatagtġat	ġġatġġagġ
91561	ġġatġġġġġ	tttġtġġtġġ	ġcagġtġtġġ	atġaaagġtġ	ttġġġataa	tttttġġacġ
91621	attġtġġġġ	ġġtġaaġtġ	ġġtġġtġagġ	ġtġacttġġa	ġġtġtġtġt	ġġatġġatġġ
91681	aaacttġtġa	tġġaaactt	ġġtagġtġġ	ġtġġġaaġa	tġġaaacġac	ġaacġtġtġ
91741	ġġttġġaaġa	ġtġġġġġġġ	ġtaagaaġtġ	tġtġtġaaġ	agatġġġtt	ġtġatġtġġ

91861	gttttccgttg	gcctcgggtga	tgaatgttct	catcāaatc	fgāācgcga	ctgtcgcctc
91921	gctgatattga	aaacttgggc	cggcgatttg	gcggggccatg	tccaccaatc	cccccatcgc
91981	atcggactcg	ccggcgattg	cctcacctga	ctcgacaaat	tcttccagga	tcatcgcgcg
92041	aaccgcgcgag	gcttcttcaa	catgtttcgaa	ttgcagtaac	gcgtcttttcg	cttgccccat
92101	caccatcaag	gttgctgcgt	cgggagagga	acttgccttg	agcaatcgat	cgatttgaga
92161	aaccactcga	ctgggcgcat	ctgactttcc	tcttcgcagg	tcttcgatcg	cgaaaccgat
92221	caacacaagc	tggctgtctg	agcggacttc	cggatcggaa	tcttcttgaa	gcgactccgc
92281	caatagtgtg	aaactctcag	ccgctttcag	atcccccaaa	gacgccaagt	gtgaaagtga
92341	ttgcagctca	cctcggcggc	cgatcgcctt	ctccttctcg	gttgcatccg	cggtgttcgat
92401	caagcgacgc	gaagcctcac	gtttccacgt	ggcgatgcgt	tttagctcgc	tgaagcgggt
92461	ggcactatct	tcgatgcggg	actgaccgct	tgtgatcatc	cgcactctga	tatctgcttc
92521	ggagagaac	gtccggagct	gctcgggctt	caaatcattt	gcgagctgct	tctcgcgacc
92581	atccaactga	gaagcaacgc	tctgaggcac	gtcaatcacg	gctgggtcat	cgacgactgg
92641	ctgcgcagca	acctcgccat	tctgattatt	actggtggcc	ggtgactcgg	gcgttgaagc
92701	agcgttgcta	tccccgacca	gcaatagatc	gtcgtcggac	gtctggtccg	tctcctcggg
92761	ctgaccatcg	ttggtctcca	aagatggagc	ccccgacgca	ggatccgtcg	actcagcaga
92821	aggctggcga	gtgcagcctc	caacaatttg	ggtcaacaag	atcgcaaaga	cgcactgtcc
92881	gatgggtttc	ggcaacgtgc	ccatcacgac	ggcaatttga	gcttgaatca	tccaatgaca
92941	tccctgaaga	acgaaagcca	ctattctact	ggccaacggg	ccagttcgaa	taccgttcgt
93001	tcaattctgg	tccgattgga	tgaccgacat	tctgagatct	gacaaaggca	tttccgggtca
93061	cgtccgttga	tacgactcgg	tagacgctcg	aaataaacgc	caccaattga	atcaggaact
93121	gactgccgcg	ttatgccggg	gaccggttcg	gtgcagacgc	caacttggcg	aacctgcaca
93181	aatcatcatc	tcaggcagcg	gtgtgctcag	ccgacagagc	atcgagcaag	tcggcggaagc
93241	gatcatcggc	ttcgcgacga	cgacgcagac	gttctgcgac	gctccagctg	ctgcggatct
93301	tcatgacacg	gcgagtgatc	tcagcgtcgg	atggtgctgt	ctcattctgc	gatgcagttg
93361	agatcatcga	gacgttttct	agcgtatggc	tggtttcggg	caacattgcg	attcttctctg
93421	aaacggggct	ttcataaggc	tccgtaccac	gttgacgccc	gtaccgattt	ggatgcctcc
93481	atccgaggca	ttggcgtctg	gatttggtgt	aatgcaacca	gggtgccaaa	actccgaaaa
93541	ccagaaaaaa	cgttccaact	gtttccaact	caccggagca	aaccatgcgt	ttcgcagaga
93601	aatcgttggg	aaaaagagcc	aaatgagtct	ccgcttgaat	ccattcgttt	tttggcggct
93661	gataaatcag	cgatcagagg	cgttggtcga	acagacgtct	ttttcaaaac	cttgtaaatac
93721	ttgccatgtc	cggtcgggaa	tccgcatcag	cgagaccgat	gctggttcgc	caaacgctga
93781	aaacagcgtt	cgcagacggt	ccatcaacaa	ttggcgcccc	tccgcggatg	aaccacggcc
93841	gtgtaagtca	acgtactgaa	tggcctgacc	gttgctcgtg	acggtgccat	cgatttgcca
93901	gctttgcgac	tgatttgccc	aagtaaacga	accatcccat	tcāaagaaca	gtccttcag
93961	tgcctcgaat	cggcctgcga	cgttctccat	tgagacgtca	aatgcccccc	gatcaggtcc
94021	gtaaacgtaa	gtctgaaacg	tāaaagcagc	agtcatcgga	tagaaaatcg	ccaattgagt
94081	tgggaatggg	tctāaaacgc	gacacttctg	atttgcctagc	aaaacagggc	gttttcgcaac
94141	ctgaaccctt	ctaacaagcg	accaccaaaa	gattttttcac	tgtttgtcaa	cccggatttc
94201	cttgaccgaa	ccgttttttg	tcctagagtt	gttggacca	ggatctctgt	ccgtactccc
94261	tcccaaac	tgtccactat	tctcgtttga	ctaggcagtt	gttactagga	ggcaggcgcc
94321	cgcāaaagg	aatgagccat	tgttggtact	tcgcgaaaga	aaaacgaaag	cattgtcatc
94381	acaaacgata	tcaaaatcgt	tgtggtggaa	atccgtggag	acaaggtccg	cctcggcggtg
94441	gaagctcctc	gcgaagtgcc	agttcatcgt	cgtgaggtct	acgacgcgat	ccagcgggaat
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104521	ċċċtċċgtac	cċċgacċċtċ	acċgatċgt	ċtggaactg	cacċacċċg	tċtċggaaga
104581	gaatċċggċg	gacċċggaac	agaatgatgċ	cċgagaatgtg	tċagċċgtċg	aagaggagga
104641	agċtċtatga	ċtċċtaaaaa	ċċtcaacċta	atgggċatċt	tċċgagcact	tgtċċggggc
104701	agċgtċċatt	ċċcattċacc	tċtċċċċċga	ċċatċgtċċg	gggagaggtc	ggacċċggċg
104761	ttcagċċċtċ	gtċċgggtga	gggggċggat	cacatggċċg	tċgaaatċċg	tatgċcag
104821	aacċċċċcat	gtcagċċgga	cċċċċċċtca	ċċcagċcaac	gċċtgaagg	cgtċċċċgac
104881	ċtċtċċċċca	atgaaattgg	gggagaggtg	acaactċċgt	tċacċgtċċg	tgaacagac
104941	caaactċċċc	agcaatċċac	ċċċtċtaacc	ttċtċtċcaca	aacċattċċg	ċcacċgtċgt
105001	tggatttttċg	ċċċċgttgat	tgtċttgatg	ggċggggċċg	cgtttgtċta	acċaggttac
105061	tggggacċgtc	gcaacċgatc	gċtċċċċċc	gacċċgaacg	gtgtċċcaac	atgggaagtċ
105121	gatċċacċgat	tċċcacaaga	cagċttċcag	ttċċgtċgaa	tċgaatacga	ttċċtaċċg
105181	gtċċgagċac	gaggtggċċg	aggċtċgtċg	acċgactatc	cċgacagċga	tċtċaacttċ
105241	tċacttċċgtt	tċcagċcaact	gacċgtċactg	aagggtcaatc	ċtgatċċċgt	gggtatċtċg
105301	ċtgacċgatg	atgaattgtt	cċactacċca	ttċatċtaca	tċatċgaacc	cċggggċċċt
105361	gtċtċtttċcag	aagaagaggt	gaaagcactċ	cċgaagtatt	gċċtcaacċg	cċgttċċta
105421	atgggtggatg	atċtċtċggg	cċactċċcag	tacgaaaaca	tċċggagċga	actcaaacċg

105541	ĕaċgacĉtĉā	aagāāāaacc	tcagġtĉĉcc	gcgatĉāact	ĉġĉĉagacg	ĉĉgcgĉġac
105601	ggĉagtgĉg	gtĉĉgtggga	atggĉgĉgt	gacggaagĉg	acaccagtgĉ	tcĉtĉactac
105661	ĉgagĉĉatĉa	ĉĉgatgacga	agaccgĉatĉ	atggĉtttĉa	tttgĉĉacaa	ĉaccgacĉtg
105721	ggĉgatggĉt	gggaacgaga	aggĉgaagac	ĉaatggĉact	tcgatgagĉt	ĉtĉĉgtĉaag
105781	aaagĉttĉt	ĉgatgggaat	ĉaĉatĉĉtg	actĉatgĉga	tgaccĉactg	aatĉatĉĉt
105841	tgĉatĉaacc	atĉgacggĉt	ĉĉgacĉtĉĉ	tcĉaaccĉga	ttgĉactĉa	tgacaaĉgga
105901	taccatgacc	ĉacgaagacg	aagĉĉĉaagĉ	ggĉggagĉaa	attĉĉĉgacg	gacgagaacg
105961	aatĉĉttĉaa	gaattgĉtĉa	aggĉĉatĉat	ĉggĉĉaagaa	gaagĉĉatĉg	agĉagĉtgĉt
106021	gatĉĉĉttg	tttgĉĉggĉg	gtĉattgĉtt	gatĉacĉggĉ	gĉaccaggaĉ	tgĉĉāāāāac
106081	attgĉtgĉtĉ	agĉagĉĉtĉg	ĉgāāāatĉt	tcattĉgaac	ttĉĉagĉgga	ttĉagĉttĉac
106141	ĉĉĉĉgattĉg	atgĉĉggĉgĉ	acatĉacĉgg	aacagaāatĉ	ĉtggaĉĉat	ĉggĉĉgacgĉ
106201	tcaccgacaa	ĉtgĉāattĉg	tcāāaggacc	aatĉttĉĉĉ	aacgtgatĉt	tgĉĉĉgatga
106261	aatĉāāĉĉgĉ	acaccgĉĉĉ	agacgĉāagĉ	ĉĉĉgttgĉtĉ	gaagĉgatgĉ	aagaacacĉa
106321	ggĉĉacĉĉgĉ	ggaggĉĉāac	gattĉgaact	ggāagaacĉg	ttĉtttgĉtt	tgĉĉĉacgĉa
106381	āaatĉĉgatĉ	gāaatggāag	gĉactĉacĉĉ	gĉtgĉĉĉgāā	gĉĉĉāactĉg	atĉĉttĉĉt
106441	tttĉāatgĉg	ĉtgatĉĉact	actĉtgĉĉĉ	ĉāāagacgāā	ĉtgĉĉggĉtgĉ	tcĉtgĉāāac
106501	gacatĉgacg	aagĉĉĉgaac	ĉgatĉĉagĉĉ	aatĉttĉĉĉ	ggĉgaagacg	tcĉgtĉĉĉt
106561	tcacgĉĉĉgĉ	gtĉĉgacgĉg	ttĉĉgatĉtgĉ	ggāatĉgatĉ	gĉĉĉĉatāĉg	ĉĉgtĉĉĉgtĉ
106621	ggĉĉĉĉĉĉgĉ	actĉĉĉĉĉĉgĉ	gacgagatgg	aacĉĉĉgĉac	ttĉgtĉāacĉ	aatāĉĉĉttĉ
106681	ĉtgĉĉĉgtĉĉa	ggĉĉttĉĉggĉ	ĉĉgtĉāāac	attggĉgtĉtĉ	ggĉgĉāagĉ	ĉgagagĉttt
106741	gĉtĉāāĉĉgĉ	ĉacgĉtĉatg	tcĉgaacgga	agacatĉĉag	gĉtĉtĉĉĉĉ	acĉĉgacgĉt
106801	ĉĉgacacĉga	gtĉttgĉtga	gĉtatĉgagĉ	ĉgaggĉĉgāā	ggĉttĉāacg	ttgagaacĉt
106861	ggĉĉacacga	ĉttĉttĉāāg	āaatĉĉĉĉac	ggāagĉtĉga	attgagĉtgĉ	ttĉĉāacgtĉ
106921	aatĉtĉĉĉtĉ	gtĉgtĉĉāāg	gĉĉāĉĉāĉg	gĉagacĉggĉ	tacactĉĉag	ggĉāactĉĉt
106981	ĉgaagĉtĉgtĉ	gĉggĉgtĉĉĉ	gĉttĉĉĉĉgĉ	ĉggĉtgĉĉāā	ĉggĉāāāacg	gĉĉĉĉĉtĉga
107041	tggaĉĉĉĉĉa	tgĉtĉtĉgatg	ĉggatĉāāga	atĉtgĉāact	gĉgatĉĉāāā	ĉttgtĉgtĉgĉ
107101	aagĉtttĉĉt	tgĉĉggactĉg	ĉacĉgaagĉĉ	ĉtĉttĉāĉĉgĉ	ggĉĉtĉĉgtĉ	gagĉttĉagĉgĉ
107161	aatāĉĉgagĉ	ĉtactĉĉĉĉ	ggĉgacĉgatĉ	ĉacggĉgĉact	ggattĉgāāā	ttgtĉtĉĉtĉ
107221	gĉacagatĉgĉ	ĉtattāĉatĉ	aagāagĉttĉg	aggāĉāāac	ĉaacĉgtĉĉĉ	tgĉtactĉgtĉ
107281	tagĉgacĉāā	aagĉĉagĉĉg	atggĉttāĉg	ggĉĉactĉga	atāĉāĉāāg	atggaatāĉg
107341	ĉgāāāĉĉĉt	ggĉĉĉgĉacg	ĉtĉĉĉtact	tcĉtĉactĉt	gĉāāĉgtĉac	ĉatgttgĉac
107401	tgatgacĉtt	ĉgacĉatāĉa	atĉĉĉĉacgĉ	tcĉtĉĉĉĉĉ	gĉĉĉagĉĉga	gtĉĉĉĉĉĉĉ
107461	tgĉgtĉāāat	ĉtttgĉĉtĉgĉ	ttggĉtĉgtĉ	ĉāāĉgtĉggĉ	atĉtggaacg	gatgtĉāāĉg
107521	gacĉgatĉtĉ	tcāāattĉĉĉ	gĉgatĉāĉĉĉ	gtĉĉĉĉgagĉ	tttgĉgtĉgtĉ	ĉtgatĉagĉgĉ
107581	acatĉgtĉtĉ	gĉĉgacĉgāā	gacĉtgĉāāĉ	ggĉtĉtĉtĉĉ	actĉgtĉgtĉ	tgĉĉgāāāĉ
107641	atgaagtgat	ĉgtĉttgaga	atĉĉtĉgatĉ	ĉtāāĉgaagĉ	gaatĉttĉĉg	tgĉgāĉgāat
107701	ĉāāggĉtĉt	ggĉtgāĉatg	gāāāĉggĉac	gĉāāāatĉĉā	agĉĉgatĉĉĉ	gatĉĉgactĉ
107761	gĉāāāĉĉĉtā	tcaggĉĉĉĉ	ttĉĉāāgaāĉ	āĉĉĉĉgagāĉ	gattgaatĉg	atttgĉāāĉg
107821	ĉĉgtaggagĉ	ĉĉĉgattĉtāĉ	acĉāĉĉāĉga	ĉĉgatĉĉĉĉ	ttĉgĉāggāā	gĉattgtĉtĉg
107881	attĉgtĉtĉ	ĉgtĉĉatĉāā	ĉgtĉgtĉĉgĉ	tgĉgtĉĉĉāg	tcgatĉggĉĉ	atĉgtĉagĉt
107941	ĉaggāggāāĉ	ĉttĉĉgatga	gĉatĉgtĉĉĉ	ĉĉĉgtĉtttĉ	ĉtagĉĉggĉgĉ	ĉactĉggĉĉgtĉ
108001	ĉĉĉĉĉāĉĉĉ	atĉttgtĉttĉ	acĉgtattĉgĉ	gĉāĉāĉĉĉĉ	aaggĉtgĉĉgĉ	tgĉĉgtĉĉāg
108061	ĉtĉĉgtĉgatg	ttĉĉtĉĉgagĉ	aggĉĉĉĉĉĉ	āĉgactĉgāĉ	ĉĉĉĉĉāĉĉĉ	gtĉttgĉatĉā
108121	gtĉĉĉĉattĉg	ĉtgĉtĉĉttĉ	gagĉactĉĉĉ	gtĉgtĉgtĉgĉ	ttggĉĉĉĉĉgĉ	ĉttttĉgtāgĉ
108181	acĉgtĉttĉtĉgĉ	ĉgtĉgtĉgtĉgĉ	āĉgāĉĉagĉt	ĉāāāāĉāĉā	ĉĉĉgtĉtĉĉĉĉ	ggatĉĉĉggĉt
108241	gtĉgtĉtĉgāĉ	ĉgaagĉtgĉĉā	gĉatĉgĉāāĉg	ggāāāĉĉĉt	tgĉgāāāāgĉ	ĉaatĉĉāāāā
108301	agĉtgāāāĉg	gtĉtĉgatĉtĉ	atĉtatāĉgĉ	gĉāāāĉĉāā	ttĉĉĉgtĉgtĉ	ttĉĉĉgtĉga
108361	ĉāĉāāāāat	gaāĉĉĉatĉtĉ	ggĉgāāāĉatĉ	gtĉĉĉĉgĉĉā	āĉatĉĉgatĉgĉ	aāĉgtĉāgāā
108421	ĉĉactĉĉgtĉ	ĉtgāāgtĉtĉ	tcāĉggaagĉ	tcāāĉĉĉact	tgĉĉgagĉĉā	ĉĉgatĉtĉggĉ
108481	aāĉĉĉĉĉtĉt	ĉĉĉgaagĉĉgĉ	ĉĉgatĉggĉĉ	āĉagĉtgĉĉĉgĉ	acĉgagĉtĉāĉ	ĉgāĉāĉĉggĉ
108541	āgaāgāĉĉgga	ttāgĉĉĉāĉgĉ	aāgaāgĉgatĉ	tāĉĉĉgāggĉ	ĉagĉtāĉĉĉgĉ	gtĉĉtĉĉĉāgĉ
108601	ĉatĉgtĉtttĉgĉ	attĉtĉĉgatĉ	tgāāgāĉĉgĉ	ttĉĉāāāĉtĉ	gatĉĉactĉgĉ	agĉāāāāĉāĉ
108661	ttĉĉĉĉgāā	ĉāagĉttāĉtĉ	tgāāāĉĉĉgĉ	ĉĉgagĉggĉgĉ	ĉĉgaāggāāgĉ	āāggĉtāĉgĉ
108721	gāĉĉĉĉgātĉ	atgātgaatĉgĉ	atĉāāāĉĉtĉ	ggāgāāĉtĉgĉ	ĉāgaātĉatĉ	ĉĉĉgtĉĉāā
108781	tgĉāātĉĉĉ	aagĉttĉĉĉgĉ	ttĉĉggĉtĉgtĉ	ĉāattĉĉāāā	ĉtĉgtĉttĉĉĉ	agĉttĉgatĉtĉ
108841	gāĉgtĉtgāā	tggaāĉgāĉgĉ	ĉāgtĉgāāā	āāāāĉgātĉ	ĉaggtĉĉgaāgĉ	ĉtgātĉgāāĉ
108901	ĉĉagātĉatĉ	ĉgtĉtĉĉgāĉĉ	āĉĉĉĉĉĉgga	ttĉĉgtĉāĉĉ	gĉāātggĉtĉĉ	tgĉtĉĉgtĉga
108961	ĉāactĉĉĉĉĉ	tttgāāāatā	ĉgtĉttĉactĉgĉ	ggĉttĉgtĉĉĉ	gāgāāāĉgtĉ	ĉgtātĉgāĉt
109021	gĉtgātĉgtĉ	ggĉgāĉgtĉtĉ	aāgāĉgatĉĉ	ttĉĉgāāagĉ	ĉtgĉtttātĉ	acĉtggaāĉgĉ
109081	ggĉttĉĉgtĉgĉ	gāāāāĉĉāā	ĉĉĉgāāĉggĉ	ĉtĉgatĉtāā	āĉĉāĉāĉĉĉgĉ	tcĉĉgāagĉtĉ
109141	gĉĉgāĉĉgāĉ	ttggātĉĉāĉ	gtgāātĉĉĉĉ	gtĉĉatĉggĉt	gtĉāĉĉgatĉgĉ	tcĉgāāāāĉāĉ
109201	ĉgāĉĉĉtĉtĉ	atāĉagĉtĉāĉ	tgĉgāāĉgtā	ĉāĉĉgāāgĉā	ggĉĉĉĉĉgāgĉ	tgĉttgtĉttgtĉ
109261	gtĉtgātĉgāā	ttĉĉgatĉāĉgĉ	ĉgaāggātĉtt	gatĉactĉtgĉ	atĉĉĉatĉāgĉ	tcāĉĉgāāā
109321	ĉgātĉactĉ	ttĉĉĉggaāgĉ	aāĉĉāĉĉgtĉ	ĉgatĉactāĉ	gĉĉātĉgtĉgtĉ	ĉĉĉgagĉttgā
109381	tttĉtĉgtĉgĉ	ĉĉgtĉgtĉttĉgĉ	atĉgatĉggĉ	ggāāĉĉĉgāā	ttĉātĉgātĉ	tcāgāāāāt
109441	ĉĉāattĉttĉgĉ	aatĉatĉĉgāā	āĉgtĉttĉāgĉ	actĉgāāgāā	gĉĉggĉttgga	āĉatāĉtĉggĉ
109501	āāattĉttĉgatĉ	ttĉgtĉgtĉāĉ	ĉggĉactĉggĉ	tcāāāĉĉggĉ	aāĉgtĉttĉggĉ	tgĉtgāāāāĉ
109561	ggĉgtĉggāā	ĉĉgtĉttĉĉga	gĉĉāactĉggĉ	ttĉgtĉĉāā	āāattĉāĉĉĉ	ĉgtĉgatĉĉĉ
109621	tcāāatĉttĉ	āĉĉĉgāāāĉgĉ	aāgggāĉgāĉ	gāgātātĉgtĉ	gĉtĉggĉāĉgĉ	tgĉgtĉggāāĉ
109681	gĉĉgtĉttĉĉgĉ	tgĉĉĉĉĉāā	ĉĉgāggĉĉĉ	āgāātĉgtĉt	ĉĉtĉĉgāĉgĉ	gtgāātĉāĉ
109741	gĉĉttāĉĉgāgĉ	āāggĉĉĉtĉgĉ	atĉgtāĉactĉ	ĉāĉgatĉĉgtĉ	ĉĉĉgtĉgtĉ	atāāttgāā
109801	gĉtāĉĉgāĉ	gaāggĉĉĉā	tcāātĉtĉĉ	gāgāātĉtĉgĉ	ttĉĉgātĉĉĉgĉ	āgāgtĉāāāĉ
109861	ĉgāĉĉĉgatĉgĉ	gāĉgāāgāā	ĉgtĉĉgāāĉgĉ	ttĉgtĉgĉātt	ggātĉggĉĉgĉ	aāggĉĉĉāĉ
109921	ggĉggaāāāā	ĉtgāĉtĉāāgĉ	ĉgāĉtĉtĉgā	actĉĉgāgātĉ	ĉĉgāātĉtgĉ	āāāĉĉtĉtĉgĉ
109981	āĉgtĉttĉgtĉgĉ	ĉāātĉgtĉttĉgĉ	tāĉtĉgtĉgĉ	gatĉggaātĉgĉ	ttgtĉgatĉgĉ	

110101	gācḡācṭḡcḡ	tttṭṭḡḡcaa	ṭcḡcṭṭḡḡḡṭ	ggcṭḡḡcṭṭḡ	gaccāṭcācc	tṭḡāṭcḡṭṭc
110161	ṭṭcṭḡṭḡḡcṭ	ggṭḡṭḡḡḡacḡ	cagcḡacḡcḡ	ṭṭḡcāṭṭcṭcṭ	ḡṭcḡṭcḡatḡ	acacṭṭṭcāa
110221	cṭcṭṭṭcḡcṭ	ṭṭccacḡṭcc	ḡṭcḡcḡatcḡ	ṭatcḡacḡṭṭ	ggṭḡatṭḡcḡ	atggṭḡḡcṭṭ
110281	ḡcṭṭḡatcḡc	cḡccḡcḡṭṭḡ	cḡaātccḡaa	acātṭcagṭc	cḡṭḡḡcṭcḡa	aagatcḡaac
110341	atcḡatācc	ggacṭcḡac	caacḡṭcḡa	ṭacccḡcḡḡṭ	cḡacḡatṭcc	ḡṭṭḡccāaac
110401	aaccagācaa	ṭṭatcṭḡaac	caacḡṭḡḡḡa	ṭḡcḡagāaḡc	ccḡṭḡagcāc	ḡṭcḡṭcḡcā
110461	acḡatṭḡḡcc	ggacḡṭcḡḡḡ	ṭcḡṭcṭcḡṭṭ	ggṭṭḡcṭḡḡṭ	caaccḡatṭḡ	ṭṭḡḡatṭḡṭ
110521	cḡḡḡaacḡcṭ	agcḡacḡcṭṭ	ḡcṭṭṭḡḡcḡḡ	ḡcṭṭcṭṭṭcṭ	ḡcṭḡḡccāaa	ccḡḡacṭcṭṭ
110581	cḡḡccāaḡc	ṭṭcṭcṭacḡṭṭ	ḡṭḡṭṭḡccca	aaccḡcḡacḡṭ	ggṭḡatācag	cccḡḡcagcā
110641	ṭḡḡāaatcḡa	acḡcḡḡcagḡ	aacṭṭḡṭṭḡḡ	ṭcacḡḡcḡḡa	atṭccaḡcḡc	gatṭḡḡatṭḡ
110701	ḡṭcḡccaatc	cḡcḡḡṭḡḡḡa	ccagāacṭcḡ	ṭcṭcṭacagc	ḡatcḡacāat	caaccagṭcḡ
110761	caaacḡṭcḡc	aaacḡṭcḡca	aacacṭḡḡaa	cagṭṭccḡḡa	agaccaagcṭ	ḡaacacḡḡḡ
110821	ṭṭḡcācḡḡcṭ	ḡcccātḡcḡḡ	cḡaagcātḡḡ	cṭḡatccḡat	ṭṭḡḡḡḡḡḡṭ	ṭṭḡḡṭṭcccḡ
110881	aagṭcḡacḡa	ḡṭcṭṭṭcācṭ	ṭaccḡagṭcḡ	ṭatṭḡccṭcā	cṭḡḡṭcāaḡc	ḡagḡaatācc
110941	ḡṭḡṭṭḡaagṭ	ṭṭṭcḡaātāc	ccḡḡccḡṭcā	cccḡaagcḡa	cḡcṭḡāaatc	ḡatṭaccccḡ
111001	agṭṭcāccḡḡ	acṭṭcagāac	cḡacḡcātṭḡ	aagacacḡcṭ	ḡcḡagṭcṭcḡ	ḡṭḡḡccāaaḡ
111061	ḡcagcḡaagṭ	cacṭṭḡḡḡḡḡ	ḡṭṭcḡaātca	acāaacḡagṭ	cacḡṭcḡḡcc	caacṭcṭṭcc
111121	ccaagccāta	caaaaḡaac	ḡagḡḡcāacṭ	acḡaagacṭc	cḡcṭccṭṭḡḡ	ḡagatḡaccc
111181	aagatcccḡa	ḡcḡṭccacṭḡ	ṭḡḡḡḡḡṭccḡ	ṭcḡcāatcāa	ggṭḡḡaagāa	agccaacḡat
111241	acḡatḡṭḡḡa	acṭḡāaagac	ḡacāaagacṭ	ḡcacḡaacca	ḡcṭcṭcḡacṭ	cagṭṭcātḡcḡ
111301	ṭṭcḡaatḡcṭ	acccaaccaa	ṭṭagccāaaa	ṭṭcḡccccac	ggṭcḡḡḡḡḡc	ḡacḡṭṭṭccḡ
111361	ṭḡṭcḡḡcātṭ	ḡḡaagagṭṭṭ	cṭcātḡcḡccḡ	cḡḡaagṭṭcḡ	ggacḡatcāc	ggḡṭcṭcḡṭc
111421	ḡcḡcḡḡḡcḡṭ	cṭcḡcṭḡacā	ṭṭṭḡccḡḡcā	aaccacḡcḡa	ḡḡacātḡḡḡ	ṭḡḡḡṭḡḡḡa
111481	acātḡcḡṭḡc	caātcaaaḡḡ	caaacḡatcc	agcacātḡḡṭ	cḡacātḡḡḡa	ṭcācṭṭḡagḡ
111541	ccaaccccḡa	cḡatṭṭḡḡṭḡ	ṭcḡṭacṭcṭṭ	ṭṭṭḡḡḡccḡa	ggacāagḡṭc	ḡcagḡṭḡaat
111601	cṭṭccḡagac	ṭḡaagṭccḡṭ	cḡcacḡcāaa	ḡcḡatṭṭḡṭa	cṭṭṭḡccḡāa	ḡṭccḡacḡṭṭ
111661	ṭcḡaagatāt	ṭṭṭṭcḡṭḡāa	ggcḡatcṭcṭc	aātccagcca	acṭṭṭcḡḡāa	cccṭcṭḡaac
111721	caagcḡaaca	agaacaācaa	ḡccḡaagagc	ṭḡatṭḡāaac	ḡcāaaagcāa	atcātccagḡ
111781	ccātṭḡḡḡāa	ḡcṭacṭḡcag	ṭccacḡṭṭc	ggṭḡḡaācḡa	ḡcāaacḡacḡ	ḡcḡḡacḡṭṭc
111841	cḡḡṭḡatcḡc	ḡḡacṭcḡcāa	cagḡatḡṭcā	ṭṭḡcṭcagṭṭ	ggatḡaācṭḡ	ḡcṭcāagagc
111901	ṭḡaacḡaagc	cḡaagccāaḡ	cagcacḡccḡ	ccaacḡṭṭcḡ	acaātḡcātḡ	caaaccḡccḡ
111961	ṭcḡcḡḡaācṭ	ḡaacḡḡagcḡ	atṭcāaacca	ḡcḡatcḡṭḡa	accātṭḡṭcḡ	ḡcṭḡccḡṭcḡ
112021	ṭḡḡcḡḡaaca	acccḡcṭṭac	ḡcḡḡḡccṭḡṭ	ṭcḡḡḡatḡcḡ	agccagṭḡāa	ṭṭcḡaagṭcā
112081	cacḡṭṭcācā	acagcagcāa	caaccḡagṭc	aagḡṭṭcḡḡc	ggḡṭcāacāa	cḡcāagcāac
112141	aacāatṭḡḡa	ṭḡaātṭḡḡāa	cṭḡḡaccagḡ	aacagḡaccḡ	cṭacḡāaacḡ	cagcāaacḡḡ
112201	cḡcāaatḡac	cḡccḡḡagcag	caagṭcāaac	ḡṭḡagātṭcḡ	ḡcāagṭḡcṭc	agccḡḡcṭḡa
112261	ḡṭḡaacṭcḡc	ccḡṭcḡccag	cagḡatṭcā	acḡagḡaacṭ	ggcccaacṭṭ	caātḡagcḡa
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112381	ḡcḡagcāaca	ḡcagḡatātḡ	cṭccḡccāaa	ccḡatḡagcṭ	ḡatḡḡaacḡc	atḡaacṭcāc
112441	ccḡḡagāacḡc	ḡṭccaacātḡ	cagḡaagcca	cḡcāacaacṭ	cḡagcāaacṭ	cḡcḡāaaaac
112501	ṭṭcḡṭḡagḡc	ṭḡḡcḡaagcḡ	atḡḡaacagc	aagacḡcṭḡa	aacḡḡcṭṭṭa	ṭccagcḡḡcā
112561	aacḡcḡccḡa	cḡcḡḡaacṭc	ḡaātccḡṭṭc	ḡagāagāaat	ṭcḡcḡaacag	ḡcṭḡcḡḡḡṭc
112621	agṭṭcāacḡa	agcḡatḡcag	ṭcāatḡcḡṭḡ	atcḡagcṭcḡ	cḡaātṭḡaac	acḡcāacāaa
112681	agḡaacṭcḡa	ḡḡaacāatṭḡ	ṭccḡāaatḡḡ	acḡcacccag	cḡaatcḡcṭc	ggcṭṭḡcḡṭṭ
112741	ccagcḡḡcāa	ṭcḡcḡaagāa	cṭcāaggacḡ	cacṭḡacccḡa	ḡcagcḡṭḡāa	ṭcṭṭṭḡḡḡḡcḡ
112801	aacṭāatḡḡa	ḡḡacātṭḡḡḡ	ḡagḡṭcḡṭcc	agḡaagccḡa	agagṭccḡāa	ccḡṭṭḡcṭcḡ
112861	cacāaaacṭṭ	ḡṭacḡacḡcṭ	ṭṭccḡcḡāaa	cḡcāacāacḡ	ccḡḡacagāa	cḡacḡacṭcḡ
112921	atḡccḡccag	ccaacṭṭcṭṭ	cagcḡṭḡḡcṭ	ṭṭḡacḡagcā	ḡṭcḡcagcāa	atḡḡcḡḡḡḡc
112981	aggccḡḡṭḡa	agcḡatccag	ḡaātṭaagcḡ	agcāaatcḡa	aacḡḡccḡcc	ḡaaagcḡṭat
113041	ṭḡḡḡcāacḡa	agcagāagḡa	ṭṭḡcāacḡṭḡ	cagcḡagṭṭṭ	ggcṭḡagcāa	ṭṭḡḡaatccḡ
113101	cṭḡṭḡṭcagā	cḡaagṭccag	caagcacḡcḡ	ḡagacḡatṭc	cḡḡcḡḡḡḡcā	ggḡcagḡḡḡc
113161	aaacṭcācā	ḡccaacḡḡāa	cḡṭcagccag	ḡagāagācāa	accccaacāa	ggacagccḡcḡ
113221	ḡṭḡagāacca	cḡcagḡccāa	ggḡcāagāac	aagḡḡḡḡaagḡ	ggāagḡcāaa	ccḡḡḡccāac
113281	aacāaccḡḡḡ	cḡagḡāaagc	caaccḡḡḡṭc	aagḡṭḡḡḡcc	cagṭcāatcā	caagatḡḡḡc
113341	aagagccḡḡḡḡ	agaacaātcc	ḡcṭḡḡcḡaat	cagāaacḡḡḡ	ṭcāaccātḡcḡ	aatccḡcṭcṭṭ
113401	cḡcagṭcāac	cṭcḡccḡḡḡḡḡ	cagḡḡṭḡḡḡḡḡ	cagḡḡḡcagḡḡ	cḡḡacāagcṭ	ccagacḡāag
113461	aacṭṭṭcḡac	cḡagccḡacṭ	ccḡḡḡcḡāac	cḡṭcṭḡāaaa	caccḡaacḡcḡ	caagāatcca
113521	cḡḡagcḡṭcc	ḡcāagḡḡcāa	cṭṭḡḡṭcṭṭc	ḡccṭagṭṭc	ḡcāatcḡcag	caagḡḡcāac
113581	cacagccḡāa	ccaaccḡcāa	ḡaagḡṭcāat	ccḡḡcḡḡṭcc	caātccātcc	ggcḡcccaag
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113701	cṭḡatḡḡatṭ	ḡcḡagacātḡ	ḡaagagātḡḡ	ṭṭṭccḡaccc	cḡagṭṭḡcḡṭ	ṭcacḡṭcḡcḡa
113761	cacḡaatṭcḡ	ḡḡaacḡagcc	cḡcḡacātḡc	ḡṭḡagḡāaat	ṭcḡccḡcḡāa	ṭccaacccḡc
113821	cḡcāatḡḡḡḡa	ṭṭḡḡḡṭcḡag	ḡagātḡatcḡ	ṭcḡaacccāt	ḡcḡagāacṭc	aaacḡcḡatc
113881	ṭcḡccḡāagā	atācātḡcḡṭ	cḡcagcḡcāa	agāaacāatc	ḡcṭḡḡṭṭccḡ	atcḡatcḡṭḡ
113941	atccḡḡṭācc	ḡḡaccagṭac	ṭccḡaagcḡḡ	ṭcḡcṭcḡatā	ṭṭacḡaacḡa	atcḡḡḡagcḡ
114001	ggcṭṭṭḡḡaac	ḡacḡcṭṭṭcā	atṭcātṭcḡa	caacṭḡḡagc	cagcātṭṭḡḡ	ṭṭṭḡḡḡḡḡḡc
114061	accḡḡagṭḡḡ	atcṭṭṭcṭcṭḡ	cḡḡḡcātccṭ	agccḡṭḡḡḡḡ	cṭṭacccḡccḡ	cḡatṭḡḡḡṭḡḡ
114121	ḡṭccṭacḡcā	cḡṭṭcācḡcḡ	caaccacḡcc	ḡatṭcḡcḡṭḡḡ	cṭcḡcḡḡṭcā	cḡcṭḡāaacṭ
114181	ḡatcḡccḡḡḡḡ	ḡcātṭḡatḡḡ	ṭḡcṭḡṭḡṭṭṭ	ḡcṭṭcāaccḡ	atḡṭḡḡcḡag	ḡcḡaacḡṭcc
114241	ṭcḡaccḡcag	ḡccaacṭṭḡṭ	ṭṭccḡatṭṭṭ	ḡḡṭcḡacacḡ	agccagagcā	ṭḡcagṭcca
114301	agātḡṭcḡac	ḡagḡaacṭṭṭ	cacḡṭḡḡḡcā	ḡaacṭṭṭḡcc	aacḡcḡṭṭḡḡḡ	cṭḡccḡacṭc
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114421	acṭḡagccḡṭ	atḡḡccḡcāa	ṭcḡacācāat	cḡaātṭcḡac	ggcātḡcāat	cḡṭccātācā
114481	aacṭṭcḡatc	ḡatḡcātṭḡṭ	cḡcagcḡacṭ	caaagḡacḡc	cccḡṭcḡccḡ	ḡṭḡcḡṭṭḡṭṭ
114541	atṭcagcḡat	ḡḡcāatṭcā	ccḡatccṭcṭc	cḡcḡḡaacag	atcaccḡḡcā	ccḡatṭcācc

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114901	acaacgtcaa	tcgatccgtt	ctcaaatcga	tgaaggcaat	gcgtggctgg	aaggtatc
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115681	attggcccaa	ttggaaacga	gttctggcca	accgcctccc	gccttcatca	ccagcgatt
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119101	gttgatatcg	gcaaccgttg	ggatgtcgat	gatttcaatg	ggttgcttgg	tcgtgttctc



119221	tcccgctcga	cgggtacgac	caaecgggtg	cacatacga	tcgctgctg	gcggcaa
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119341	aacccaaacg	tcgagttgac	cacgcttgag	ttggtcaatt	gtccgctctc	gaaccttctg
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119461	actcagcgtg	gagtcctttg	tcttcgtgaa	gacgatcact	ccatcggttt	cttcacttc
119521	caagatgcga	gtcaacgc	caattttgtc	gcgtggtgaa	acaaacaacg	cacgctggcg
119581	aaccgaagcg	gcggtgatcg	tctttgactt	gatcgtgatc	cgagctgggt	cgttgagata
119641	ctcgtcagcg	atcttgccga	ttggcttttg	caacgtcgca	gagaacaacg	cgacttgccg
119701	tccttcaggc	gatttttcga	ggacaaactg	aacgtcttcc	agaatccca	tgttgagcat
119761	ttcgtcggct	tcacgcagca	caaggcaatc	gagcgaaccg	agatccaacg	taccgcgttt
119821	gacgtgatca	atgactcggc	ccggtgtgcc	gacgacgact	tggacaccgc	gacggagctg
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122461	aacgtggggc	cccatgctgc	acccaatgaa	aagaaccaat	gtcgactgga	tcggtcttat
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122641	acgatcttgg	ctccaaacgc	gcaactctgc	tcagaaggaa	ccgaccaccg	agatgtgggt
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123601	cgcacgcgag	gcagccagac	gcatgagctg	cagcaacaat	ttcaagcaaa	ttggcttggc
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123781	tētḡtācātē	cēḡḡttgga	ēētḡccgtt	cctḡāacāḡ	āaggcctt	gggaacaāt
123841	atccaatcca	ctcagcgtga	atcḡgatgg	atcḡaccaag	agcccaccat	ggcagcccat
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124081	gggcḡctaca	ttgcccctatc	gaaccgacac	cgcgcacgcg	gcgḡcttcta	atcagccca
124141	gḡcgcḡcatg	ttcḡtcaacg	gtcḡagaagt	tcaatttcgc	gatacḡctcg	acḡḡactttc
124201	caacacḡatt	atḡtḡcḡḡcg	agatcacḡac	ggacttgggc	aacaacḡaca	aacḡcacḡac
124261	ḡḡttccḡacc	aataccḡḡtg	ḡacatḡcḡḡc	gccaacḡaa	aagaaccagt	gtcḡactḡga
124321	tccatcttat	gcccḡagccct	acatcḡatcc	tḡaacḡccct	cagttttḡḡt	caccatccḡḡ
124381	cttgaccaag	caagctḡttt	ggḡḡagctḡḡ	ttttcḡctḡḡ	cacḡactaca	tḡccacccta
124441	ttcccagatḡ	accacḡḡḡt	tatcḡcccaa	cgcḡgaacta	tḡctccḡacḡ	gtcḡagacca
124501	tcḡcḡatḡḡ	ḡtatcḡcccc	cttcḡagcca	acaccagḡḡc	ḡḡagtccatḡ	tḡttḡatḡḡḡ
124561	agacḡḡcḡca	gtcagḡttcḡ	ttaccḡactc	ḡattḡaagct	ḡḡtaataaaa	atḡcaccḡca
124621	ḡḡtatcaaac	cḡagccḡḡḡt	cḡccccḡccc	aggcagcccc	agcccatacḡ	ḡactḡḡḡḡḡ
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124741	cḡaatccatt	ḡccaactatt	acḡaactḡcc	ḡccatḡagtc	actcatḡḡḡḡ	ḡcagttctt
124801	tḡtattcaga	actctcḡctc	tagaccḡact	cagḡaaacag	tḡcḡtccagt	ḡtaagttḡḡc
124861	tcacḡḡttt	cagḡḡtḡctḡ	cḡḡttctḡḡḡ	ḡḡagtḡḡtt	tacḡḡaaacḡ	aactḡacctt
124921	cḡḡcḡḡḡtt	ḡḡcctcḡttḡ	ctḡḡḡḡacḡa	ḡtḡḡttḡctc	caagatḡaag	cḡatḡḡacḡa
124981	ctcccaagḡtḡ	caccḡḡacca	acttḡcḡttḡc	tḡḡḡḡtcata	aagcaaacct	tctcḡttḡat
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125161	ḡttḡḡcḡḡḡ	cagacḡttt	tcactcḡaac	caccaccḡḡḡ	agtḡtattḡa	aaccattḡḡa
125221	ccḡcḡcḡḡc	agccḡḡatcc	gtccactḡca	tcaccacḡta	ḡḡḡatcaat	tḡttḡaaac
125281	tḡḡatcḡḡḡ	ctccattḡca	ccḡcḡḡḡḡc	ḡataagacaa	ttcḡtḡcḡḡ	ḡcaḡaatag
125341	ḡctḡcagḡḡa	tḡḡtccacḡ	ttḡcḡḡtcaa	acccttccaa	atḡcccaatc	ḡattcḡatca
125401	aggḡcḡcḡḡḡ	aatḡacaagḡ	acḡḡḡttctt	cḡḡḡḡḡḡḡc	ḡttḡḡagḡac	attctḡcaat
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125641	ḡḡcctḡcḡat	attccḡattc	ḡagḡcḡḡḡḡ	ḡḡḡacacḡa	ctḡctcḡḡaa	ḡctḡḡḡḡacc
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125761	cḡcḡagagat	tḡḡcacaaac	ḡḡccḡḡḡḡḡc	cḡtḡcḡcaat	ḡctcttccḡt	cḡḡtḡḡttc
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125881	ccḡḡatcaaa	actḡccḡaac	cacagccḡac	cḡatcḡḡḡc	accagattca	cacagḡctt
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126001	tttctcacc	cḡcḡcactḡt	ḡactcḡcagc	atcḡcḡactḡ	ḡacagḡtagḡ	cttḡḡḡttc
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126121	ctḡḡcḡagcḡ	acḡacagcḡḡ	ḡacḡagcḡḡc	aaaaaattḡc	ḡactḡcaacḡ	actḡcḡtḡcḡa
126181	tccccaatcḡ	atcagccḡat	cttctcḡtḡc	atcctcacḡḡ	aactḡattt	ḡctttḡcatc
126241	attcatcaaa	acaaacttat	cḡcḡcḡcḡḡt	ḡḡḡḡatḡcc	catcḡacḡḡḡ	ḡatccḡattc
126301	ccaacḡḡaat	ḡatḡattḡḡt	caatcḡḡḡḡc	ḡḡatcḡctt	ḡatcagḡttca	ttccaagatt
126361	cḡaḡaacḡa	aggḡḡaattḡ	atcḡacttḡḡ	ḡagacḡtḡcḡ	aattttḡccḡ	ḡḡttḡḡḡtca
126421	acactcatac	ḡcacctḡḡaa	ttcagcḡacc	tcccaaaacc	cḡtḡḡḡacac	accḡḡcatḡḡ
126481	aattḡḡccḡa	ctḡḡattcḡc	ḡaagḡcatca	cḡactcḡagḡ	ḡatḡḡtḡcat	caccaaacḡc
126541	ḡacaacaaaa	cḡttctcaaa	ḡḡḡacacḡḡ	aagcaactḡc	ḡtcagḡcaca	cḡctḡḡatcḡ
126601	cḡḡacatcḡa	ḡaccacḡcḡ	atḡḡaatcḡa	tḡcḡaccaaa	tacḡatcḡca	ttcḡcḡḡaag
126661	tctcḡḡact	cagccagḡaa	cḡagḡcḡacḡ	aacḡḡatḡtḡc	acagḡctḡaa	cḡacatcttḡ
126721	ccaacaacac	ttcḡcctḡat	tḡcḡḡatḡḡ	acḡtḡcḡcḡc	ḡatcagccḡḡ	cacḡtccct
126781	actcḡacacc	tttḡcḡḡttḡ	atcḡagcḡct	ḡcḡḡcḡaagḡ	tḡcaaagcaa	cḡcaagacḡa
126841	cactcḡccat	ḡcacḡttḡcḡ	ḡaatcacctḡ	ccḡaacḡḡḡa	actactḡaca	aacḡḡatccḡ
126901	ḡcccatttḡc	cḡaatcattḡ	cḡaactctag	ḡattḡcctat	cḡagḡcḡttc	tttccctḡḡa
126961	caaaagcḡaa	tccagtctca	cactḡattc	agḡtḡcctḡc	caaactacct	cḡtḡcḡttḡa
127021	tḡtḡcḡcḡḡ	aaatḡatttḡ	agtḡagaccḡ	aaatcḡagca	agtcaaactḡ	caccḡgaact
127081	ḡcagcatcḡt	ḡtactḡccca	agaacḡcatc	atttctttca	ḡcattccaat	catcccḡtḡcḡ
127141	cagaattḡct	agccḡcagḡa	atcaacḡtag	ccatcḡḡḡḡac	tḡattcacḡc	ḡccagcaatc
127201	ctḡatctḡḡa	tctttḡḡḡḡc	ḡagḡtccagc	acttḡctcaa	ḡcatcḡḡcct	ḡacctḡaatc
127261	cḡaccḡagcḡt	ḡcttcḡcatḡ	ḡcḡaccḡcca	acḡḡḡcḡcḡa	cḡcattḡḡḡa	cḡctcagcaa
127321	ctcacḡacḡ	ḡttḡḡccḡcc	ḡḡḡatḡccag	ccaactttat	caccḡtḡcḡa	acaagcḡctḡ
127381	atcḡagḡtḡcḡa	tcaḡctttḡḡ	tḡḡactttt	catcctcatc	cḡtḡtcatct	tcattccatḡt
127441	cttccḡccḡc	tḡcḡccagca	ccccaaagct	ḡaacḡcḡtḡc	ataaagacḡa	tḡagcagḡḡa
127501	tḡḡḡaatcag	cagattḡccḡ	ḡtcacaaatca	ḡcaagḡcacc	aaagḡacaaa	cccatcaacḡ
127561	cḡḡḡḡacḡac	ḡatḡtacagḡt	ttḡḡḡḡattḡ	ḡatḡḡaacat	tccaaacḡcḡ	aatḡagḡḡaḡa
127621	ccagccagḡc	tḡcagḡttaat	tcccatctc	cḡagcḡḡaga	ccaccaagcc	agcaaacctt
127681	cttccḡcca	agcḡaatcḡ	ḡtḡactḡagt	ttḡḡcaaact	ḡcccagccat	ccḡccataag
127741	cccaccatcḡ	cḡatḡḡḡḡct	tccaaatcag	ḡagcaagcḡa	cḡcḡḡcḡtct	ccḡccaacc
127801	aagḡcaacaa	ccaaccḡcḡa	aacaagagḡt	cctcḡccḡac	ḡccḡḡcḡcac	aaactḡatcḡ
127861	cḡaacaattc	ccagḡcḡttc	agtḡcḡcagca	tcaagccḡat	catḡḡḡḡḡḡa	tḡctḡḡagct
127921	tḡtḡcḡagḡttc	ttcḡattḡcc	ḡḡḡḡḡttḡa	ttcḡccḡcaa	cacḡḡcaacḡ	aacaacacca
127981	atḡḡaatḡḡt	cḡcaacaatḡ	cccagcccḡa	taccḡccaat	ḡaccḡcḡḡac	ḡaagcḡactt
128041	cḡttḡtagcḡḡ	cḡḡaaccatḡ	tcacḡḡḡcac	tḡḡḡaccag	cagḡtatccḡ	agaatcaacḡ
128101	ccagḡḡcacc	caagccḡḡct	tḡacḡcḡcḡa	cagcagḡtccḡ	aaagacatcḡ	tccḡḡḡḡttt
128161	ḡttcḡtḡcḡtḡc	cḡcḡttḡḡḡt	tḡcḡtcaac	ḡcctctctca	ḡḡatḡḡḡctt	cḡḡḡḡcḡḡt
128221	aggḡattḡaa	caacaagḡtag	ttcaagḡḡḡc	ḡatacagatc	actḡḡaatc	agcaactcḡḡ

128341	gtaācgtctt	cagccggtga	ggcaacātg	ccacāācga	tccgcgatcc	gccaacctc
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139021	aaaacttġtġ	atttttġcġt	ġġccacaaaac	cactcagcġa	agtġagagġt	caagattġġc
139081	caaaagġtġa	aaagcaatta	acġagcagġa	atcatġtġca	aaagacacġt	tāaatcaacc
139141	gattttġcaca	ttagcatġca	aatatġcac	gttttġġcc	atcġttcact	cccġaaactġ
139201	tatġgatttġ	aagaagttġg	cġtġttġcġa	tatġġġcġca	ġccatacġgaa	ġġagġaaagā
139261	gtcatġġġtġ	gāaaaccġtġ	ġccāaaaacġ	catġġġcġġa	ctġaaaaccġ	ctcġtġcġtā
139321	ġcġaagġaag	ġcaccġcaaa	ġcagġcġtat	agagagactc	agcaactġtag	agacacagġt
139381	ctġtttġcġg	ġcġaacġġtġ	tacġagccag	atcagcttġg	cttġtġtġca	ġcġatcagāā
139441	tġactġġatc	cccġatttġg	accġġcaccġ	cġġtġacġġt	ġacttġġtġcġ	cccġcactġcġ
139501	ġcttttġġġc	ctccġatġag	agtġccatġt	cġagcġtġcat	catcġtġtġcġ	cccġtġġtġcġ
139561	tāaacġtġgac	ġactāagtġt	tġtttġccac	ġġacġttġġc	agtġtġġtġ	ġactġaactt
139621	ġaccġġtġta	cġġactġccġ	ġagcġttġcā	cġttġtacat	tccġtġcttġ	ġġtāaatġcā
139681	cagcġġtġcġ	cactagcact	tġcttġtġcġ	cccġtġttac	catcġġtġcca	tāgaagġtġġ
139741	cġtġġtġcatc	tttġaatagc	tġġactccġġ	ttġcatġtcc	ġccġagatca	atccagacġt
139801	cttttġcġctġ	ttġcġacttġ	acġtġcatca	tcaacġagta	ctcġttġcġt	cġttġaacġġ
139861	ttttġatātġ	ġcġaacġġtġ	cccġtġactt	catġacġttt	ġccġctcaag	cġġtġtttā
139921	cġġtġtġġcġ	ġatccġġġac	ġġtġġġaccġ	cġttġcttġga	cġtġctġccc	agctccġaat
139981	agtġġtagġt	ttġġtacacġ	ccatġcġcġt	cttcatcġtġ	ġtagġtġacġ	tagġcġtcat
140041	ttagġtāatc	accġtġcactā	tġġatġtacc	ġcġtġġatġcġ	ctcġtacġtt	ccġtġcġcat
140101	cġcġatġcġtġ	ġtagġacaca	tagcttġcġt	tġtagtġcġtġ	ġccatagāāā	ġtatcġġcġġ
140161	ġġatġatcag	ctġġtġtġg	tġtġagġcġc	tġcttġtġtġcġ	agcġtġttġca	tagġāāāagā
140221	tġtġtġcġtġ	ccāacġtġccġ	atagcġtġcġ	cġġtġġġtġ	ġtāatcġttġ	cġġtcaaacġ
140281	atccġagat	ġcġtġaccag	ġcatcġtġcġ	caacttġtġcġ	ġccġcġġtġt	tccġġġtcaa
140341	agtġcġcġġt	ttġtġccatc	ġcġaccġġcġ	tġcaagccāā	cġġāāāagag	accġcġġcġġ
140401	tġcġġaccāā	ġġaacġaagġ	agtġġtġtġt	ġġcġatġaag	ġaatttġcatġ	ġġġtġaacġt
140461	tttġattġġt	ġttġtġcġagt	ġcccġcġact	ġctġcġġgaca	tġġġtġāāāā	caccacāāāā
140521	ġaagġcāāac	ġġcġcġccac	cttġcccġtt	tacġġccġca	tġacagacġt	cacġcġattġ
140581	caccacġtġa	tġtġcġacāā	ctġġġtġcġ	cġagcġatca	tttġcġatcġ	tġcġcġgāāā
140641	tġġactġcġa	cccġāāāaat	ġcttġġcatā	ttġcġġcatc	ccġcatcāāā	tġġtġcāacc
140701	agacġġtttġ	cġġtġtġcġtġ	aaccġaccġġ	tagactcġġġ	cġatttġtġcc	tttttġacġc
140761	tāacaagagā	ttġcġagcat	ġagcttġġġt	ġccġġtġcag	acacġcāatt	cġāāaccatġ
140821	cġcġġtġcġg	aatttġcġtġc	ġattcġtġcāā	ttcaccatct	tġcġagāāā	ccġagtġġġġ
140881	cagtġtġctġ	agġtġtġtġcġ	ġcġattġtġag	ġġġactġġġā	tccġaatġtġ	ġġccctġtġcġ
140941	atcaacġagcġ	cġġcġġaatġ	tġcġtġcġtt	cġcttġtġtġa	tġagcġacġc	ġġaccġġġc
141001	cġagagattc	ttġagcġagc	cġġġtġġġc	atcatcġaat	ccġatctġġt	tġġcġtġġag
141061	cttcccġaag	ġcccccāacc	actġtġcġġt	gtttġcacġġ	cġttġtġtġcā	agcġġaactġ
141121	aacatcatcc	agġcġtaccġ	cttġtġcatġ	cġtccġcacġ	ġcāagccagc	ġġtġcġġatc
141181	atġġtagagā	acatcġactt	ġġcġatġāāā	acġtġacġġ	agāāagġttt	ccġaatcatc
141241	accġagġatġ	acttġġacġc	tġacaatctt	cġcġcġcāag	acatctactġ	agtġacttġ
141301	cttġtġcagġc	cġcaccġtat	ġatġġtġtat	cġctcġġtac	ġatġġcġttġ	caagġccġtġ
141361	ġaatcġtatġ	ctġġcġactt	cccacġġcca	tġtġaatcag	cagġtġcġac	agcġttġġāā
141421	ġġacatcġcā	catctcatcc	aactġccġcc	ttġttġactt	cccġccatġa	ġtġaactġcc
141481	tġcttġacġat	tġġtttttġc	tġġtġtġcġt	tġġagġccġġ	ġagġġġcagġ	acġatġtġat
141541	ġccġtttġtġc	ġāāāacġttt	tġcġagġcāā	ġaacġtġccġ	cġcġāaccġġā	tġctġġaagġ
141601	cġccġagcāc	tācāāacact	tġġġcġġtġt	cācġcccatc	aacġagcāāā	accġtġcagct
141661	tātġcġagcā	ctġcāāāagc	ġatttġacġc	caacġġaatc	ġacttġccġa	tġctactġġġġ
141721	caatcġġaāc	tġġġatccat	acttġtġccġa	cacġctġcġ	cāaatġaagġ	cġġatġġcāā
141781	ġaagcġatcġ	ctġġcġtttt	tġaccagcat	gttġcagctġc	tacagcġġtt	ġtġcġcagta
141841	tġcġcġāāac	atcatġcagġ	ctcġcġāāgā	agtġġġcġag	ġġagcaccġc	tġġtġagāāā
141901	agtġccġgatġ	ġġcttġcāacc	atcġtġġcġt	catcġtġcġg	atġġcġġacā	acġtttġcāāā

142021	cātċccgatg	ggcatgġċtġ	acaaġtgċga	ctācgaaaaa	ċaāctġcgag	aatcatgċcġ
142081	tttggttgcc	gatgċttgċg	gtgċggtgga	ttgggacttg	gtttaccaaa	gtcġcagcġg
142141	gccaccatcg	cagċcttggt	tġgaaccaga	ċgtġċtgġac	gċgatcġċcġ	agatġġacga
142201	ċġctaaaaaa	ttġgaatċġt	tġgtgatċct	tċċgatċġga	tttġtcagcġ	accacatġga
142261	gġttċtgġtt	gactġġgacġ	aggaagċċġ	ċċagċttġġ	ċgagaacġġ	gaatċaaaat
142321	gġċacġgċc	tċċġġġġġ	gaacċċacċ	agatġtċġtċ	gagatġatċt	gċġġattġġt
142381	gċaagaacġġ	ċtċġgaaaaċ	tgaacġaaaa	acċċġtċtċa	ġġtgaactġġ	gtċċċtġġca
142441	tġatġtċtġċ	ċċġcagġatt	ġċtġċttġta	ċacġċċacġġ	ċġġċċtċċġġ	tġġġġġġġġ
142501	gġġacċġġtt	ċaagċċaatt	gatġġġġġġ	ċtāgaatċac	ċġacġagċċa	tċċtġattċċ
142561	ġġċċacatċġ	ġċttċġtċġt	ċtġtċċacġa	agċġġtġttt	ċtġċċċċċt	ttċġatċċt
142621	ċġtgagcacc	atġċċċċac	tċċċċacċa	agġtċttċtċ	acġacċaaag	acċġcagċga
142681	ċġaaaccatċ	aacġġġttġt	tġġacġattġ	ċċaaacċtat	ċtgaacġatċ	atċċġġttt
142741	ġġtgagċttċ	ġċċġtġġġac	ġċtġġġagċc	ċgaataċġat	ċġtċġġtċa	acatġġactt
142801	ċġatġtġġtġ	ċtġċataċag	tċttċgaaga	ċċġtġċġċċ	ċatġacġċt	atċaaacagċ
142861	acċtċġġċac	ċtġgaattċa	tċġagċġtċa	aaaacċċaat	tġġġċġgaag	ttċġġtġtt
142921	ċġattċġaat	ċttċġġact	gatġċċatċċ	aacċttċaca	accacġtttċ	actċttttt
142981	aaaagċtaat	atċacċatġa	ġtġttttġġt	ċacċċaaaaa	ġċċċtġatt	tċacġġċac
143041	ċġċġtċatġ	ċċġatġġċa	ċġttċaaag	ċġactċaaġ	ttġtċġġatt	acaaġġċaa
143101	ġtāġtċċtġ	ttġttċttċt	ġċċactċġa	ċttacttttċ	ġtċtġċċċaa	ċġaaatċat
143161	ċġġttċagċ	ġacċġġġċċa	agġacttċġa	agacċtċġġċ	ġtgaacattġ	tċġġġtttċ
143221	ġatċġacagċ	ċatttċactċ	acttġġċatġ	ġacċaaċacġ	ċċacġċaaċġ	aagġtġġċat
143281	tġġċaaġacċ	ġċttacċċat	tġġtċġċġa	ċttgaacaaġ	ċaaatċtċġċ	ġtġattacġa
143341	ċġtġġttġtġ	ġacġġġġġġ	tċġactġġġ	ġġtttġttċ	ttġatċġacċ	aagaagġġġ
143401	tġtġġtġġġ	ċaagġġtġċa	acġatġtġċċ	ġġtġġġġġġ	agċġtċġacġ	aagactġġġ
143461	aatġġtċaaa	ġċċtċċagġt	acttċgaaac	ċaatġġġġaa	ġtċtġċċċag	ċċaactġġġa
143521	agaagġġtċġ	ċġtāċaatċa	aagċġġacġt	ġgaagġġacġ	aaagagttċt	tċġġġġġġa
143581	atāċaaaagċ	tāagċaaġċa	atċġagġtġa	tċċċatġtġġ	ċaatttċaaġ	atġttċġġġċ
143641	ġċġacċċċt	ġġċtċġġtt	ġtġacċġaa	ċġcagġċċag	tġċttċacċġ	ċġactġġaa
143701	tġġġacġġġ	ċacġactġġġ	tttġċċacċ	ċġġġġġġġ	tċċaaagġaa	tċagġtċġġ
143761	ċġatċċġat	ġġttċttġġċ	acġtgaactt	ġttġġġġtt	ġġġacġacġ	ċġċtċċġġ
143821	ċġċċacġġaa	ċaatċġtċċ	ġagġġġacġt	ttġgaacġtġ	acġċttċċtċ	aagċġacag
143881	ċċagġactċa	ċttċġtġtġġ	ċtċtġġagġt	ċġtġgaagċċ	acġgaactċ	ġactġġtċat
143941	tgaacċċacġ	ċtġtċġattċ	aaacactġtt	ġġtġġacacġ	ċacċċaaċġċ	tċġacċtġac
144001	ċġċtttġġġċ	ġattġġġġġġ	tġatċttċġa	ċġagġġġġac	acċċtġġġtġ	acġġġġtċċ
144061	acċġatttċa	acċġttċaat	tġġatġġtġa	aacċġġċtċċ	atġġġġtġġ	tġġġġġġġ
144121	ċacġacġġċ	ċġġttċacġa	ċġġatttġġġ	tċġagaagġġ	ċacċtġċaac	tġġtġtċtt
144181	ċġġġgaattċ	ċtāgaaaaaġ	ġġtġatċċġ	ċaagġtċġġ	ċċttġġattġ	tġġtġġatċġ
144241	ċtċġgaacag	ġġġtttċġġ	agġġġatċt	ċċaagġtat	ttgaaacġat	tġtġġgaaac
144301	ġċċċtġġċt	ttġacġġġtt	ġagġttġġġt	ttttġġacċt	ċċagġtġġċ	tċġġġattġ
144361	agtttġġġtt	ttċaagaacġ	ċġtġġġġġġ	ċaagaatagċ	ġġġttċċċċ	acċġġġtċċ
144421	ċttċtġattġ	ġċġacagtt	ċagġġgaacġ	ċġactattt	tġġttċatċċ	tċtġtġġat
144481	ġġġtttttċ	ċtġatċtāċa	tġtċċċttċġ	ġacċatġttċ	ġġġċacċac	tġċċacċġga
144541	ġgaagacġġġ	atċġċġgaag	tċġacġġġġa	aacġttġaa	ċġagċġagġ	acttġġttġġ
144601	ġġacacġġat	ġċatċġġagċ	ċġġġġgaagġ	tgaagġġġaa	gaagġtāacġ	aagacacġġa
144661	tġġġttġag	ċġtċċċagġt	ċġċċaacatġ	ġtċġacċċtċ	ġġttċċatġġ	atċġġacċag
144721	tġġġtatġtġ	atġġtġġtġa	ċattgaacag	tċġġġġġġt	ġġċatċgaac	gaattġaact
144781	ġacċgaacġċ	aaagagaacġ	ġacġtġtġaa	atāċġacġġ	ġtġatġttċ	ġtċġġġtā
144841	ċċtġġġġac	tġġġġġġġ	acċġacġġġ	ċacġġatċtċ	ġġġatċġag	tċaacġtġġt
144901	ċġġacġġġga	actċċġġġġ	atċtġġġġac	ċġttċġġġġ	ġtġġaagġtġ	ġċċtġaaacċ
144961	ċġġġacatċ	atċacġġġġt	tċaacċaaaa	ċaacġtċaac	aacċtġtċċa	tġċttċġġga
145021	agġġatġġtġ	gaacċċaaac	ċagġġġaatċ	ċġċacċġtċ	acġġttċtġġ	ġgaacġagaa
145081	atġġatġġac	ttċacġacċa	ċġtġacġġa	acacċġġtġ	ġacttġattċ	ġattġġtġga
145141	acacġġtġġġ	ġacġatġaaġ	tċgaagġċaa	ċċtċtġġġġ	ċtttċċtġġġ	tġtġġacġġt
145201	ġġġacġġtġ	ġġtġġġġġġ	aaattċaatċ	ċġġġġagaag	acċatċgaag	ġġatġġtġġa
145261	ċacġġġġat	ċtġatttġġġ	atġċċtċċċa	agacġġġġac	aacġtttċċt	acċagġtġġa
145321	ġttġtċġġac	tċtġagatġa	agċġġġttċ	ġġġtāaatċa	ġtġġactġġ	aacġġacċtā
145381	ċtġġtġaaa	ċġagacagġt	actġġtġġga	ċatġġacġtt	ċagatċġāċa	acċġġġġġa
145441	ġgaagċċċaa	ġagġtġġċtt	acċġaatċġa	agġtġċċaac	ġġċatċacġġ	tġgaagġtġġ
145501	ġtġġtāġacġ	aacāaaatċa	ġtċċċactġ	ġġġġġġtġġ	ġġġtġġġġ	acatġġtġtā
145561	ċaaaaccacċ	ġċġgaagġtġ	acġaaactġġt	ċtċġġttac	ġġactġttġa	agġġġġġaa
145621	gaacġaatċċ	gaagġġatġ	acċāaacact	ġttġġtċċċ	ġattċġġac	ċacġġġtġġ
145681	ċaacċtġagġt	tācatġġġġ	tġġatġċċā	ġtacttċacċ	ġtġġġatġt	tġċċacċġga
145741	agġāċaagag	tactċāaga	ċattċġtġġ	tġċġġġġġġ	aatattatċġ	ċġacċċaaġ
145801	tġġtġttċċċ	ġāċāāaaġ	aacġġġġġ	ċaacġċagġ	ttċtatċtġġ	acagttċċat
145861	ġġcagacġtġ	ċċċġġġat	ġtġġtġġaaġ	acaaċactċ	ġgattġttġġ	ċtġġġġġaa
145921	acagċċġġac	ġtġatġġaaġ	ċċactġġttt	ġġġġactġġ	atċtactacġ	ġttġġttċtċ
145981	ġttġtġġġt	aaacċtċttġ	ġġġġttġġt	ġġactġttt	tċċaacġtġġ	ġġactacġġ
146041	ċttġġġaatċ	ġttġtġġtġa	ċactġtġtġt	ġġagġtġtġ	atġttċċġġ	tttġġġāaa
146101	agġġġġatċ	aacġtċāac	ġġatġġāga	ġttġġġacċt	ġagġtġāga	agattġġġga
146161	gaagġāċāaa	ġacġacatġġ	aagġtġġġt	ċġgaċċċaa	ċġġgaactġġ	aacāacġġt
146221	ċġġġttāac	ċġatġġġġġ	ġġtġtġċċċ	ċatġttċċtġ	ċagttġċċaa	ttttċattġġ
146281	ċttġtāċġga	acactċtċġġ	tġġacattġa	actġġāċaa	ġtġġġtttġ	ċċtġtġġac
146341	ċacċtġġġġġ	tċaaacċtġġ	ċġġtċċġga	ċatġatġtat	tactġġġġġġ	actġġatġtġ
146401	ġġactacttġ	ġġagġġġġġ	ġġacġġttġ	ġttġġġtċġ	tacttċāāā	tċċtġġġat
146461	ġatġtġġtt	tġtttġttċċ	tġġtġġāġa	aaagatġttċ	atġċċacġġ	ċtāġġacġa

146581	cttccgtgtc	ccggctgggt	tgtgcatcta	cttcatcac	agcagtctgt	ggggaatcgg
146641	cgagcggatc	ttgggtcaaga	aaacgctgcc	atcgaagcct	cacttcgatac	cagcaaccct
146701	gcagggcgcc	gccgcgggtg	gcggcacggt	cgatggcaaa	gtcaacaatt	cggcgggtgc
146761	caatggaaag	aaaagctccg	acggcaaac	caaaacgatg	gccgaccgac	ttcgcgagcg
146821	attgggaact	cccgaagaag	aagccgcccc	gctacccaaa	gacgcgaaac	gcccaccatc
146881	gaagaagccc	ggcaacaaga	aacgcgcta	gcgtcttaag	acccccgacc	gcgcagcggg
146941	agggttcggg	taacgagcgt	tcagcgagat	ttctggggga	gggcaatccg	cgccacgtcc
147001	cacgctcggc	ccccctccctc	gcgtatgcct	gaacggcgtc	gcttgacctc	ccccaaaact
147061	tcgtttcggg	agaggtgcg	agggtgaaaa	tcgcgcggaa	agcgttctct	gaaaacggca
147121	ggccgcagct	tcgcgtactg	cgaggccaga	gtagaaccgt	tgtctcaact	gttccgcggg
147181	gcaaccctca	acggccaggc	ctcatcacca	tccatcaagg	tccgaagggg	cgacagatcc
147241	attgtcagag	tcgtcaggcc	ccggaacgat	gaaccactca	aacagctcag	gccgacggag
147301	ggcctccgct	ggcaacagg	aactcaacac	tcccacgaca	acctcgtccg	tgacaatgcc
147361	gggtaatgtc	gaccgcaacg	cggtgcaggc	gaatacgccg	atttcttgac	gttgcgatcg
147421	gggcagggca	gggcggagtg	tcattccgcc	acttcccaac	ctttctttgt	caaaaccagc
147481	tcctgcgact	tgtccactgt	ccttgcttcc	aagccatcaa	ctcgaaacgt	ggttggaag
147541	cagcgtttca	tgtcacgggt	cgtccgtggc	ggcatctcga	actcgtcgac	actctcgttg
147601	gtttcgtatc	acaccgttgc	agctttgccc	gaacgggtta	gcaccgagat	ctcaatctgc
147661	gctgatttgg	gtcgacaaa	caaataaacg	gcgtagttaag	tcgtttgatc	tttcgtcgcg
147721	acagccgccc	ccgtttgcgt	gatgtgtttg	gccacgatgt	tctcatgggtg	cggcgggtgaa
147781	tcgatccatc	ccggaacaaa	gatataaatc	aaactcttcg	cagtgacttc	accagtgttg
147841	gtgcgataag	caatgtttctc	tctcacgacg	cagtactcgt	accccccgcc	ttcggcacgc
147901	tccgcccggc	tcttgccatc	cgcgtgatga	ccgtacttgc	ccgattcagc	catgaactcc
147961	gcaaaccttc	tcgcggttgc	ctgcaactcg	tcgtttcacct	gcaactgacc	gagccccctc
148021	tttttgcggg	agtcgltgat	ttgcttgacg	attgcctctt	ccacttgctg	gaccaattcg
148081	ccatcgcttt	ccgaatcagc	agcgaccgcc	gtcgattcct	cttgagccat	caacggaccg
148141	acaaacaaca	gacatccaag	catcaaccaa	ccacgcactg	catcactcct	ggtagagaat
148201	ttgaattgaa	accgaatcac	ccaatgagca	gcgatgatga	atcgatcatg	ctattctttg
148261	cctcgtctgt	ttcgtcacag	cgccgaccca	aatcaatcgg	tcacgaccag	cgattctctc
148321	cgccttcacc	gagctggtaa	aacgttgctc	acccctgatc	aacagcgccc	ctttcgtctg
148381	cccactcac	tgatttgaca	ccgtcccaac	tcagcatgcg	aattcaagct	ccttctttcg
148441	tcgatctcga	aacgcccacc	ggtccgatgc	ggacgcattt	gtttcgcccc	gacggtcccc
148501	gccgctatcc	cggtgtgatt	ctttacagcg	agatctacca	gatgacggcg	ccgatcgctc
148561	gcaccgctgc	tgtgctggcg	ggacacgggt	tgtggtcgc	cgttccggat	gtctaccacg
148621	agtacaccga	actgggcgag	tcattcgcgt	acgacaaga	aggcaccgac	cgcggcaacc
148681	gattgaagat	cgaaaaggaa	atcgccgct	acgatgccga	cgctcgatcc	gtcatcgact
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148801	gccacctggc	atttcgggca	gcgatgaacg	aggaagtcaa	agccggagtc	tgttcttacg
148861	ccaccgacat	tcataaacga	agtctcggca	aaggcatgca	cgacaacagc	ctcgaccgca
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148981	ccgaaggacg	ccggtatgatt	tacgacgcga	tgactgctgc	cggcgtcagt	ttttcctggc
149041	acgaattcaa	tggcgagcac	gctttctatg	gagacgaggg	gcacgcgtac	gaccagaaac
149101	tcgccttgct	gctcaactcc	atggcgtgcc	aacacctcaa	ccgccatctg	cggtagcggc
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149221	aatcgtccca	cttacgaatg	agcgacgatc	gcgtatcctt	tgcggttcgt	tttcgcgaaa
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149341	tgattttcgac	ccgtgttacg	aaccacacc	tcggcgcg	ttcgcaaatc	tgcgtcggc
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149521	gaagcactga	tcaaacagc	tggccacgtg	ccaaacgaaa	gcgtgatcct	gatccgcggc
149581	gtgggtggcg	atcgcttggg	aggcaaaacc	aacgcgaaat	tggaaaccgg	tgaaatcgaa
149641	gttcgcagcg	aacacttcga	aatcctttcg	gcctcggaaa	cgcctccctt	cacaccggcg
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149761	aaagaaatgc	agcaggccct	gatccgtcgc	agcgaaatca	tcaagtgcac	gcgggactac
149821	tttgcgcgag	acgatttcat	cgacgtcgaa	acgcccatcc	tcggtcgcag	cacccccgaa
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149941	caatcgccgc	agctttacaa	acaaattctg	atggtcgcgg	gtttcgaccg	ctacgtccaa
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150181	acctacgaag	aagccatgcg	tcgcttcggg	tccgatgtct	ccgatttacg	attcggtttg
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150481	gaagaacact	tggctgaaat	caaagcactc	atgggcggcg	aaccgggtga	cttgctgatg
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150721	gctcctctcg	aagaagacct	gccgcttctg	aaagagtcgc	ccgagaaatg	tctgtctcaa
150781	gcctatgact	tgttcacata	cggatcggaa	gccggtggcg	gaacgattcg	gatccacgac
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150961	ttgggtgtcg	atcgctgggt	gatgctgttc	gctggcctcg	aaaacattcg	cgaagtgatc
151021	gcgttcccca	aaacgcaaaa	ggctgccgac	atgatgaccg	gagctcctgg	cgaagtggac

151141	ċgċātcaatc	tagttġcccg	ġctcacċtċg	ttġġtċacċ	aaccaaātċ	tgctaċaaac
151201	gġtggttgga	gċgaggtcgg	agcagggcag	ggċtgċgtg	cġttcactgc	cġtctggtct
151261	cġccgattga	atċtċttttc	tatcġacgga	tċgcatċatc	gċcġtaatc	gccacċtċgg
151321	tttggttgga	gccaccagcg	tċggcġtċgg	cġcġatċgtg	ggcġgġgga	tċċtċcact
151381	ggcġgagtc	gċgtttġcga	caacaggtċc	atċcġcġtt	ċtggcġttg	gċċtcaacgg
151441	cġtcatċcg	atċċtġaccg	cġċtġagttt	cġcġgagatg	gċtġgaagt	tċċċġaatc
151501	cġgġgġact	tacacċttca	gċcġcaaagt	ċċtċtġagtc	gaatċġċtt	tċacġgtggg
151561	ttgggtċgtt	tggtttgcat	cġatċgttġc	ċċcġttċtċ	tatġcġatċg	gċttċġgtag
151621	ttttġcġacg	ċtġttġctga	gġgaactġta	tċcġactċag	ggttċġgtċc	cacattġgġt
151681	tggġgaacċc	tggagċgtċc	ċtġtġgtttc	gċttġcġacg	acġtċġgta	tġggcġgċċt
151741	gatġacġttt	cġaacġtċcġ	gtġgaggagc	ċtġgatċaac	gtġcġaaag	gtġgtġċtt
151801	ċtġgtttċtġ	atċatġcġg	gattċtġgat	gġtġacġgg	caacċġttt	ċcaaaccac
151861	cġcġgaattg	cġtċcġtttċ	tċcġatċggg	ċtġggġcġgt	ttġgtacaag	ċcatġggata
151921	cagċttċatc	gċċttġcagġ	ggtttgactt	gatġcġcġca	gtġggġgtg	aagtċġcġga
151981	accġaccaag	aacatċċċac	gagġatġtt	gġtġtġġtġ	gtċattġġġt	tgġtġatċta
152041	tttgċcactt	ttġtttġtġc	tġaccacġġt	ttġgtaccġat	ggatċċċaaa	gċattċġcġga
152101	attġgġcġga	tċcġatċċċg	aagċġgtġgt	cġcactġgċc	gġcġgġact	acċtġgġac
152161	atcagġċtat	tġgtġgtġc	tġatġcġgġc	ggttċtċtċa	atġttċtċġg	ċtċttċaagc
152221	caacċtġttt	gġgġatċġga	gaattġġtċt	cġcġatġtċt	cġggacaaca	cactċċġaa
152281	cġcactġagt	cġtttġgċġg	ċġgatċċġg	ttċċċċtġg	atċtġgtġt	ttġgtġacġac
152341	cġgtttġgtġ	tġċttġctga	ttċagġtttt	gċcagacatt	gġgġcġgċġg	ggġcġgġatċ
152401	cagċttġatc	ttċċtġgtġga	cattċġcġat	cġċċattġg	ttġgċcatat	ttġgtacġgġca
152461	acġcagġgtg	ċtġacacġcġ	cacġgttċcġ	agtċċġgggt	tacċcagġcġ	ttċċtġtġġt
152521	tġgġgġċttġ	gċttġgttġg	cġttġgtċat	ċttċcaaggc	atġcġgtġc	ċtgaagġtġg
152581	aatċatġcġg	tġcatġtġgga	tġcġatġtġg	cġgġtactġ	ttċċtatċċt	ttġttġġtġc
152641	tġgagċċġg	ċtġaccġatġ	tġtċcaacat	cġcġagġaat	ċċtgaactċt	cġcġatġġcġ
152701	cġgtaaċtġc	ċġttġgtat	ttġgtċċaat	cġcġaatċġg	aacaacġtċ	gġcġatġat
152761	tġcġttġgġc	gacacċttġg	ttċċġcġcġ	ċċtġggacġc	gtġtġgttċ	aaacġttġt
152821	cġtġcġacċt	cacġactġgg	atċġttġgt	caatcacġg	ċċċtġġtċ	aaċtċactċ
152881	ggġtatġaac	gaaatċttġc	acġċtċcġc	gagtċtġgggt	gtġcġgtġcġ	aaacċċtġac
152941	cacġgtttċt	gġgaacċca	tġatġgaaat	cġċċġcġtċ	gċcaaactġc	acċaatġċca
153001	atġgtġtġtġ	ttġggġttġga	gġgagatċac	ttċġgagġca	cġcġacacġc	cġtġgaagg
153061	tttġtġcġgg	caactatċca	gġatġttġt	cġtġtċtġcġt	gġtċċcaagg	attġgġcġgt
153121	cġaccaaaġc	cagcagatċt	tġgttċcġgt	cġgtġgacġt	ggġgġcġacġ	actactġgt
153181	cactġcġactġ	ċtġagcagtc	tċtċtġcġta	acaacaaga	caagtċaagt	ttċtġcġagt
153241	gatċċċacċc	gatacacttċ	gtġcġatċca	aaaacġtatt	cġcaaagagt	ttġgatġggac
153301	aactġcġatċ	aaġcġggġca	gggtttġtġga	acġcġagġtċ	gtġcġgagġca	atġatċcagġt
153361	caaaacaatċ	gġcġaccġag	ċġgġcacġgġc	aggactġatċ	attċtġgggtġ	ċtcaacġact
153421	gggaccacġg	caaaagġċat	tġgtġactt	cacċġcġaaġ	gtġcġġtġcġ	aatċġcġactġ
153481	ċċċġtġatċ	atċatġacġc	gġcġcġgġta	aggaaġgaaa	acċtataaaġ	tġcġtġgġcaa
153541	ċtġacagactġ	ċcagacatġc	gcaatċtċat	tġċċtġcġac	ċtġtġgaga	gċċaatġcġc
153601	ċtġtġcġat	tġgtġcġgtt	cagġcġacġ	gagġġċtċc	gtġcġgġgaca	agtaactġga
153661	ċatċtċċcaa	gacġgċċċġg	ttċġggġcaa	ggaccġcġag	gċcagagtag	aacagttġtċ
153721	tcaactġttċ	cġtġggġcag	ċttċcaaagg	ċcagġcġatġc	tġgġcaacċa	agtċacttċ
153781	caacġgttġcġ	cġtġacġcġga	ċtġcagġgaca	gġcagġgċċc	acġcaaacat	ttġgggacaa
153841	atġttċtact	ċtġtttċċca	cġacagċċċc	gtċġgagġgġc	aggċġatġc	aacġaacġaa
153901	tġagċċacat	tġcċaatċac	ċatġgttċca	ċċcaacaagg	tċcġaagggt	cġcacagġca
153961	attċċċcġga	gġcagaagtc	gġtġgġaat	gacagatātċ	agacttġgġc	gagġtċattġg
154021	tċtġacacċt	gġtagġgagc	ċcaatġġtġt	gġtġcġattġ	actġtġatċa	cġacaactċt
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187741	acggtctcat	tgcgagcctg	ttcgggtgac	aagtagcccg	gtḡtgccgac	gacḡctgtca
187801	ccgcgagcca	agccttgac	cgcagatcct	gcgaccgcca	agccgaagtc	caaaatcctg
187861	acccḡttcgg	aaggcgattg	aatccacaag	ttcgccggct	tḡatḡtctcg	ḡtḡaatḡatt
187921	cctcgatcgt	ggggcgcttc	caatcccaag	gcgactḡgat	ccgcḡatcgc	ḡatcacttct
187981	tccgagctga	attḡḡcgacc	ḡḡattḡcagc	aactḡctcca	gcḡttcctcc	ctḡcaacagc
188041	tccatcgcca	agaatḡḡtḡt	ḡccattḡcḡt	tḡcccaactt	cḡaacagcḡt	cḡcaacḡtḡ
188101	tcatḡatḡḡa	ccgcḡḡccat	cḡagcḡḡcḡt	tcctcḡacḡa	tcḡḡtḡḡcḡ	actattcḡḡc
188161	ḡatttccḡcḡa	atcḡctcḡtt	catcactttc	agagccacḡḡ	tḡcḡḡtḡcaa	ccḡḡḡtḡct
188221	tḡcḡḡtḡḡḡt	agacatḡccc	catḡccḡcct	tḡḡcccagcḡa	attcḡatcac	ḡcḡatacḡḡc
188281	cctḡḡtḡḡḡc	ccaattcḡcc	agctḡcttct	ḡḡḡḡḡatcca	ḡaaactcagḡ	ḡḡḡḡaatca
188341	ḡḡtḡcḡḡḡcḡ	ḡtḡaatcḡḡt	catḡḡḡtḡc	cḡḡḡḡtḡcḡa	tḡḡḡḡaaacca	atḡcattcca
188401	cḡḡḡtḡḡtḡcḡ	atḡcḡḡtḡḡa	cḡḡḡtḡḡcc	agcḡcḡcccg	cccaactcḡt	tḡḡcḡḡaat
188461	ccaaccctḡc	agḡḡḡaaaca	ctḡḡcacatc	ḡcccaacaac	tcttccḡcca	cḡḡḡaatctḡ
188521	tccccatḡḡa	atccatḡccḡ	ḡḡtctḡḡata	cḡattḡḡccḡ	ctḡḡattḡḡḡ	ccḡḡḡaccac
188581	cḡccctḡccc	tḡtcccḡctc	tḡaacatcta	ttcḡccttct	acccḡcḡacḡ	agccḡḡḡtḡc
188641	acḡaacccḡct	atccatḡatc	tcḡcḡcagḡḡ	aatḡacḡttḡ	ḡcccagccḡt	tccaagḡḡḡc
188701	tḡacaacaac	ctḡcḡḡtca	atcḡcagḡḡḡ	tḡḡcaagta	atcctḡḡtḡa	agttatccḡa
188761	cḡḡḡtḡḡḡḡc	acḡatcḡtḡcḡ	ḡḡatḡatḡḡḡ	ḡaatḡcḡḡac	ḡaaaccacct	tḡḡacacctt
188821	cḡaccḡcḡḡḡc	ḡactacatcc	attḡcaccḡḡ	tḡḡaacccag	ḡtḡcacaacḡ	ḡttccctḡca
188881	ḡḡtḡatcctc	acccḡḡatcc	agcḡcātḡḡa	ccḡḡḡcḡḡḡa	ḡtcḡaccaaa	ḡcḡatttḡcḡa
188941	cḡḡcttḡcḡat	ḡccaaccaag	cḡḡacaacaa	cttcacḡcḡt	ctḡḡḡḡḡḡḡ	tḡḡḡḡccac
189001	ḡatctcaca	ccḡcactḡc	attḡcḡtḡḡc	ttcagtcata	ctḡaacḡacḡ	attcḡttḡḡt
189061	tcaatcḡttt	cḡccagḡccḡ	cḡcḡcḡḡḡt	ctccaatcac	catḡcctatc	cḡḡḡcḡḡact
189121	ḡctcḡaacac	accḡtcaaca	tḡatḡḡaat	ḡḡtccḡactḡ	atctcaccḡc	ḡatcḡccaa
189181	agtcḡacacḡ	ḡacctḡttḡt	tḡatḡḡḡḡḡc	cttccctcac	ḡacttḡḡḡḡḡa	agattḡatḡa
189241	actḡcḡḡḡcc	agcḡḡcḡḡḡa	tcagctacac	cḡaccḡḡḡḡt	caactcḡttḡ	ḡacacatcḡt
189301	catcḡḡcḡḡt	cagcḡtttḡḡ	ḡcḡḡḡḡḡḡḡ	cḡcḡḡḡḡḡḡ	ḡaagcctcta	ccḡḡccaaa
189361	ḡttttcḡacc	ḡḡactḡcḡḡc	accaattḡḡḡa	acactḡḡatc	ḡtcagtcacc	acḡḡḡḡtctt
189421	ḡḡaatccḡḡc	agtcḡḡḡḡḡa	ttccagtcac	ḡctcḡḡḡḡḡc	ḡttḡcḡttḡc	atcacatcḡa
189481	caacctcḡat	ḡcaaḡcḡtḡcḡ	cttcḡtactc	ttcḡatcatt	ḡattccḡḡac	tḡcḡtḡḡtḡa
189541	tḡḡḡḡḡḡḡḡ	acḡḡḡḡḡḡḡ	ccccatcḡat	cḡḡḡḡcḡḡḡḡ	ctttḡḡḡḡḡḡ	ḡcḡactcḡḡḡ
189601	aattccacct	cḡcaatcaaa	aacḡḡḡḡḡḡ	ḡcccaacaag	atḡctḡḡḡḡḡ	agccḡḡcḡḡḡ
189661	ttḡctḡtccḡ	ḡtḡḡactḡḡḡ	cagcḡccacḡ	tḡtḡḡḡḡḡḡ	tḡcḡccḡcḡḡ	ccaagḡḡḡḡ
189721	ḡaagttcctḡ	ḡatḡḡcctḡ	cḡcḡtaccḡḡ	caacḡccatḡ	acḡḡḡḡḡḡḡ	tḡatcḡḡḡḡḡ
189781	ḡcaaaacaag	ccagcctḡat	ḡḡḡcḡtḡḡḡ	tḡcḡaccḡḡḡ	tḡatcḡacat	tḡacctḡḡḡḡ
189841	cagcttḡḡḡḡ	ḡatccḡctct	ḡḡtḡḡactḡḡ	ttccatcḡccḡ	tcccaaaatc	ḡḡatcatḡḡc
189901	ḡacaaaatcḡ	cḡḡḡcḡacat	cccḡḡḡḡḡḡ	tacḡtccḡḡḡ	cccḡcaacac	aatcttctḡḡ
189961	tḡḡtacḡctt	tḡḡcḡḡttḡc	cḡḡḡḡḡḡḡḡ	ḡḡatcḡcḡḡḡ	acatcttcat	ḡḡḡcḡtcaat
190021	ḡcactcḡact	acagcḡḡḡḡḡ	cccḡḡattḡc	cḡtccḡḡḡḡ	tcattcagcḡ	atttcaaacḡ
190081	atḡḡcagcḡt	tḡḡccaccaa	agcagḡḡḡḡḡ	ḡaagacḡḡḡḡ	attcḡḡttac	cattcacacḡ
190141	cḡḡtḡḡctt	actḡḡaccaa	ḡḡccḡḡḡḡḡ	atccagcḡḡḡ	ḡaatcḡḡḡḡ	ḡḡḡḡḡḡḡḡ
190201	tactcacaac	cḡctḡtccḡḡ	ctatḡaccac	caagḡcagcḡ	ḡcḡacḡḡḡḡ	ḡcḡtccḡḡḡḡ
190261	ḡḡtcaatḡcḡ	acḡcctḡttt	ḡctḡḡḡḡḡḡ	aaagḡcttḡcḡ	cagaaaacḡḡ	ḡatcḡccḡḡḡ
190321	ccḡḡcaatcḡ	ḡctḡḡḡḡḡḡ	cḡatctḡḡḡḡ	ḡacḡḡḡḡḡḡ	tḡḡttḡcḡḡḡ	ḡtḡḡḡttḡḡḡḡ
190381	cattḡḡḡḡḡḡ	tḡccḡcagcḡ	aaacagttḡḡḡ	ḡacacatḡḡḡ	ctactctaga	ḡtḡḡccctcḡ
190441	tcaacḡcḡḡḡ	cḡcḡattcḡḡ	ḡcagattḡḡc	cḡḡḡḡḡḡḡḡ	ctcḡḡḡḡḡḡ	ḡḡattḡcaaa
190501	ḡtḡcaaattḡ	atcaatḡcaa	attḡcaaagḡ	atttccḡḡḡḡ	cḡḡcaactḡḡ	cḡtḡḡḡḡḡḡ
190561	cagacctḡcḡ	actḡccaatt	tḡcaatḡtcc	actttḡcaat	ttḡcaatcḡc	cccḡtctcḡc
190621	cattcctctc	atḡḡcagḡtca	cḡccagaccḡ	cccḡḡḡḡḡḡ	agccḡtḡcḡt	cttagctcḡḡ
190681	ḡḡtḡḡḡḡḡḡ	ccḡḡḡḡḡḡḡ	acḡḡḡḡḡḡḡ	ccatcagḡtḡcḡ	cccḡḡḡḡḡḡ	ḡḡccḡtḡcḡḡḡ
190741	agcḡttccḡḡ	cḡttḡttḡḡḡ	aaḡcacḡacḡ	cḡaacḡḡttḡḡ	ḡaactḡḡḡḡḡ	ḡḡḡttḡcḡḡḡḡ
190801	ḡtḡḡctḡḡḡḡ	cattḡḡḡḡḡḡ	ḡḡcccaacḡḡ	aaacagttḡḡḡ	ḡacaactḡḡt	ctactctḡḡḡḡ
190861	ḡḡtḡccctcḡ	tcaacḡcḡḡḡ	cḡcaattcac	cḡacattḡcc	cḡḡḡḡḡḡḡḡ	ctcḡḡḡḡḡḡḡ
190921	ḡḡattḡcaaa	ḡtḡcaaattḡ	atcaatḡcaa	attḡcaaagḡ	atttccḡḡḡḡ	cḡḡcaactḡḡ
190981	cḡtḡḡḡḡḡḡ	cagacctḡcḡ	actḡccaatt	tḡcaatḡtcc	actttḡcaat	ttḡcaatcḡc
191041	cccḡtctcḡc	cattcctctc	atḡḡcatcac	ḡccagaccḡc	cccḡḡḡḡḡḡ	ḡccḡtḡcḡḡḡ
191101	ttḡctccḡḡḡ	atcḡtccagc	cḡcacḡacḡt	cagcḡḡttḡḡ	acctḡḡactt	ḡḡttḡcḡḡḡḡ
191161	tḡccttḡḡḡḡ	ḡttḡḡḡḡḡḡ	ḡccḡcagcḡḡ	acagttḡḡḡḡ	acaactḡttc	tactctḡḡḡḡ
191221	cḡḡtccattt	caacḡcḡatc	ḡcḡattcac	ḡacatctctt	ctactḡḡḡḡḡ	ctcḡḡḡḡḡḡḡ
191281	ḡḡattḡcaaa	ḡtḡcaaattḡ	atcaacḡcaa	attḡcaaagḡ	atttccḡḡḡḡ	cḡḡcaagḡtca
191341	catḡatttca	ccḡacctḡcḡ	attḡccaatt	tḡcaatḡttt	actttḡcaat	ttḡcaatcḡc
191401	cccātḡcḡat	ctcḡcḡḡḡḡḡ	ttccḡcḡttḡḡ	ccccccḡcag	ḡttttcccta	cttcaacagḡ
191461	aaaccḡḡḡḡḡ	ḡatttccaacc	ḡḡtctcḡḡḡḡ	ḡtttcaacaa	atccḡaacḡc	ḡttḡcḡḡḡḡḡ
191521	tacttttcaa	cctcḡḡḡḡḡḡ	cḡctḡḡccat	ttactḡacḡt	tcaaacḡcctc	ḡatḡḡḡḡḡḡḡ
191581	tccḡctttḡḡḡ	ḡctcḡtḡcḡcc	ttcḡaacatc	cḡccḡḡḡḡḡḡ	acḡacḡccaa	ḡaccḡḡḡḡḡḡ
191641	ctḡttcttca	attcḡccttḡḡ	acḡttḡcagḡ	tḡḡacttḡcḡ	cacḡcagcḡḡ	ctḡacḡcḡḡḡ
191701	cḡcaccacḡc	ḡttḡḡḡḡḡḡ	cacttcatcḡ	ḡctcccattt	cḡctḡḡḡḡḡḡ	tttcaagagḡ
191761	tctttḡactt	cḡtccaagḡt	ḡḡccagcttḡ	tḡcḡccctcḡc	cḡḡttḡḡcḡat	tḡcḡttcḡḡḡ
191821	acatcḡḡḡḡḡ	accattccac	atḡḡctḡḡḡḡ	aaaccagḡḡḡ	ḡtḡacttttt	ḡḡḡacccttḡḡ
191881	ccagcḡḡḡḡḡ	ccattḡḡcḡat	ḡḡccagḡḡḡḡ	ttcaagagcḡ	ḡḡḡttḡḡḡḡḡ	ttcatcḡḡḡḡḡ
191941	tcttcttḡcḡḡ	aaactḡḡḡḡḡ	atcḡḡḡḡḡḡ	tḡḡtcatcca	ḡctcḡtcatc	accactḡcḡḡḡ
192001	tḡtttḡacct	ḡccaaatttc	aaacḡccḡḡḡḡ	acḡḡḡḡḡḡḡ	ctttḡḡḡḡḡḡ	ḡtḡcḡḡḡḡḡḡ
192061	acctccatcḡ	ctttḡcḡḡḡḡ	cḡccḡḡḡḡḡḡ	atcḡcatcag	cattḡḡḡḡḡḡ	ttcḡatcḡḡḡḡ



192181	tgctcāgaaa	ḡattcḡgcaa	aacgṫtṫṫṫ	ṫcaatgṫcḡa	tttgṫḡḡccṫ	ttcctcatcā
192241	tcgcgḡatgc	cttcaatgct	gggcccgaag	atttcattgt	cgaacgcttc	atcgaccaaa
192301	gtctcgaccḡ	cccaaaacgc	ttcttcgatt	ttccagttca	ctcgcggtg	actggctgta
192361	ttggcagḡaa	cccatgcccḡ	aattccttcc	agcggcggtg	ttggaaattg	gagcattcga
192421	gcccḡcaaac	gatagcggct	gggtttgtcg	gtcaccḡḡag	gagcatgcac	gtagccacga
192481	ṫcgacaaḡt	cḡaatṫḡcc	ctgacccacḡ	accḡcgatac	cgccagctgc	ttḡcaagḡca
192541	tcḡaaaccṫṫ	gattctccaa	cagattcaaa	atḡcḡaaacṫ	tḡttḡccṫcg	atccactṫṫḡ
192601	ḡcḡacḡtcḡc	gaatgatccḡ	ḡcccātḡṫc	aaḡḡṫṫṫḡa	caaaccattc	ḡacctḡcḡaa
192661	ccttcḡactṫ	caattṫṫḡṫ	ācḡṫḡaaḡa	ḡcctḡṫṫṫc	aaacḡḡṫṫcḡ	caacaatḡḡṫ
192721	ḡcctṫḡṫcca	agḡaatcṫṫc	ccḡḡccatcḡ	ttḡḡcaatcḡ	cḡṫccḡaaṫ	ttccagcacc
192781	accḡaatcac	ḡatccḡatḡc	ḡatcacḡcḡa	tcctṫḡḡṫca	ḡacagacaac	aacṫṫḡṫṫcḡ
192841	atcṫṫcagṫṫ	ḡcccḡḡṫcḡ	cḡṫcṫṫḡḡṫ	cḡḡṫacacḡc	ḡṫacḡḡṫṫṫc	accagcatḡa
192901	ḡṫḡacatcḡḡ	tcḡḡḡḡṫcḡc	ḡccḡṫcḡḡṫ	ttcagatcṫṫ	ḡatcaactcḡ	cṫṫcaagaca
192961	ḡcṫṫccḡcṫṫ	ccḡcḡṫḡṫṫ	tcḡcḡcḡaatḡ	tcḡḡcḡacaa	cḡcaaacḡḡa	agacḡḡṫcḡḡ
193021	cḡḡṫṫḡṫcḡṫ	ttṫcaaacḡḡ	caaccāaaacc	ḡcḡatcactṫ	cṫccḡḡṫcḡc	ḡatcṫcḡṫac
193081	agṫṫccṫṫṫcḡ	ḡacḡcaatcc	ḡactṫṫṫḡṫca	cccagṫṫṫṫṫ	cccacacḡḡc	acṫṫḡḡḡṫḡ
193141	ccḡaaattḡḡ	catcḡatcaa	ṫḡḡcṫṫcatc	ḡagḡḡatcat	ccḡṫḡatḡcc	agacagagṫṫ
193201	ḡṫṫṫṫṫṫṫṫ	acḡaatcaca	cacacḡḡṫc	agḡṫṫḡḡḡaa	tacḡṫactac	accagcḡḡcc
193261	ḡṫḡṫcḡḡḡca	acāactṫcaa	cḡccḡṫcatc	aaaacḡḡḡṫṫ	ṫḡḡcacḡḡcc	cṫḡṫṫṫḡcc
193321	ccḡḡcṫṫḡṫ	tcḡcagḡccc	agcḡṫṫṫṫṫ	tcḡagcccḡḡ	cṫṫcṫṫṫḡc	ḡḡḡḡḡccḡca
193381	tcṫṫḡḡḡḡcḡa	tcḡaatḡṫḡa	tcāatcaaa	cacacḡḡcca	ḡaacḡḡṫḡṫ	catcacatḡḡ
193441	agcacḡcḡcḡa	ḡḡcḡḡcaagc	cṫḡṫḡṫṫcḡa	ccḡṫcḡaaḡṫ	ṫḡḡaaaaata	ṫḡṫṫcḡcḡṫḡ
193501	ḡḡattḡatca	cṫcḡṫṫṫḡṫc	cḡccactṫḡc	accḡṫṫḡaa	aattcattca	agatcḡṫṫṫ
193561	ḡaaatcatcḡ	ḡaatccatcc	ḡagccḡcḡṫ	cṫṫḡcḡcḡa	cṫḡḡṫcagc	cḡḡccḡatāt
193621	cḡṫaaaccṫṫ	tcṫatṫṫṫcḡḡ	ḡccḡaaatḡc	cḡatḡṫcacc	atccatcḡcc	ṫḡattṫḡṫḡc
193681	cṫṫṫḡcaagā	ḡaccaaaatḡ	accḡaaacḡc	agḡaaactcc	ḡṫaccaaaac	cccṫṫḡattḡ
193741	agcḡṫṫacḡc	ḡṫcacḡagaa	atḡḡcḡṫṫṫc	actḡḡḡḡṫcc	ccagcḡḡḡcḡa	ttcḡcatcṫṫ
193801	ḡḡcḡaaagḡṫ	cṫḡḡattḡcḡ	cṫagcḡḡagḡ	ccḡaaacaagā	ḡṫcḡḡaaṫc	ḡcaatcacḡḡ
193861	atḡcccāaat	cḡaaacaactḡ	aagṫcḡṫṫcḡ	aaaacaāat	aaatcṫḡḡac	ḡcḡḡcḡḡcca
193921	aatacḡaaḡc	ṫḡaaactṫcḡc	cacḡatṫṫcḡa	ṫḡḡcccacḡṫ	ccacḡṫṫac	ḡḡḡcṫcagṫ
193981	ḡcccḡḡacḡc	cḡḡṫḡḡatc	atccacṫṫcḡ	ḡcḡcḡaccag	ttḡṫṫṫcḡṫḡ	accḡacaacḡ
194041	ccḡacṫṫḡṫ	ḡṫḡattṫcḡc	ḡaagccṫṫḡḡ	agṫcactḡc	ṫaaacḡṫṫḡ	ḡcḡḡccacḡa
194101	tcḡaccaaat	ḡḡcaaaatṫc	ḡcḡḡccḡagc	accḡcḡacṫṫ	ḡccṫṫḡṫṫc	ḡcṫṫṫṫacc
194161	actṫṫṫcaacc	agcccagccc	acāacḡḡṫcḡ	ḡcaagcḡagc	atḡṫṫṫḡḡḡ	atṫacḡacc
194221	ṫagṫṫṫṫṫḡa	tcṫcḡaaḡcḡ	atcḡaaatcṫ	ḡṫṫcḡaaac	tcṫḡcḡṫḡca	cḡṫcagcca
194281	aagḡcaccac	ṫḡaaaccḡag	ḡcḡagṫṫṫṫ	ṫḡḡaatḡḡṫṫ	cṫccḡḡcḡac	cacḡacaagḡ
194341	tcḡḡṫcḡḡṫṫ	ḡḡaaaaacḡa	atcḡṫḡaaā	agṫṫṫcḡṫṫ	ṫḡagṫcḡḡṫc	ṫacḡccḡṫca
194401	ccḡḡacāaac	cṫaccṫṫcḡc	aaḡṫcḡacḡ	cṫcaattḡṫṫ	cḡacḡccṫṫḡ	tcḡḡḡḡatcḡ
194461	ḡḡcaaagcṫṫ	ḡcacaagatc	ḡccaccḡaca	tcḡḡṫṫḡṫṫ	ḡḡccḡḡṫcḡc	aaḡaagṫcḡ
194521	aagagccḡṫṫ	ṫḡagaagaaḡ	caaatcḡḡca	ḡṫcḡḡcaat	ḡḡccṫacaaā	cḡcaaccḡcḡa
194581	ṫḡcḡḡagcḡa	ḡcḡaatcṫḡṫ	ḡcactcḡḡṫc	ḡattṫḡṫcat	ḡagcṫḡcāā	ḡagcṫḡcccḡ
194641	cḡatḡacccḡ	agcḡaccḡag	ṫḡḡagṫaaac	ḡcactṫṫcḡa	cḡacagcḡcc	aaaccḡccḡṫ
194701	ṫḡḡṫcatccṫ	ḡcaagcḡṫṫc	ṫḡḡcāaatcḡ	accḡḡḡcact	cḡṫḡṫṫḡatḡ	caaāacḡṫṫḡ
194761	ccḡacḡḡaaṫ	ḡḡṫcḡṫṫac	ccagccacḡa	tcḡcaaaaaā	cṫṫḡḡḡḡḡcc	ḡagṫṫṫccḡṫ
194821	tcātḡḡcḡac	cḡagaacatc	ṫḡatḡcāag	cḡḡṫcḡṫḡc	ḡḡḡcḡḡḡḡac	cḡṫcaagatt
194881	ṫḡcacḡagca	aattcḡcḡṫḡ	cacagccāag	cḡḡcagcact	agaagṫcāā	cagaacḡṫḡ
194941	ḡcḡacaacḡa	cṫḡṫḡḡḡaa	cḡṫṫcāaaḡ	ḡcḡacḡagaa	cṫṫcḡccḡḡc	atcḡactḡḡḡ
195001	aagṫḡcḡat	ṫḡatccḡcac	ḡcṫṫcḡḡḡḡ	ḡḡcḡagṫcc	ccaacaagṫc	ḡacḡagṫṫca
195061	ṫḡḡaaḡcḡat	catcacccṫṫ	atccḡccacḡc	ḡṫṫactṫṫḡḡ	cagcḡacagc	ṫṫḡagcḡṫḡḡ
195121	aagṫcacḡḡṫ	cṫḡattṫcḡa	cḡḡḡcḡactḡ	cccṫṫaaacḡ	caaagatṫṫc	ḡccḡḡcḡḡṫḡ
195181	catatcḡccḡ	ḡcḡagatcaa	atḡṫṫṫṫṫṫ	ṫḡḡatcḡṫṫ	ḡṫṫṫṫagaaā	caataagṫṫṫ
195241	ṫagaacaagā	agatcḡṫḡṫc	aatḡccḡaaṫ	ḡṫḡḡṫṫḡḡṫ	cḡṫṫṫṫḡṫṫc	ḡṫṫṫṫcāag
195301	atḡccḡḡṫca	cḡṫcḡḡṫṫṫc	ḡṫṫcḡccacḡ	ṫccacḡcḡaa	ṫṫṫcḡḡacḡ	ḡatcaagacḡ
195361	ṫṫḡcḡṫcḡcḡ	ḡṫṫṫḡacṫṫ	ḡḡcāccāag	ḡṫṫaatḡcḡṫ	agacḡṫcāac	ḡṫṫcḡṫṫḡḡ
195421	aagacacccḡ	cḡṫcḡḡcḡṫc	ataccactcḡ	aagcḡactḡc	ccaagccāā	acaatcḡṫṫḡ
195481	accḡṫḡṫagā	tcagḡṫagṫṫ	ḡṫṫcagḡccḡ	ṫagḡṫṫṫṫṫ	ṫḡaagṫṫḡcc	accattḡccḡ
195541	ṫṫṫṫṫṫcḡṫ	ccatḡṫaatc	cḡactḡcāag	acataactḡca	ḡṫṫḡatcḡḡṫ	caacḡcḡatḡ
195601	tcḡḡṫḡacḡa	tcḡagṫḡcat	ḡṫagccṫṫḡc	ḡacḡṫḡḡṫḡc	cḡḡṫḡḡṫṫc	atccḡcaāāā
195661	cḡṫccagcḡa	cagṫṫḡcḡṫa	ḡḡṫcacagṫḡ	accḡṫcḡṫcac	tcātḡḡṫṫāā	cḡagacaccḡ
195721	cccāagaacḡ	agṫcḡccḡṫṫ	ḡṫṫṫṫcḡaaā	cḡḡṫṫṫṫṫṫ	aaccāaaḡḡṫ	ḡṫaaccaccḡ
195781	ṫaaacḡḡṫca	agṫcatcḡṫ	agcḡṫṫḡṫag	ḡṫcḡccaatḡ	caccḡḡṫḡṫḡ	ḡḡṫḡaagḡḡc
195841	tcḡṫḡṫṫḡṫ	acatcḡṫḡṫa	agcḡṫḡḡṫḡ	ṫagaagaagṫ	ṫḡṫcagḡagc	ḡḡcaacaact
195901	tcḡṫagccāā	ṫḡatcḡṫḡaa	ḡaagṫḡacca	aactṫcacḡḡ	acagḡṫcḡcc	ḡṫagccāact
195961	tcaccḡṫagā	cṫṫḡṫḡḡcag	ṫḡcactṫṫccḡ	ṫactcḡccat	ḡcṫṫccaacc	ḡḡṫḡṫcccag
196021	ṫḡḡccattḡṫ	cḡatḡccḡaa	cḡcṫṫḡṫḡḡ	ṫcctḡagcḡṫ	cḡatḡccḡṫa	ḡḡḡṫaatcḡ
196081	atḡcḡṫccḡcḡ	cḡaagṫcḡaa	accḡṫṫcḡag	ḡṫḡṫcḡatḡḡ	cṫṫṫṫṫcagc	ḡṫagaaccaā
196141	ḡcṫṫḡatḡca	ḡḡṫṫḡṫattc	ḡṫcḡḡḡacḡa	ṫḡḡṫṫḡaaā	aagḡcaatḡc	ṫṫṫḡṫṫḡḡḡ
196201	ṫagcccattṫṫ	ḡaaccāaac	ḡccḡacḡḡag	ṫagccacaag	cṫṫcacḡḡaa	ḡagcḡṫḡaac
196261	ḡḡatcḡccḡa	ḡḡṫcacaatc	aaacatccḡḡ	caaccḡccḡṫ	catcaaacag	ḡccḡccaccṫ
196321	atḡṫcḡccac	agcccātḡṫc	ḡccḡcaacca	ccatcḡcagḡ	ccaactcacṫ	ḡcagccacat
196381	tcṫatṫṫcag	ḡaaatḡṫḡṫc	acagḡattca	tcacagṫṫḡḡ	catcaagṫḡ	cccḡṫḡḡḡa
196441	accḡactṫcḡḡ	cṫṫḡactḡḡṫ	ṫḡḡcattccḡ	ccctḡḡṫaac	ṫṫḡcḡṫcḡḡc	cacḡaatcḡḡ
196501	tcḡḡcagcag	aagcḡccatt	ḡagḡṫṫṫccṫ	aatccaacca	agccaccḡag	ḡḡccaaccac
196561	aaagcagṫṫc	ḡṫṫṫṫcattṫṫ	catṫṫṫḡṫṫc	ḡṫccṫṫatc	ḡattṫcāaat	ḡḡattcḡccḡ
196621	cḡṫccacagṫ	ḡactḡccacc	ṫṫccatḡḡca	ḡcaaacagṫ	caaccḡṫḡṫc	ḡaccḡccaag

196741	ccātāgāāāc	cccagcccgā	ātcāccggāa	aatccggcāc	ācggttaaac	tttgcgggtt
196801	aggggattga	tccggcgatc	cacgaggcgt	cggccgatcg	gcctgagatc	ttgagcgcaa
196861	acgaaaaaaa	gccggctcat	cgcatttctg	cggatgaacc	gcctcttgga	tctcacgaaa
196921	tcttcggtcg	gggcagctta	gaacgtgaag	atcgatatcg	aaccgaaggt	ggtttgatcg
196981	tcgtcatcat	tttccaagat	tccggctcgt	tcccatcaa	cccagtccta	gcgaacttcg
197041	ggacgaatca	agacgttggc	gtgaggacgg	tagttgatac	cagtcgtcag	agcgtagacg
197101	tcgcttccgg	tgttgttgcc	atcatcgaag	acgccttcgt	tttggtacca	ctcgaagcgg
197161	ccacccaagg	acaagcaatc	gttgacgctg	taaaccaagt	actggttgat	accgaacgtg
197221	tcacgtgcgg	tggcaccagt	ttcgtcttcg	gtgtccagca	agtccgactg	gatgatgtac
197281	tgcaagttgt	cactgacagc	gtagtacgca	acgatcgagt	gcattgtagcc	ctgctcaact
197341	ccaccagcgt	tgtcttcgcc	gaagcgaccg	atggttggtg	cgtaagtcag	agtcaggctg
197401	tcgggtcaaac	cggccgagaa	cccgccagg	aagtgtgcgc	cattgtcttc	gaatccgctg
197461	tcccagccca	tggtgtatcc	accaaagacg	ctcagggtcat	ccgagacgtt	gtacgttgcc
197521	aatgcaccgg	tgtgggtgaa	tggctcgtcg	ttgtacatcg	tgtaggcgtg	gctgtagaag
197581	aagttatccg	gagcggcaac	gacttcccaa	ccgatgatcg	tgaagaagtg	accactttg
197641	accgacaggt	cgccgtagcc	catttctgtg	tacagctgag	gaatggcgtg	accgtagtcg
197701	ccaccgttgt	cccagtcggt	gtcccagtg	cgttctgtga	tcccgaacgc	ttgcgtgtca
197761	ggtccgtcgg	taccgtagac	gtaattcgata	cgctccaccg	tgtcgaagcc	acacgaagtg
197821	tcgatggctt	tttcagcgta	caaccatgct	tgtgtcagct	gaacgttgtc	gggacggctg
197881	ttgaacaaag	gcaacgcctt	cgtgtggtag	ccgatcgacg	cccatccacc	gacttcgatg
197941	ccacaaacat	cgccgaacag	cgtgtaaagg	tcatccaagc	agcagtcgcc	caaaccgggc
198001	aagcagcttc	cgaggccacc	gccgcagagc	gaatcacaac	cgctgtcgca	acctgctgtg
198061	cagccacagt	cgcccaagca	gccgacggtt	tccgaaccgc	aagtcacttc	gttctcgcaa
198121	ccgggtgtcg	agccgcaca	aggctcacaa	ccacacacgg	gctcaccaca	atcgcaaagc
198181	gacgaggtgc	aagagaccaa	tccaatatca	tttgcgtgaag	cgccggtcag	gttcgtggcg
198241	ttaacgccgc	atgcaaccgc	tgcgatcaga	gctagtttac	taagcttcat	tgttttctcc
198301	gttgatatac	caatccaatt	gggtcgtttc	gtgtcaccaa	gattcaaaat	ggatgctgtt
198361	agaacgggaa	gctgtgcccc	caaaatgtgg	ggagggccga	tctctcgctc	acaacgatga
198421	aacaaacgca	gtccatcgct	ttttcaacgc	acacgtcgcc	tgcccgccgat	ggcacatcga
198481	aacttccagg	caatcgcttc	ggaattcgaa	tcaatcacct	cgaaagattt	cgagtgaagt
198541	gaaagcaatc	catcatgtcg	tcgggagaa	tcatcggtgg	gtttgcgaga	tctgtcctca
198601	accggtgctc	aaaacgactt	agaaaccgcc	cgcggggtgc	gcaacgcgcc	tgttaatcct
198661	catctgcggg	tcgctcccaa	cgttccgtct	gggcaaactt	tgacgcttcc	cgacccgaac
198721	acgccccgca	tctgaaaatc	ctgctttcaa	taaaacgttc	cacccgctat	cctgcggggc
198781	ttctccctga	aatcagggat	tttgaccgtc	tcaaattcaca	ttcatgacaa	tcaccgcgag
198841	cggtagcgga	gaatcagatg	gcacgacagt	cgaagcgctg	cggcaaaaaa	gtccaaatgg
198901	gcaaccgtat	cgaaaccggg	ggtaaagcga	agtacttggg	cggtgtcggt	accaagatca
198961	ccggctgtac	ccgccgtaaa	tttgtcccca	acctgcaaaa	agttcacgtg	acattgccaa
199021	acggcaccaa	caaatcgatg	cgagtttgca	cgagtgcat	ccgcagtggt	gtcgttcgca
199081	aaacggtgaa	aacaaaaccg	tttgacgtca	gcggcagcaa	aaagtcctga	tgtccagttc
199141	cggcagtagc	aacggcggct	cggtcgacat	ccaaaaattg	gctcgactgg	ctcgccttca
199201	gcttacggag	caggagcaaa	ccgatttcgg	tccgcaaatc	acggacattc	tcggtttcgt
199261	cgaacaattg	tccgaactcg	acacttcggg	tgtcgagccg	atgacgagtg	cgctcgacgt
199321	cgagaatcga	ttccgcgacg	acgttctctga	ccaaagcctg	tcagccgaag	tggcgacacg
199381	cacggcgccc	gcctctcaag	atggcacgtt	tctggtgccc	ccggtcctgg	gaaacacttc
199441	ttccaagaag	tgaagcatca	cgagcaacgt	ttgcgggaag	gattcatttc	caggaatccc
199501	gcgaacttcg	ggccggaagc	atcgctgcga	acttgccgga	caatcgataa	atcgctacgg
199561	ctataaatgc	cactcatgcg	tgaatgatgc	atatggattg	gacaaaaacc	caggctgctt
199621	gatcacgcaa	gcgaagcgac	acctagattt	cattcgggaa	cgacgaaggc	accagacgcg
199681	aatcttttat	agatcgacga	ccgtatcgct	cgccgaatcg	tcctgatgct	tccgcaactg
199741	ctccatcgcc	gccaaagtag	cgtcgcaata	cgatgagacg	gctgttcccc	aggcctgttc
199801	tttcgtcgcc	tggcgagctt	gctgcaaaag	ctggtcgacg	ttttgccagt	ccaacatcca
199861	atcttcgctc	tcggaagtct	gacgaagctg	agtatcacca	tcgtccattc	gaagcaagaa
199921	cgcttcatgc	gaattggctt	taaaacggcg	gtaaggcccc	gtccccaag	cggtttcccc
199981	gcttccgata	tcgagcgatt	cacccgaatc	ccaggcatca	ccagccaagg	ccggatcgct
200041	cgaaccaccc	tgccttgccc	cggactgacc	gggcatcccc	gggttcgatg	acgcacctgc
200101	cgaattccgg	tcccgcacgc	gacgcgtttt	cagcggtcgc	ctgcttccat	tcggcttgaa
200161	gactccactc	gcccaaaccg	cgcccgaaat	tgaccccagg	atgaacgcaa	cgattgccga
200221	gcccaacaac	cgcgggctga	ccagagcggc	gcgcaaacca	aaaccgactg	ctcccgcca
200281	acaaaaatgc	gtggttccaa	tgagcgcccc	agaggaaacc	tcattccgctc	ccagagaacg
200341	ggctttccgc	ggcgcacccg	cattctgagt	cagatgctca	tcattcgactt	caaccacgat
200401	caacgtgata	ttgtccggac	cgccccgtaa	attggccagg	tcgatcatca	cccggtccgc
200461	tttatcgaca	tcgagcgaat	ccagcagaac	tgcgagctcg	tcgtcttcga	tttgcccagt
200521	cagcccatca	ctgcaaacca	tgaagcggtc	gccaaacttc	aggtcaaacg	gcccctccag
200581	atccaccaac	acttctggcg	aaggccctag	cgaccgagtg	atcacgtttt	tgggaattga
200641	cttactgaag	acactgtcgc	tgtgaaactt	gcccgtggct	tgcatttccc	aaaccagcga
200701	gtgatcaaac	gtcaattgct	caagcacgcc	ctgccgaagt	cgataaactc	gcgaatctcc
200761	gacgtgtgcc	acataggcgg	caccattgac	cagaaccagc	gaactggcgg	tcgtcccat
200821	gttcaggaac	tcgggattgc	tctgtccgcg	ctcgtaaact	gcggcattgg	ccagatgcac
200881	ggcctcggaa	atcgcggtgc	caggagcctc	ttcccgcgat	tgatagtagt	gcattgcaat
200941	gcgttcaact	gcaatctgcg	acgccaaact	accggccgcg	tgggctccca	ttccgtccgc
201001	gacatacga	aggtggccgc	gttggttcag	acgttcggcg	gactcagcga	ttaaaaccgc
201061	catgaatctt	tgattgttcg	cacgtcgcat	cccgcacatg	gtctgctcag	cgaacttcac
201121	tccggggcgc	catgaacctg	acaaacgatt	tgtgaccgag	aacttgtgac	cgagaacaca
201181	ttcaaccgac	gaacttacac	gcctcttaca	gactacttgg	caaattgtaa	gtcgccacgt

201301	ĕtġġġġġtca	cgġġġatcgġ	tġġātccaġa	āāaccġācca	agġaatġāgc	tġācactcġt
201361	ttcccgaccġ	ttccgatġca	cgccġctcag	ġcagġġġcġa	tcaactccġc	agccaatcġa
201421	cacġcġtcca	agaactcġtc	ġaccatcagġ	tactcġtġca	ccġtatġaat	ġġacġcctġa
201481	ccacacccca	atġtgaccġc	ttcġattccġ	tġcagcatca	accaattcġc	ġtccaaaccġ
201541	ccattġġcġa	cttcacactġ	tġġagagcġc	cccaattġcġ	aatcaattc	cġttġccġc
201601	agaactġacġ	ġatġatcctc	cġtāatcġa	aacġttcat	aatcġactcġ	ġctġġtġaat
201661	tcaaġcġtġc	ctġttcġġcc	ctġaacġtcc	ttġaccġact	ġaacġcġatt	ttcġatcġcc
201721	ġttcġcatct	ġagacacġat	ttcġġccġcġa	aactcġġcat	cġtgactġcġ	agcctccġcc
201781	cġtagctġta	cttctġġcġt	ġatcacġttc	ġtcġcġtġc	caccctġaaa	aaccccccacġ
201841	ttcġcġġttc	cġcġacġccc	ġtcctttttca	accagtcġcca	ġccaaccġtt	ġcġatġcġa
201901	ctġctġatcġ	cttcġġatġc	aatcacaaatc	ġcactġacġc	ctttctcġġ	agccacġccġ
201961	ġcatġagcġ	cġtġġcġtġ	aatġġtcacc	tġcactcġtt	cġccaccġat	cġctccatġa
202021	cġġattttat	cġagttġctc	ġccatcāaaa	ttġaatġctc	ġatcaacatġ	ġccġactttġ
202081	ġacacġtcca	aatġacġagc	cccctccaac	cġġacctctt	cctġaatcag	ġaatġtgact
202141	ġcġġcagġag	ccagttttcaa	atcagġġttc	tttġcctġcc	ġtgatagctġ	ctcġacġatc
202201	ġcactġagaa	tcaccġcġca	accġctġcġġ	tcactcġġc	ccaagccġġt	cġġcccatcġ
202261	ġccacġacaa	ttcġġcccaa	ttġġtcatcġ	tctcġaagct	ġtġġattġca	accaacacag
202321	atcġġaacġc	tatccatātġ	agcġġaaagc	aacġtcġcġ	ġcaacġaatc	ġtcġcctġġc
202381	aacġtġacaa	tcaaattġcc	cġcġttġcca	tccaacagag	tcttġġtġcc	agcġtcatcġ
202441	ġattġaatcc	aatccġġatc	cactcccġca	tccaccagca	ttttctcaat	cġcġġccġaa
202501	attġcġġctt	cġtcġccact	cttaccagġa	atccġcġtta	ġctcġagaaa	ġcġatccaag
202561	ġcagcġġact	catcġatcġc	agcccaagac	atagcaccct	tcccġccatc	atttatcġct
202621	tġġactġġc	tcactcġcġt	cġattġġcac	ġġcagġġcġa	ctġatcttc	acacġaattġ
202681	ġctġtġctġc	ġġtġccagtt	tġcġactġġt	ttaaactġtc	cattġcġaac	cacccaacġġ
202741	ccaacagcaa	tccġtġġcġ	ġcaaactagġ	ccaacattġġ	aacaactġga	ġcġġġttccġ
202801	tġġcġtagtġ	agtcaaactc	tctġtġctġc	catġccctġġ	ġtgagccġaa	ġcġġġaacġġ
202861	caaaaaccaa	agcġġcaatc	ġagccaatġa	ġtġaacġcġa	caaaatġaac	tcacaagaat
202921	caagagaaat	ġagaagagcc	ġattcacġġġ	cġġatttcac	cttcġġcġac	caaaccat
202981	ġcacctġcca	accġatġagc	ġġġatcġtġġ	agccġġatca	ġccġactġat	tataccctt
203041	ġġtcġagctġ	ttġttġacġc	atccġtġcag	ġttttcġctġ	ttcġtagġtc	acttcġcġġ
203101	cacaacġcġa	acaagccacġ	ccacġttcġt	aatcġġaatġ	ctġcttcatt	tccġġġtca
203161	acġġccatcc	acatccġtġa	cacaactcat	acġccccagc	ctġcaattġġ	tġatcġacġcġ
203221	cġacacġatt	ġtcġaacaca	aaacattcġc	cctġccaacġ	agaatcctct	tccġġcatct
203281	tttccaaata	attcagaatc	ccġccġcġca	ġġtġġtacac	ctcttcġaat	cġcġġttcct
203341	tcaġatacġc	ġġtcġacttt	tcacaccġġa	tccccccġt	acaaaacatc	ġcaactttġġ
203401	ġġtġcttcġt	cġġġtccaag	ttttcttcġa	caaactġġġġ	ġaattctcġa	aagġattccġ
203461	tatġagġġt	ġatġġcaccc	tġġaacġtġc	caatctcġat	ctcġtagtġc	tttcġġġtat
203521	cġatcagcġt	ġacatccġġa	tcactġacca	aagcġttcca	atcctġġġġc	tccġatġtagġ
203581	tġccaaccġa	tccġacġġġa	tcaatġctcġ	acacġcccat	cġttacġatc	tcacġcttca
203641	ġccġaacttt	ġġttttġcġa	aacġġġatct	cttcġcagta	cġaccatttġ	acatccattc
203701	cġcġaaaagġ	agtġġcttġġ	tcatcaagct	ccatcġacġc	ġagccagtcġ	ataaacġġtt
203761	ccatcaactc	tccagġtccc	ġcġatcġttc	cattġatġcc	ttcġccġġcc	agcaacaacġ
203821	atccccġaat	ġccatcatct	ġacattcġct	ġġcġġaacġġ	ctctcġcagc	ġattcaaact
203881	ġtġġcaatġġ	agtġaagcaa	tacagtgccġ	cġacġġccac	cġġcaaatca	ġcġġcaccag
203941	cctcġġcagġ	cġattcġġcġ	ġġcaattcġġ	cġġġtacġġa	agaagcġtġt	ġattcġġtca
204001	tġaccġaaaa	cttaccat	catttgaccc	attġcagcca	agcatccacġ	tagġcaatcġ
204061	ġtġtcatġtt	catccccġcc	tġaaatġcct	cġġġaaacġġ	ctġccccġat	tġcagġtttc
204121	ġcaacacġġc	ġtcġaagccc	cġġcġattct	ġtctġġacaa	caagġactcc	ġcġatcġcġa
204181	cġġccatccġ	ġtcġġctcġc	tccġġcġġca	ġctttccġtt	ġagġaaatcc	ttġcccġact
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204301	ġtttġġattc	ġccaccġġat	attġcġġtcc	caagtccttġ	agcaaaccat	cġġġcagcġ
204361	cttcġccġcġ	ġctġaccaca	ġccagactġġ	caaccġġagc	cacġaccġcġ	ctcġcġattt
204421	cctcttcġct	cġctcġttcc	ġatġcġacġa	cġcġacata	cġcġcġġata	cġġcġtact
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204541	tġtagtcata	cġccttcġġc	aaaacataga	tccagctttt	ġccatġġaag	aaatcctccġ
204601	ġcġagccatc	cġcctġġġġc	agġaacttac	ġagcctġctġ	cagtcġġġct	tccġcġġact
204661	ctġcaaccġt	ttcġagcġtt	ġccġġcġaaa	cttcccccca	aaccġcġaag	tġatcġctct
204721	ġġtgattttġ	catġcġattġ	acatcġġcac	cġcġcaaccġ	ġaattcatct	tccġġaat
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204901	ttġaaatcaa	ctġaatatca	ctġtcagaaa	ġagġagġacġ	cccaccġġca	ġġcatcġat
204961	cġccagcact	cccġcġaagt	ttctġaacta	ġcaagcttġc	ttctccġtca	cġġġccttca
205021	tcaccġatcc	ġctġtcaccġ	ccġcġaagca	tttġagcaag	ġġtġtccatc	cġcaaaccġc
205081	cacġġġtctġ	catcġcġtcc	aagtġġcaac	cġġtġcagtt	tttaaccaac	agcġġtġcġa
205141	cġtccttcġa	ġaacġatācġ	ġtttcattġc	ġġttġġġctt	cccġaccatt	cġġġcġtġag
205201	cġġcctctġġ	cġttġcġġġc	ġtġacġġġag	ġctccccġcc	ġctcttcagġ	ctġġtġcagca
205261	tġcġcġtġġġ	atcġġġġcġ	tcaaacttġġ	ctccttctġt	cacccttġc	ttcaatttġt
205321	ccaattġctc	cttactġact	tttctctctc	cġcġagġcat	ġtcġccġġtt	tccatcġttt
205381	cġatcaatcġ	actġġcġatc	acġtcaccag	ġaaaaatcac	ġactccctcġ	ġġġġccctt
205441	ccatcaactt	ġġcaaactt	ġġcatcġcġa	acccactttt	ġctġccġcġa	attġġacaac
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205741	tġccġġccac	ttcġatctġc	ttġatcġctt	tġcġaagagc	atcaccġġac	ġtctcġtagt

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213601	ctcgcccaac	gtcaaaccct	tcgcctgtca	ccgctcgaag	ccgtcagtga	tcctgcaaa
213661	tgggaaacgtt	tagttgaatt	catcaaactt	tacggcgacc	caatcttcac	ccaaggtttc
213721	ctgcaactga	gcaacgttcg	cgcggtgctg	caccaagacg	tctcgatcatg	gctggaaacgc
213781	gccatgaccg	atggcgacga	cttggttgga	gacaccacgc	tatttcgcga	tctcgaaatt
213841	ggcaagatca	agatcaacga	agcctcgca	tggtcacgc	tggtgtttga	atcgctgtct
213901	gatcaccacg	cggaaatacca	agactacaac	agcacgacga	cacaaagcga	tcgcggcgaa
213961	ctgatctaca	cgttctctga	tttttctcgt	ctgcgaactc	gatacgaacg	cgtcgcgtgg
214021	aatttaaaac	cgatcatgtg	gacccacgaa	gtcctcgtgc	ggatgggcct	cgatcaaacg
214081	tactgggtt	ggcgtgaaag	cctcaacgaa	cgcacgcgag	ctgaagccga	gctatatgtt
214141	cagaagcttc	gtgaattgca	acgtcgacat	tccatgcgaa	tgccaacgat	tgccgatcgc
214201	atcgaagaac	gattcgttca	accaatgacg	atcgaccgaa	tgcatcgct	tgtcgaaacc
214261	gccatggggc	atgcgggaagc	ggaccgcttt	agtgccgcgt	tcgaacaact	cgaagcagaa
214321	gccaacgaac	tttcgcgaac	tcgcgttggc	gtcggactcg	atctgcccgc	ttgggtgagt
214381	gctctggaag	atgaagtgga	aaagatcggg	aaacgaaatc	taatcagcga	gattgaccgc
214441	caagaattga	tgaccattcc	cgtcagccca	ctgacgctgg	acgaactcaa	aacgcaactc
214501	gcgacggctc	aaaccacaag	ccgcgcggtg	cctcatatgc	gtcgccgcaa	atcctaagtt
214561	gcgcgttccg	tctggttcgc	ggtcggcttt	gcgcgtgacc	gctgcacggg	tgaacgaacc
214621	gcaaacttct	tcgcctcccg	gttgctgtga	tctcgctttc	gaaagtgaca	agcaaaacgg
214681	cgatgatttt	tcagcggaat	ctcgaaaagt	caaaaaaact	ttgactcaag	tcgcgactgaa
214741	aatggcgctg	cgaggcgagg	tttcagaggt	caaccgcgaa	gacattgcag	gaactcaggg
214801	gaatgatccg	ctcctctaaa	gacccaaatc	ctcccatcc	ctcctatttt	atcgcgccat
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214981	tccaacācgc	t̄t̄t̄ccgctcc	gc̄c̄ḡaatgct	t̄ctccḡaccg	āc̄ac̄ct̄c̄gt̄t̄	tccacāt̄ct̄t̄
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215101	gactc̄gactg	acaaacaaaa	cagcgaatac	ct̄ttaccaag	cct̄tḡgc̄gat	tacaḡtt̄c̄gc
215161	gacc̄gct̄tḡ	tgccaatctg	gct̄gḡaaact	tggaagaaga	cct̄gc̄ct̄gag	cgaagat̄c̄gc
215221	aaḡgt̄ctact	ac̄ct̄gt̄cact	tgaatt̄ct̄tg	at̄c̄gḡcc̄gt̄	cḡct̄cac̄caa	cgc̄ḡgt̄cgaa
215281	aac̄ct̄cgact	tggacgaaga	c̄gt̄cc̄gcaaa	gct̄ct̄gc̄gag	cct̄acagc̄gt	cḡgaat̄ggaa
215341	gaaḡtc̄gctg	acaaagaact	cgat̄gc̄cḡgt	tt̄gḡgcaatg	gt̄gḡc̄ct̄c̄ḡ	cḡgt̄t̄gḡc̄g
215401	gcat̄gt̄tt̄cc	tggacagctg	tgcaaac̄ct̄g	caḡct̄t̄cc̄ḡ	tc̄gt̄t̄gḡct̄a	cḡgc̄at̄cc̄gt̄
215461	tac̄gaatac̄g	gaat̄gt̄t̄cca	cc̄aḡcacat̄c	gaagac̄gḡgc	gcc̄aaḡtc̄ga	aḡacc̄cḡgat
215521	cḡct̄gḡtt̄gc	gt̄gat̄gḡcaa	tc̄ct̄t̄gḡgaa	at̄caaac̄gcc	ct̄gaagacac	tc̄gc̄cc̄ḡc̄gt̄t̄
215581	cḡct̄t̄ct̄ac̄g	ḡcc̄gc̄acc̄ga	aāact̄act̄ac	gac̄gaacac̄g	gāact̄t̄t̄gc̄g	acc̄aḡt̄t̄t̄g
215641	gt̄c̄gact̄c̄gt̄	ac̄gat̄gt̄t̄ct̄	t̄ḡcc̄gt̄t̄cca	t̄tc̄gacat̄gc	ct̄gt̄t̄c̄ct̄ḡ	gt̄acc̄gcaac
215701	gacac̄ḡt̄ca	ac̄ac̄gt̄t̄gc̄g	att̄gt̄t̄gḡaaa	gc̄gt̄cḡac̄ga	c̄cḡac̄gt̄ct̄t̄	cāac̄ct̄c̄agc
215761	gaatt̄caat̄g	c̄gḡgt̄c̄gt̄a	ccc̄cḡaaḡcc	gt̄c̄gc̄gḡcaa	agaac̄gac̄gc	c̄gaac̄aaat̄c
215821	tc̄gat̄gḡt̄gt̄	t̄gt̄at̄cc̄caa	cḡac̄gc̄c̄aḡc	gaaaat̄gḡca	aḡgaact̄ac̄g	act̄gaac̄caa
215881	caḡt̄act̄t̄t̄c	tt̄gt̄t̄ct̄c̄aḡc	at̄c̄gt̄t̄cc̄aa	gac̄gt̄gat̄c̄g	ccc̄gt̄t̄gḡgt̄	t̄gaac̄aḡcac
215941	gḡtḡagḡact̄	tc̄aḡt̄gact̄t̄	t̄gḡac̄gcaaa	aāct̄ḡct̄t̄cc	aāct̄caat̄ga	cact̄cacc̄cc
216001	gc̄ct̄gt̄gt̄c̄g	tt̄ccc̄gaact̄	cat̄gc̄gat̄t̄g	ct̄gat̄gḡac̄g	aḡcat̄gḡact̄	t̄gaat̄gḡgac
216061	gac̄gc̄ct̄gḡg	ac̄gt̄gḡt̄gac	ac̄gt̄t̄gc̄at̄g	gc̄tt̄ac̄acca	acc̄acac̄gt̄t̄	gct̄t̄ccc̄gaa
216121	cḡgt̄t̄gḡaāc	gat̄gḡt̄cc̄gt̄	c̄gḡt̄ct̄gt̄t̄c	aḡtc̄ḡct̄t̄gc	t̄ḡcc̄gc̄gt̄t̄t̄	gct̄c̄gacat̄c
216181	at̄ct̄ac̄gaga	t̄caac̄ḡct̄c̄g	gt̄t̄ct̄t̄gaaa	ct̄c̄gt̄c̄gat̄c	aḡcaḡt̄gḡcc	cḡgt̄gac̄gt̄t̄
216241	gc̄gat̄gc̄gt̄c	ḡc̄gaat̄gt̄c	gt̄t̄gat̄t̄gaa	gaaḡgt̄gaca	acc̄cc̄gc̄acat̄	cc̄gaat̄gḡc̄g
216301	tac̄ct̄gḡcca	tt̄gt̄c̄gḡaag	tt̄t̄ct̄c̄gḡt̄c	aāc̄gḡt̄gt̄t̄g	c̄cḡgt̄ct̄gca	cac̄ac̄aḡt̄t̄g
216361	tt̄ggaat̄cag	ḡct̄ct̄gt̄t̄caa	ac̄act̄t̄caac	ac̄gt̄ct̄gt̄gḡc	ccc̄gcaaḡt̄t̄	caac̄ac̄aaḡ
216421	acaaac̄gḡcg	tḡacc̄caac̄g	tc̄gt̄t̄gḡt̄t̄g	tc̄gc̄act̄gca	acc̄caḡgc̄ct̄	tc̄gt̄gac̄ct̄c
216481	ct̄caac̄gaaa	cc̄att̄gḡc̄ga	aḡgt̄t̄gḡcaa	aāaḡac̄ct̄ca	cc̄aaaat̄caa	aḡaḡt̄taact̄
216541	c̄ct̄t̄ac̄gc̄ga	cc̄gac̄gc̄c̄ga	ct̄t̄cc̄gcaag	aāgt̄gḡat̄c̄g	at̄gt̄caaḡca	aḡaaaac̄aaa
216601	ḡct̄c̄ḡct̄t̄gt̄	caḡact̄t̄gḡt̄	gḡt̄c̄gc̄gḡaa	acc̄gḡc̄gt̄t̄c	ḡct̄t̄tḡacac	gt̄catt̄cat̄g
216661	tt̄c̄gac̄gt̄t̄c	aaḡt̄caaac̄g	gatt̄c̄ac̄gaa	tac̄aaāc̄gt̄c	aāct̄ct̄tgaa	c̄gt̄t̄t̄gt̄cat̄
216721	at̄c̄gt̄gc̄acc	t̄gt̄ac̄gat̄c̄g	catt̄t̄t̄gc̄gt̄	gḡt̄gaaac̄cg	c̄gḡgc̄at̄gḡt̄	ccc̄ac̄gt̄t̄gc
216781	gt̄c̄ct̄gat̄c̄g	gc̄gḡcaaaḡc	aḡcccc̄cḡgt̄	tacc̄ac̄gt̄c̄g	cc̄aaat̄tgat̄	c̄gt̄gaaḡct̄g
216841	at̄caac̄gat̄g	tt̄gc̄gaaḡaa	gḡt̄caacaat̄	cac̄ccc̄gc̄aḡ	cc̄aat̄gac̄ct̄	gct̄caaḡgt̄g
216901	gt̄ct̄t̄ct̄t̄cc	c̄gaact̄at̄c̄g	c̄gt̄t̄t̄c̄gt̄c̄g	at̄gḡaaḡt̄ga	tt̄tḡccc̄aḡc	aācc̄gaḡt̄t̄g
216961	t̄ct̄gaḡcaaa	tt̄t̄caacc̄gc	gḡgcaaaaḡaa	ḡct̄t̄cc̄gḡca	c̄gḡgcaac̄at̄	gaaat̄t̄cat̄c
217021	at̄gaac̄gḡtg	c̄gt̄t̄gac̄gat̄	t̄gḡcac̄gt̄c̄t̄	gat̄gḡt̄gcca	ac̄at̄c̄gaaat̄	cc̄gaḡaaaac̄
217081	gc̄gḡgt̄gc̄cg	agaact̄t̄ct̄t̄	ct̄t̄gt̄t̄c̄gḡt̄	t̄t̄gḡac̄gt̄c̄g	cc̄gaaḡt̄aac̄	cc̄gaat̄t̄gaaḡ
217141	aaḡgact̄at̄c	gt̄ccc̄aac̄ga	aat̄cat̄c̄gcc	ḡct̄gat̄gaḡg	ac̄at̄c̄gt̄t̄c̄g	cat̄cat̄gaac̄
217201	ct̄ḡct̄gḡaaa	gc̄gḡac̄act̄t̄	caat̄c̄ct̄gac̄	aat̄cc̄aḡgt̄t̄	t̄gt̄t̄c̄gat̄t̄t̄	gt̄tḡacc̄aḡc
217261	gḡc̄ct̄ac̄gca	acc̄ct̄c̄aḡga	tc̄ct̄t̄gḡgt̄c	acc̄at̄c̄gc̄cḡ	ac̄ct̄t̄c̄gt̄gc̄	gt̄ac̄at̄c̄gac̄
217321	ḡct̄caaḡcc̄g	aaḡt̄t̄gḡcaa	gḡcatacc̄caa	gac̄gt̄c̄gat̄c	act̄ggaat̄ca	gat̄gaḡcat̄c
217381	ct̄aaat̄acc̄g	caḡgc̄aḡc̄ḡ	ct̄gḡt̄t̄caḡc	aḡc̄gac̄cḡaa	c̄gat̄t̄caḡca	at̄ac̄gc̄gac̄
217441	gac̄at̄ct̄gḡg	ac̄gt̄gc̄ḡacc̄	act̄gt̄c̄gt̄aa	gc̄ccc̄aāc̄ct̄	gat̄t̄gḡt̄cca	aac̄gaaaaḡg
217501	ḡct̄c̄gḡt̄gaḡ	aaat̄c̄acc̄ga	gcc̄ct̄t̄t̄t̄t̄t̄	ḡt̄t̄gt̄t̄gaḡ	aāc̄gaat̄t̄gc̄	ct̄aḡt̄act̄ac̄
217561	aḡc̄ḡct̄aāct̄	gḡt̄gt̄t̄gt̄aḡ	aḡgḡc̄c̄gḡgc̄	tt̄t̄t̄c̄gt̄ga	gaat̄aḡc̄aḡc	t̄gḡaḡat̄t̄t̄t̄
217621	gt̄t̄t̄ḡct̄gca	c̄gḡaḡaḡct̄t̄	gḡcat̄gḡat̄g	tc̄ḡct̄gaact̄	ggaac̄aāct̄c	gaaḡat̄c̄gḡt̄
217681	t̄aaat̄ḡct̄t̄a	ct̄t̄gḡct̄c̄gc̄	tt̄t̄gḡc̄gat̄t̄	gt̄t̄t̄t̄c̄gac̄g	aāgc̄gac̄ac̄g	aḡgḡct̄catt̄
217741	t̄gac̄gac̄cta	t̄gt̄cc̄gt̄gḡt̄	caact̄t̄t̄cc̄gt̄	ac̄ct̄t̄gḡac̄gc̄	caaḡaḡt̄gt̄g	gaḡcc̄gat̄t̄g
217801	c̄gt̄t̄gcaat̄g	c̄gḡt̄ac̄acc̄g	gt̄gc̄gaac̄ct̄	t̄gc̄aḡgaat̄t̄	tat̄c̄gc̄cc̄aḡ	cat̄c̄gḡt̄gḡg
217861	ac̄gaaḡat̄gḡ	act̄t̄c̄gc̄aḡg	aḡḡct̄gat̄cc̄	ac̄at̄c̄gt̄cc̄ḡ	t̄gat̄gaḡcat̄	gt̄caac̄aaḡa
217921	ac̄act̄gt̄c̄gc̄	gat̄catt̄gac̄	gaaacc̄aḡc̄ḡ	ac̄gt̄caaḡaa	gḡgc̄gac̄aaa	ac̄gc̄ct̄gḡc̄ḡ
217981	t̄gcaac̄gaca	gt̄gḡt̄gc̄gḡc̄	aaaḡt̄c̄gḡca	aḡcaḡgaḡaa	ct̄gt̄at̄c̄gt̄c̄	ac̄ḡgt̄t̄cat̄c̄
218041	t̄gḡct̄gc̄gḡc̄	gaac̄gaaḡac̄	tt̄t̄cact̄gca	t̄gḡt̄c̄gat̄gḡ	t̄gaact̄gt̄t̄c̄	ct̄ccc̄cḡaga
218101	ḡct̄gḡaḡtaa	c̄gac̄cc̄gc̄gaḡ	c̄gt̄t̄gt̄gc̄cḡ	c̄cḡcc̄gḡcat̄	t̄ccc̄gat̄gaḡ	at̄ḡgt̄ct̄at̄c̄
218161	ḡcccc̄aḡt̄g	gc̄aḡat̄c̄gc̄ḡ	t̄t̄gḡaāt̄t̄gc̄	t̄t̄gat̄c̄gc̄aḡ	taaḡgaḡgaḡ	gḡgatt̄gaat̄
218221	at̄c̄ct̄t̄gḡgt̄	aacc̄gc̄t̄gac̄	gaaḡḡct̄ac̄ḡ	gc̄gḡt̄aāacc̄	t̄gḡatt̄c̄ct̄ḡ	gaaḡct̄ct̄t̄ḡ
218281	cc̄gac̄cc̄gc̄ga	tc̄agaaḡt̄t̄t̄	gt̄ḡct̄t̄gaaḡ	t̄ḡcc̄gc̄gaac̄	gt̄t̄t̄t̄c̄gḡt̄t̄	t̄gḡgaḡaaḡc̄
218341	at̄ccc̄gaaḡt̄	gac̄cḡaḡc̄aḡ	cc̄ct̄at̄c̄gca	aḡgḡc̄gc̄gḡc̄ḡ	c̄gḡcc̄gaḡgt̄	c̄gcaaḡac̄ac̄
218401	ccc̄gc̄gt̄caa	gaḡc̄gḡgḡgaa	aḡt̄t̄c̄gc̄c̄gc̄	gaaḡt̄gt̄t̄ga	aācaḡt̄gt̄t̄c̄	t̄gḡcac̄gḡc̄ḡ
218461	aācḡgat̄gaa	aḡc̄gaaac̄gc̄	t̄gḡaaac̄ḡct̄	acc̄gc̄gt̄caa	aḡac̄gḡc̄gaḡ	aāaḡgt̄ccc̄a
218521	t̄cat̄ct̄gḡga	aḡcc̄aāgc̄gḡ	gt̄t̄c̄gc̄gt̄ca	cact̄caaaḡḡ	caḡc̄gac̄gḡa	ct̄acc̄gḡgḡc̄
218581	t̄gt̄ct̄ct̄gt̄g	gt̄t̄gḡt̄gḡt̄c̄	gc̄gaḡaaac̄ḡ	t̄ḡct̄t̄gac̄gḡ	c̄gaact̄gaaa	tt̄ct̄t̄c̄gt̄ca
218641	gcaac̄gc̄gaḡ	c̄gaḡt̄t̄c̄gt̄c̄t̄	tc̄gat̄gḡc̄ga	t̄ḡct̄ḡct̄aca	gḡt̄t̄gc̄gt̄t̄t̄	caḡc̄gat̄gḡc̄
218701	gaḡt̄ggaac̄ḡ	tt̄gt̄t̄t̄c̄gaḡ	gat̄caḡaaac̄	aāgaḡgt̄c̄gḡ	ct̄taḡact̄gt̄	tac̄gaḡgḡgc̄
218761	ḡcc̄gat̄act̄t̄	gḡgt̄ct̄gaaa	c̄gc̄cact̄t̄ga	tc̄at̄c̄ac̄gt̄c̄	gt̄tgaḡct̄at̄	ct̄gt̄t̄t̄ct̄t̄t̄
218821	c̄gcaaac̄ct̄ḡ	cc̄aḡc̄aḡgaḡ	c̄gḡgaaaaaa	aāt̄c̄cḡgaḡt̄	gḡacaat̄t̄c̄a	ḡgaaat̄t̄c̄gc̄
218881	gac̄gc̄gḡt̄c̄ḡ	ac̄gc̄caat̄c̄gt̄	t̄gt̄c̄aḡct̄gḡ	tc̄act̄cc̄ct̄c̄	gt̄gaḡaḡt̄c̄ḡ	tc̄gc̄at̄gt̄t̄ḡ
218941	ct̄t̄gat̄caḡg	tc̄gc̄ct̄c̄ac̄ḡ	gat̄caact̄ac̄	cat̄caat̄cac̄	gcaac̄ḡtaḡc̄	gḡct̄c̄gc̄at̄c̄
219001	aḡcc̄atac̄gc̄	aāac̄gaaḡct̄	c̄gac̄aḡatac̄	gcc̄gaact̄c̄ḡ	gt̄at̄c̄gac̄cc̄	c̄gaaaḡcat̄c̄
219061	ac̄ac̄gat̄gcc̄	gat̄gḡcc̄caa	aāct̄taḡc̄gc̄	t̄gt̄agt̄act̄a	gc̄aḡḡct̄gt̄t̄	gḡt̄t̄taḡac̄ḡ
219121	cat̄acc̄gat̄t̄	gacaat̄catt̄	aḡcc̄gt̄t̄gḡḡ	c̄gt̄taḡcccc̄	gḡt̄t̄gḡc̄gt̄c̄	taat̄caac̄cḡ
219181	cc̄ḡct̄aāc̄gc̄	gḡt̄gc̄gḡct̄c̄	aātaaāt̄caa	caḡc̄ct̄ḡcta	gḡac̄aaac̄ct̄	ac̄gt̄gt̄gḡccc̄
219241	gaḡcccc̄at̄c̄	gc̄ac̄gt̄c̄gc̄c̄	aāgc̄act̄gaa	tt̄gḡcc̄gat̄ḡ	t̄gaaḡcat̄ca	t̄gt̄gḡcc̄ḡct̄
219301	caḡgt̄aḡaaa	c̄cḡt̄gc̄aḡc̄ḡ	at̄ccaac̄c̄gt̄	ḡct̄gaact̄t̄t̄	tc̄gc̄gaaḡat̄	gt̄t̄caḡt̄c̄ḡḡ
219361	gt̄t̄c̄gḡc̄gt̄t̄	gaaaac̄acc̄ḡ	c̄gt̄c̄gt̄c̄gḡc̄	att̄caḡcaat̄	gc̄ct̄c̄gat̄c̄ḡ	ct̄gc̄gc̄cat̄ḡ
219421	c̄gac̄gaḡaaḡ	aāct̄t̄ct̄cca	cc̄act̄t̄ct̄t̄c̄	catt̄gḡc̄gga	tac̄aḡc̄gt̄gc̄	catt̄gḡgat̄c̄

219541	cgaggtgttg	gctcāāāctt	gctcāāgcac	tgggcatgga	tacagcāacā	āatgccccāg
219601	gatgaatgcc	ggatgattcg	actcgataac	agtatcgccg	accacggcaa	aacgagcgaa
219661	ctgctcctgc	gtcactcccg	tcatcagtcg	tbtggcgat	ccgatgcaaa	gctgaccaga
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254401	agatgcgatc	cgcgcagtca	tcgctcgacg	cgcgggtggat	gtgccgcgga	ccaaacccat
254461	cgggtgtttg	ctggaggatc	caccaaacaa	agcgatcgaa	ggcgaagtga	ccttcgcacg
254521	cgatgtcgcg	ccgggtcattc	aagcaaaactg	cgcgggggtg	cattgccaaa	acggttcggc
254581	tccgttttcg	ctgttgactt	acaacgacgt	cagtggctcat	gccaaacaaa	tactagaggt
254641	gacgcattcg	cg tttcatgc	ccccatggaa	accggccgcc	ggattcacgc	ggttccaaga
254701	tgaactgcga	ttgaccaacc	acgagatgtc	tttggtgaac	gtttgggttc	gcgatggcaa
254761	accggcgggc	gacccgaagg	atcttcgcgg	ccctttgccg	ccatcaaatg	gttggccact
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254881	cgacgttcgg	cagtacttcg	tcactccaac	tgg tttgaaa	gaacatcgct	tgg tcaacgc
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255361	gttgctggac	acgggtgcgcg	acatgcatct	ctttggccgg	gaaatgaaag	tttggtcgaa
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255481	aggcaagtac	tcgtttgccg	aacctgtgcg	attgaaaaag	ggaacaatca	ttcacgtgga
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255841	atctgaaacc	acccctcaat	cgaatcacgg	catcggaatt	ctgggtggat	cg ttcgaccc
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256021	cgaācāccgṭ	ctgcaāātṭḡ	tgcggtṭggc	āctcagcgga	caaṭcḡgggḡ	tḡṭcatcga
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256141	ggaacagttt	cctgaccgcc	cgctgtacct	gatcatcgga	gccgattcac	tggcctcctt
256201	cgaccgctgg	cgagaacccg	agcaaattct	gaaacgggtg	cacctggccg	tgatcgctcg
256261	cgggcggggac	cctccgcccg	actactcgat	cctggacgga	atgaccgacg	aaacgcagat
256321	cāaaaggatt	cgcgagtctc	agatccagat	gccccagatc	gaaatcagca	gcagcgacct
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256981	gaccacacat	ggacgcttcg	tgaagcgggg	ggactggaga	acgaattgcg	gatcgacgcc
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260401	tcaaccacaca	agactatgtc	gaagtgtctc	gcagcgttcg	cgaagtctgg	gacgaagcca
260461	ccaaagccgg	acaccacttg	gaagtcctcg	acatcggtgg	cggtttcccc	gctccgtatc

260581	ĕċġtċgġċġa	ċttgċġgatt	ċġtġtġatċġ	ċġġaaċcagg	cġġgġġtġg	tġġaċġġaa
260641	ġġtġġġġġġ	ġatġġġġġġ	ġtġatġġġġ	agagġġġġġ	atġġġaattġ	cġtġġġtġġ
260701	ġġġġġġġġ	ġġġatġġġġ	ġġatġġtġġ	cġġġġaagat	cġtġġġġġġ	acġġġġtġġ
260761	cġtġtġġtġġ	cġġaaacġat	ġġġġġġġġ	agacġġtġġġ	tġġġtġġtġ	ġġġġtġġġ
260821	cġtġġġġġġ	cacġġatġġ	ġtġtġġġġġ	atġagġġġġ	tġġġatġtġ	ġaagġġġġġ
260881	aattġġtġġġ	ġġtġġġġġ	atġġġtġġġ	acġġġġġġġ	cagġġġġġġ	cġtġtġġatġ
260941	ġattġġġġġ	ġġġġġġġġ	ġġġġġġġġ	acġġġġġġġ	ġacġġġġġġ	tġġġatġġat
261001	cġġġġġġġġ	cġġġġġġġġ	tġġtġtġġġ	ġatġġġġġġ	ġġġtġġġġġ	cagġġġġġġ
261061	cġtġġġġġġ	ġġġġġġġġ	tġatġġġġġ	ġġġġġġġġ	cġtġġġġġġ	acatġġġġġ
261121	cġtġtġġġġ	tġġġġġġġġ	ġġtġtġġġġ	cġġġġġġġġ	cġtġtġġġġġ	cġġġġġġġġ
261181	tġġġġġġġġ	ġġġġġġġġ	cġatġġġġġ	cġġġġġġġġ	ġġġtġtġġġ	tġġġtġġġġ
261241	ġġtġġtġġġ	tġġtġtġtġġ	cagġġġġġġ	cġatġġġġġ	ġactġġtġġ	cġatġġġġġ
261301	tġtġtġtġġ	aaacġġġġġ	ġacġġġġġġ	cġagġtġtġġ	acġtġġġtġġ	tġatġtġġġ
261361	atġġatġġġ	ġġġtġġġġġ	cagġġġġġġ	cacġġġġġġ	ġġtġtġġtġġ	tġtġġġġġġ
261421	tġġġaaġġġ	atġġġġġġġ	aaacatġġġ	cġtġaaġġġ	ġġcġtġġtġġ	tġġġtġtġġġ
261481	cġtġġġġġġ	tġtġġġġġġ	tġatġġġġġġ	cġtġtġġġġġ	ġtġġġtġtġġ	cġġacatġġat
261541	tġaaacġġtġġ	ġtġatġġġġ	tġġġtġġtġġ	ġġtġġtġġġġ	ġtġtġacatġġ	cġcġtġġġġġ
261601	cġġġġġtġġ	tġġġtġtġġ	tġġatġġġġ	tġġġaaġġġ	ġġġġġtġġġ	agġtġtġtġġ
261661	cġactġġġġġ	caatġġġġġ	agġtġġġġġ	cġacatġġġġ	ġġattġġġġġ	cġġġġġġġġ
261721	ġġġtġġġġġ	cġġaaacġġġ	atġtġtġtġġ	ġġtġtġġġġ	agġġġġaaġġ	acġaaġġġġġ
261781	cġġcġtġġġ	ġġaaġġtġġġ	tġġġtġġġġġ	ġtġġtġactġġ	atġtġtġġġġ	tġtġġġġġġ
261841	ġtġcġtġġġġ	tġcġġġġġġġ	tġġtġatġġġ	tġġġġatġġġ	tġġġaaġġġġ	tġaaġġġġġġ
261901	cġacġtġġġġ	ġaagġtġġġġ	ġaaġġġtġġġ	ġcġġġġġġġ	atġacġtġġġġ	cġġġġtġġġġ
261961	ġġtġġaaġġġ	ġtġtġtġtġġ	ġtġġtġtġġġ	cġġġġġġġġ	cġatġġġġġġ	cġġġġġġġġ
262021	ġtġtġġġġġ	cġġġġġġġġ	ġtġġġġġġġ	aaacġtġġġġ	cġtġġġtġtġġ	ġġtġġġġġġġ
262081	cġġġġġġġġ	aaġatġtġġġ	ġġtġġġġġġġ	aaġġtġġġġġ	cġġatġtġtġġ	ġtġġatġtġġġ
262141	ġtġġġġġġġ	ġġġtġġġġġ	ġġaaġaaġġġ	ġatġtġġġġġ	atġatġġġġġ	agġġġtġġġġ
262201	cġtġġġġġġġ	ġtġġġtġġġġ	tġġtġġġġġġ	ġġġġġtġġġġ	cġġatġtġġġġ	aaġġġġġġġġ
262261	cġġġġġġġġ	ġġġatġġġġġ	cġġatġġtġġ	cġġġġtġġġġ	acġtġġtġtġġ	cġtġtġġġġġ
262321	cġtġtġġġġġ	ġaattġġġġġ	tġġġġġġġġ	acġġatġġġġ	cġġġġġġġġ	cġtġtġġġġġ
262381	aaġġtġġġġġ	ġtġtġġġġġġ	tġġġaaġġġġ	tġġaaġġġġġ	cġġġġġġġġ	cġtġtġġġġġ
262441	tġġactġtġġġ	ġatġġġġġġġ	ġtġġġġġġġ	tġtġġġaaġġ	ġġtġġġġġġġ	tġġġtġġġġġ
262501	cġaaġġġġġġ	ġġġġġġaaġġ	tġġġtġġaaġ	cġtġġġġġġġ	ġġtġtġġġġġġ	acġtġġġġġġġ
262561	tġġtġġġġġġ	ġġġġġatġġġ	ġagatġġġġġ	tġtġġġġġġġ	ġġaaġġġġġġ	ġtġġtġġġġġ
262621	atġtġtġġġġġ	cġtġtġġaaġġ	cacġġġġġġġ	aaġactġġġġġ	ġcagġtġtġtġġ	ġagġġġġġġġ
262681	tġġaaġtġġġġ	tġtġġġġġġġ	cġġaaġġġġġ	tġġatġġġġġ	ġġtġġġġġġġ	cġġġġġġġġġ
262741	taatġġġġġġġ	cġaaġġġġġġ	cagġtġaaġġ	atġtġtġtġġġġ	agagġġġġġġġ	caatġġġġġġġ
262801	acġġġġġġġġġ	acġġġġġġġġġ	atġatġġġġġ	tġacġaaġġġ	ġġtġġġġġġġ	cġtġġġġġġġ
262861	ġġġtġġġġġġġ	cġġġġġġġġġ	cġġġġġġġġġ	acġtġġġġġġġ	ġatagġtġtġġġ	cġġġġġġġġġ
262921	ġtġtġtġġġġġ	cġġġġġġġġġ	cġtġġġġġġġ	ġġġġġġġġġ	cġġġġġġġġġ	ġġġtġtġġġġġ
262981	tġġġġġġġġġ	cġġtġtġtġġġ	cġaaġġġġġ	ġġġġġġġġġ	agġtġtġtġġġġ	ġġġġġġġġġ
263041	ġtġġġġġġġġ	ġtġtġtġtġġġ	cġaaġġġġġ	tġagġġġġġġġ	caaġġġġġġġ	ġatġġġġġġġ
263101	tġġġġġġġġġ	aaġcaatġġġ	cġġġġġġġġġ	ġatġġġġġġġ	aaġtġġġġġġġ	cġaaġġġġġġġ
263161	tġtġġġġġġġġ	cġġtġaaġġġġ	tġġġġġġġġġ	acġġġġġġġġ	acġactġtġġġ	acġġġġġġġġġ
263221	aaġġatġtġġġġ	cġagġġġġġġ	acġtġtġġġġġ	cġġtġġġġġġġ	ġactġġġġġġġ	cġtġġġġġġġġ
263281	ġġaaġġġġġġġ	ġġġġġġġġġġ	cacġġaaġġġ	cġtġġġġġġġġ	tġġatġġġġġġ	cġtġġġġġġġġ
263341	cġġacagġġġġġ	tġtġġġġġġġġ	caaġġġġġġġ	atġtġġġġġġġ	cġtġġġġġġġġ	cġatġatġġġġġ
263401	tġtġġġġġġġġ	tġtġtġġġġġġ	tġġġġġġġġġ	agġġġġġġġġġ	cġġagġġġġġġġ	aaġtġġġġġġġ
263461	cġagġtġġġġġġ	cġacġġatġġġġ	ġġġtġġġġġġġ	cġġagġtġġġġ	aaacġġġġġġġ	cġġagġġġġġġġ
263521	cġtġtġġġġġġġ	ġaaġġġtġtġġġ	tġġġġġġġġġ	ġaatġtġtġġġġ	cġaaġtġġġġġ	tġġacġġġġġġġ
263581	tġġġġġġġġġġ	cġacġġġġġġġ	taacġġġġġġġ	cġġġtġġġġġġġ	cġġcagġġġġġ	ataaġtġġġġġġġ
263641	ġtġġġġġġġġġ	ġtġġġtġtġġġġ	ġġġtġġġġġġġ	agġatġġġġġġġ	cġatġatġġġġġ	tagġtġġġġġġġ
263701	tġġġġġġġġġġ	cġatġġġġġġġ	ġacġġaaġġġ	ġtġġġġġġġġġ	cġatġaaġġġġġ	cġġtġġġġġġġġ
263761	ġġġatġġġġġġġ	ġcagġġġġġġġ	tġġġġġġġġġġ	cġaaġagatġġġ	cġtġġġġġġġġġ	tġġġġġġġġġġġ
263821	ġtġtġġġġġġġġ	atġġġġġġġġġ	tġatġtġġġġġġġ	acġtġtġtġtġġġġ	caaġġġġġġġġġ	tġatġġġġġġġġ
263881	tġtġġġġġġġġġ	cġġġġġġġġġġ	agġġġġġġġġġ	cġġġġġġġġġġ	ġagġtġġtġġġġġ	tġġġġġġġġġġġ
263941	ġġġġaaġġġġġġ	tġġġġġġġġġġ	agġġtġġġġġġġ	cġġġġġġġġġġ	tġġatġġġġġġġ	ġġġtġġġġġġġġ
264001	cġtġġġġġġġġġ	cġġġatġġġġġġ	ġġġaaġtġġġġġ	cġġġġġġġġġġ	tġtġġġġġġġġġ	atġġġġġġġġġġ
264061	cacġġġġġġġġġ	cġagġactġġġ	aaġġġġġġġġġ	ġagġġatġġġġġ	cġġġġġġġġġġ	tġġġġġġġġġġġ
264121	cġtġġġġġġġġġ	acġaaġġġġġġġ	cġġtġġġġġġġġ	ġġaaġġġġġġġ	tġġġġġġġġġġġ	cġtġġġġġġġġġ
264181	ġġġġġġġġġġġ	cagġtġġġġġġġ	atġġġġġġġġġ	cġtġġġġġġġġġ	ġacġtġġġġġġġ	tġġġġġġġġġġġ
264241	agġġġġġġġġġġġ	aaġġġtġtġġġġġ	ġatġġġġġġġġġ	aaġcagġġġġġ	cġġġtġġġġġġġ	cġtġġġġġġġġġ
264301	cġġġġġġġġġġġ	caaġtġġġġġġġ	atġtġġaaġġġġġ	ġaaġġatġġġġġ	aaġatġtġtġġġġ	atġġġġġġġġġġ
264361	cġġagġtġġġġġġ	tġagġtġġġġġġġ	tġtġġġġġġġġġ	atġacġġġġġġġ	ġġcagġġġġġġġ	tġacġġġġġġġġġ
264421	cġacġġġġġġġġġ	atġatġġġtġġġġġ	cġġtġġġġġġġġġ	agacġaaġġġġġ	ġġcacġġġġġġġ	tġatġġġġġġġġġ
264481	cġġtġtġġġġġġġġ	ġaaġġġġġġġġġ	tġġġġġġġġġġġ	ġġtġaaġġġġġġġ	cġcagġġġġġġġġ	ġcġaaġtġġġġġġġġ
264541	ġtġtġtġġġġġġġġ	tġġagġtġġġġġġġ	tġġġġġġġġġġġ	caaġġġġġġġġġġ	ġagatġtġġġġġġġ	acġaaġġġġġġġġġ
264601	agġtġġġġġġġġġ	cġtġġaaġġġġġġġ	ġġġġġġġġġġġ	ġatġġġġġġġġġ	ġactġtġġġġġġġ	acġaaġġġġġġġġġ
264661	cġġġġġġġġġġġ	agġtġtġtġtġġġġġ	tġtġġġġġġġġġ	ġġaaġġġġġġġġġ	aaġacatġġġġġġġ	ġtġtġġġġġġġġġ
264721	cġaaġtġġaaġġġġġ	cġġġatġġġġġġġġ	atġġġaaġġġġġġġ	ġġtġġġġġġġġġ	tġtġġġtġġġġġġġ	ġtġġaaġġġġġġġġġ
264781	ġaaġaaġġġġġġġġ	tġġġġtġtġġġġġġġ	taaġġġġġġġġġġġ	cġġagġġġġġġġġġ	aaġacġġġġġġġġġ	agġacġġġġġġġġġ
264841	cġġġtġtġġġġġġġġ	tġġtġtġtġġġġġġġ	aaġacġġtġġġġġġġġġ	agġaaġaaġġġġġġġ	ġġcġatġġġġġġġġġ	aaġacġġġġġġġġġ
264901	tġactġġġġġġġġġ	aaġcaatġġġġġġġġġ	tġtġġġġġġġġġġġ	ġaaġġġġġġġġġġġ	tġġcagġġaaġġġġġġġ	tġcagġġġġġġġġġ
264961	caaattġġcagġġġġġ	ġġtġġaaġġġġġġġġġ	cġġġġġġġġġġġġġġġ	tġġtġġatġġġġġġġġġ	cġġġactġatġġġġġġġ	cġġġġġġġġġġġġġ
265021	cġaaġġġġġġġġġġġ	cactġtġtġtġġġġġġġġġ	tġaaġaaġġġġġġġġġġġ	tġġġtġtġtġġġġġġġġġ	tġġġagagġġġġġġġġġ	tġġatġġġġġġġġġġġ



265141	gccacgctga	fccatcgcāa	cgccaactctc	gtagagagacg	ācgcaaagaa	fccacgcat
265201	gggtcgtgcg	accggactcg	cgccctcgtc	cactaccatt	caaacaagaa	tcactcatgg
265261	atgaaatcgt	ctatcacgac	cgatacaccg	gcgaagaccg	catcgaaaaa	gtgtatggcg
265321	acaaggcatt	gcgatggacg	tacggcacca	ttgccggacg	tctttcgctt	tcgctggctg
265381	tgaaacgaac	gttgtttctg	cactggtagc	gttggcgaat	ggaccaaccg	aaaacacgcg
265441	agaagatcgc	tccgtttcatc	aaggagtatg	aactggactc	ggatgagttt	gtccgcgacg
265501	tggacgagtt	tgccaatttc	aacgagttct	tttttcgaaa	gctgaaaccg	gaagctcgctc
265561	cgattgatgc	ggctgccgac	tcgggtggtct	tccccgccga	cggccgtcac	ctttgcattc
265621	ccgacctatc	aaaatgcgaa	gggctgtttg	tcaaaggcga	gatgtttgat	ctgccaacgc
265681	tcctgcaaga	ttccgcccctc	gccgaccgct	atgcgagcgg	cagcctgctg	ctttcgcggt
265741	tgtgcccggg	cgactatcac	cgctttcact	ttcccgccgc	cgggtgtccc	ggtgagagcc
265801	gtctgatcaa	cgggtccactc	tattccgtta	atccaattgc	cttgcgctcag	aacattcaca
265861	ttctgaccag	caacaaacgc	tgcttcacgc	agctcgaaac	ggaatctttc	ggaacagtgc
265921	tattgcttga	aatcggcgcc	acctgcgtgg	gcagcatcca	acagagttac	tcgcccgggtg
265981	aaaccatctc	caagggcgac	gaaaaaggct	acttccgatt	cggtggttcc	tcgaccatgg
266041	ttttgttcga	accgcgccgc	atccaattcg	acgcggacct	cattgaaaaa	tctcgccaac
266101	atcgcgaact	ctacgctcgc	atgggcgacc	atttggggaa	tcgacctgcc	aattccactc
266161	gagcacaatt	ttcaattttg	atgtcccgat	tcgtgttctc	ggttcgtcac	cctcacaaat
266221	gacgtggcta	tgttgccact	ctcgaaccgc	aaaccttcgt	ttgaaagaac	accgatgccca
266281	aaattcatgt	ttgtttatcg	ggcggtgctg	gacgagatgg	aaaacgcctc	tcgggacgag
266341	atgcaaaaag	tcatgcaacg	gtggatggac	tggatccaag	acgggatgaa	agccgggttg
266401	ttgcttgatg	gtggcgacgg	actgaaaccc	gaaggcgcaa	ccgtcaatcc	ggatctgtcc
266461	gtcacgggatg	ggcggttcac	cgagtcgaaa	gaattgggtg	gtggctactc	gatggttcaa
266521	gccgagaatc	tcgcccgcgc	agtggaaactg	gccaagacgt	caccgatcat	caccacaaa
266581	ggtgacctcg	aagtttcgga	attggcgaat	gtgggccaagc	ccgaagaagc	atgaccgatt
266641	caagcggcca	tttggtcgag	cacttttttc	ggcacgagtc	cgcccatttg	attgcggtgc
266701	tgactcgtgc	ctttgggac	cgtcgaatca	acttgatcga	agacatggtt	caggtcgcca
266761	tgctagaggc	gatgaacgcg	tggaaagcaag	gcggagtgc	tgacaatcca	actgcgtgga
266821	tcctatcgcg	caccaagaac	cgaatcctgg	atgcattgcy	ccgcgaaaag	acgttggcac
266881	aagcgatctc	tttggcgga	ccatcgctgg	acgtccaaga	ggacaccgtg	gatcactggc
266941	taagcgaaga	acaattgccc	gacagcttgc	tcgggatgat	gtttgtttgc	tgtcacccaa
267001	ctctgaaccg	tgagacgcag	atcgcgctga	cgctgaaaac	actttgtggc	tttgggtacg
267061	ccgaaatcgc	tgccggattg	ttgctgccac	tcgagacgat	caaaaaacga	atcgctcgty
267121	ccaaacgttc	actctgcgaa	gccaatgtcg	cggtggaatt	gcccagccct	gacgagattg
267181	cacagcgccg	cggcgctcgtt	cacgatgtgc	tgtatctgat	gttcaatgag	ggacacaa
267241	cctcacacgg	atcccagccc	atccgatgag	acatttgcy	agaagcagca	agactgtgtc
267301	atctgctgag	cgaaagcgaa	catggctcgc	gcgccacgaa	agctctgctg	gcactgatgc
267361	tgtttcaagc	agcccgcctg	gaatcacgaa	ccgacgaaca	aggcaacgtg	attctcctgg
267421	aggaccaaga	ccgttcgaaa	tgggatcggc	gactgatcac	catcgcgcaa	catgagctgg
267481	ctggctcgaa	gattgattcg	ccgactacgt	accactggga	agcagccatc	gcgatgcagc
267541	actgcatcgc	cccaagcgta	gaagccaccg	actggtcaac	gatcgttcgt	ttttacaatc
267601	gcctgcttga	gattccaccg	tcgcccgttt	acgaactcaa	ccgagccatc	ccgagggctc
267661	aagcaggcca	gatcaacgag	gcactgaaag	agctgcaaac	gctccagcaa	tcgggtgcaa
267721	tgacagaccta	tttggtgctg	gattgtgcaa	tcgccagagt	gcatgaactg	ggcaaccaca
267781	cctcacaggc	aattgacgcc	tatctgatcg	cgctgtccaa	agccaaagct	gatcacgaga
267841	aacaactggg	cgaaacgaaa	ctgcgaaagc	tacaacaggc	gtagaacgaa	aaagccctcg
267901	caagagaact	tgccagggct	atctcgttgc	tcggtttgat	caagtgacct	gctggatcaa
267961	ttggctggac	gacttgactg	aactacttgt	cagtgaagtc	caagaaccac	caaccatcgt
268021	cccattcgag	cgagacttta	cgccatccca	aaggaaactg	tgggtagggg	tagaaaggctc
268081	cgatgtatgg	gaaagccgat	gggctgtact	gttgtgggta	cgtcagtgc	gcgtagtgtg
268141	gatacgctgc	gtagcctggc	catgcgtagt	tcggcgaggt	tggcgaaatc	tagcgaggtg
268201	ctccgacggg	tgccggcagga	gccattggaa	cgggttgctc	catgacaggt	gcgtgagcca
268261	ttggtgcagg	tgctgctggc	acgcggctc	catgagtcac	catgctaccg	ggcagacca
268321	tttcgcccgt	gatcatttgt	ccgccagctt	gtccgtacga	aacgggacga	gcttggactt
268381	gaccacgggt	agctggtggc	aaaggctgca	atccaccggg	gcggtgagaa	gcaggtgttg
268441	caaccaaac	ggtgttcgaa	ccagccttca	cgctcatcag	atcgcgaaac	ccgcgtgtc
268501	caggagcgtg	acgagcgatt	tcggcgatca	gttcacgttg	cgatgccgaa	gcagcttcgc
268561	cggtgatttc	gacgatgccg	tcgtatgcgt	tgacgtcgac	gccgaagtct	ttcaagtgc
268621	cgaccgatgg	ggctttggcc	aaagcagcgg	cgaccgatgg	cgtgattgct	tcgtcgctgt
268681	tggcttcgcc	gccagcgttt	tcccaagcag	ccacggtgcg	agtttgcgag	tcagcggtg
268741	cttcgccggc	gactggtgaa	accgtaccag	gaacaacttc	ttgagcttcg	gtttccaaag
268801	cacctttgaa	gtcaaacgct	tcagctggct	caacagctgc	gattgcagcg	gctttgggtt
268861	tgtaaattctt	tgcttcgaga	acttcgagtt	cgttaaaca	attgacaacg	ccgtcgacgt
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280201	acġactcġct	tcctġccġag	gtġggcġccġ	cġttccġcġc	ccġgttġtca	cġccaagcġg
280261	aagcttacġg	cġtgġatctt	ttġagcaaga	cactcaacaa	aactaacġct	gġctġatġag
280321	cġacagagġc	caaacġcttc	ggcaaatttt	cġġtgccġcġ	cactġtcġca	ġcacġcatca
280381	tcacttġcġc	ttġġacġcaa	ctġaattġġt	gcaaaccġat	tcġġġacagc	gtttġġtttc
280441	ġcaattġġta	cġġcaccaca	ctcġctattt	ggcġġġtġca	aaagatccġg	acġtġcġttt
280501	tcġcġatttc	cagaaatcacġ	tgġtgcatġt	cġacġacġġc	tactġggġcġ	ġcġcaccacġ
280561	cġtcġctcac	cagtgġtacġ	accġcttġca	gġgttacctġ	caccaatcac	gttttġacġa
280621	tġcġġcacat	ġctġccġġcġ	tactcacġca	ttacġtgacc	gatccactcc	agccġtgca
280681	cacġcccacġ	acġccġatġg	aaaagġtttt	gġaccġagccġ	attġaatġġt	ġcatcactca
280741	aaattactġg	gatctġctcġ	ctcagtgġcġ	acagġatccc	actcġaatcġ	ttttccaact
280801	ttccġacca	ccġġġatġġc	tcġġcġaagc	gatcttġcaa	tcġctcġgtt	tgġcġcacag
280861	tcactacca	acactġttġg	acaactttġa	tttġġcġġcġ	tcġġaacatġ	atcccaacaa
280921	agġtctcaac	gaagtttccc	gtcġcatcġt	ttcacaaġtġ	gtcġġactġt	ctġtgaccġg
280981	ctġġġctcġc	atcctcġagc	tgġctġctġc	ggacġctġag	cagcġaagcġ	gġcġcccat
281041	ttccacġġc	ggcctctcġc	taccġatġġt	atġttccġcġ	atccġcġtġc	ccġatcġcat
281101	gtġġctġaaa	cġġattacct	acaaaatcġa	acġagaaaag	gtġcagcġġt	tgġtġatġa
281161	atttcġacġa	accġġcġatġ	tgġagcaaaa	cttġcccacġ	gaagttcġcġ	tcctġcaacġ
281221	cġtgġcaacc	atttaccatc	ġcġaaaaaga	ataccġtcag	ġcaaagġcca	aactġġccġc
281281	cġcccġcġaa	gġgttġġtġg	cġtcġgaagc	agccġaacġc	caatccġaat	cġcacġatġc
281341	aaacġtgctġ	ccġtttġtca	ġcaccġaaga	caacġttcġa	ttġcatġtġg	ctġaccġgtt
281401	ġġtcġacġca	cġatcaatcġ	ġcaaaaagac	cġctġctcġa	ttcġcagġca	tcġġcatcca
281461	tactġtġġġt	ġactttttġa	aagccġacġa	gaaaaccatġ	acġcġġcġat	tgġccaccġcġ

283381	tātccgācāt	tgctācgcāa	agcāgaactg	gcacāgggēg	cggtgcgētt	ggaāgāgtēg
283441	ttggcgaacg	ttgcttgggt	ggcttgaaat	gtggtcggtg	tgaaagccgc	accaagccca
283501	cgggttgcga	tggtctgagg	ttgatcgagc	ttgttccaga	acaacgattg	gctgtactga
283561	gcgtcgaagt	tggtccagagc	tgcttcgaca	ccccccaacg	gatccgcgtg	agccaagcct
283621	ggcgtgaaga	ccgtcgtcgc	ggattgagga	gcgctcacca	ccgcgccacc	aatcggttcgc
283681	agcacgggac	tggatcgcaa	tgcttgctgg	accgcttgct	ccagcgtcaa	ctcgacgtcg
283741	ggcagattgg	ccgggtcttc	cagcgtattg	ggctgaaccg	cagacacggc	atccgagatg
283801	actggcgtgg	cacattgggt	gacctcgggg	tactcgatcc	gcattgccga	atgggtcatga
283861	tacgacgttt	tggtgtcgtg	aggaccgtcc	gggattttct	gcgcccaatg	gcatccgctg
283921	gtcagcgtgg	atgccgccac	cgcgacaccc	agccaagagg	ccaagcgacg	acgacgggtt
283981	tgtttgcgcg	aagagagaga	cgtttgccga	tccatggcaa	tctcgattcc	atatcaggat
284041	ggttccctct	gctcacacca	acatccttgt	cggtgcccag	tcgcagaggc	ggaatgttcc
284101	gttgtcaaat	cactcagcac	taaggcagag	cgatgattcc	gcccgaatt	gcggcggtt
284161	ctacaacaac	agcacgccgt	tcaagcgggc	cagcgtgcac	cacgcaagga	gccgatgagc
284221	cggcccggta	gtaacccttg	ctataaacga	tgctgcacgg	ttcctgaatc	gttgccaaagt
284281	aaggcaacat	tggaaatcgt	gtgaagaacc	gagcaccagc	ggcgatcggt	tgcattgcac
284341	cccatcggtc	gtgaccgtgt	cgttccaaca	ttcgggtcttc	gaagtacaac	ggatgcgaat
284401	aggtgtttgg	tgcagcccaa	ggcagtaccg	cccccgctgc	caccattccg	tcagcgaatg
284461	gttcttcggg	caaagcgatc	gcagcaacgt	cttcggtgga	atcaaaatca	cgcggcagac
284521	gaccgttgcc	aatcgctgat	gtatccaaag	aaaccgctcg	gagcgaaggc	aacacaatgc
284581	ggccaccggg	cacattgggc	agtctgtcgc	tgatgaacgg	ctgcgagaac	aaccgcgtct
284641	catccttttc	ttcttccctg	gcgtccgcga	taatttcatc	ccgcagcgac	attcggtctt
284701	tgccgttgac	ggcttccgca	cgatcgcttt	ccgcaccggg	gcgtagcaaa	tctcgcaaac
284761	gctgacgacg	agcctcatcg	gcattcgctg	gtgcagtatc	gcttggcacg	tcgctcgctg
284821	cgggtgaatc	ggcgaccaca	tcgtcgctcaa	tcattcgcaaa	accggcagcg	gcgaagaagc
284881	cactgggtag	cgacgccacg	tgctgcattg	gagtggtcaa	cgccatcggt	tcgtcagcgg
284941	tgccaacagc	cacggtcgag	gccaagcatc	ctgacaatac	ccacgcgaac	gttcgccgac
285001	ttggccggat	cccccgggacc	caacgcacca	tttcgtaaaa	tcgtttgacc	gagaactctg
285061	cgaacattct	cgatgtgtta	cgacgcagga	cggggccatc	accgaaccac	caatccccatg
285121	tagattccag	cattgcgacg	gtcttctctg	acgggtcatg	caaaaagtga	aagctcgttc
285181	aaacaacgac	cttcccgtgc	atccttcggg	tcgtgataaa	caatcactcc	aaaacagttg
285241	atccaccttg	cgcgtttgtt	acgccggatc	gacacacatc	cagcacaaac	cgcacaaacg
285301	gaccggaacg	attgccagag	acaattaggg	acctcgacga	cccccggtc	tcgccctacc
285361	gaaaccttcg	acaccgtgaa	actgacgacg	gcttcacgcg	cgaaggcagt	ttggtgggtg
285421	gacgactgct	gcaaagtgcg	ctcggcgctt	aatccgtgct	gatccacacc	ggtcgcgaat
285481	cgaagtattt	gccactgatt	cctgacgacg	ttcccggtga	cttgatcgat	cgagaactcg
285541	gcaaagagtt	ggccgggttac	gatttccatc	gcgggtgtgt	ggcacatggc	ttcagtcccg
285601	ccatcgaacc	actggagaaa	tttcgcgact	caccccagtc	ctcgtctgca	ttggcactgg
285661	tggggctgag	tgatcccga	aacgtgggca	gtctgcttcg	ctccgcccgc	gcattgggtg
285721	ttcgcgacat	ccttctgggt	ccgcacacga	tttcacccat	gaccgcgtcg	gtcattcgag
285781	tcagcatggc	atcgggtgtt	cgctcatcgct	tttatcgttt	cgacaatcca	gtgggacaac
285841	tgcgagattt	ggcaaacgcg	ggcatcgcat	cgatcgcgac	gcttttggtg	gatacccgca
285901	ttccattgat	cgatctttct	aacgctatcc	agtccaaacg	acgaattctg	atggttggca
285961	acgaggccaa	tggcttgccc	cgcgagattg	ccgaagccgc	caccaccgcg	agcacattgc
286021	caatgcgaaa	cgacaccgac	agtctcaatg	tgggggtcgc	atcagccatc	ttcctctacg
286081	agctgactcg	attgcaggac	gctgatcatg	gaaacggctg	atgtgcatga	cttgctgtcg
286141	gcgctgattc	atcatgcaaa	acagcggccc	gacgaatttg	ccttgatcga	ttcccaaacg
286201	ggcgccgcgc	ctttcacttg	gagcgaactg	acttgccgcg	tcgatgcgac	cgcgatcatg
286261	ttgcggtcga	aattctcaga	agcgaccacg	acgaaacgct	tgacctatcg	atgcaccaac
286321	cgccccgagg	atgtgggtgt	gtctctggcc	tgcgttgctg	ctggattcac	agagatcccg
286381	atcgacgcgt	tcttgcccgc	cccacaacaa	gacgtcttga	tcaaacgatc	caaagcggtg
286441	cactgggtct	agaaaatcca	tgcgaaattc	attcactcga	gcaagggtgg	ggatgcgatc
286501	tcgaacttag	aaacggcagc	tcgcgacgtt	gacattcact	cgccatcggt	ggttctttgg
286561	acgagcggca	cgacctccga	accccgaggc	gtgatgctgt	cccagcacaa	tctgaccacc
286621	aatgcgaagg	ccaaactgct	ggcggtccct	caacacacct	cggacctgcg	actgtcggtg
286681	ctgtccatcg	ctcacgctta	cgcgcgaacc	agcgacatgg	gaacgtgggt	gctctcgggg
286741	tgctcgctga	gtctcgccgc	aggccgggtc	acgttgcggt	cgctccccga	aaacctctgc
286801	ccgactttga	tcaacgctgt	gcccgtattg	atcaatgaca	tcttgaatcg	aattgaatcc
286861	gggcaatcca	gtttgcaatc	gctgcgtttg	ctcggatgcg	gcggcgctcg	aatgtctctc
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286981	gaaacgtcac	cggatgatct	cagtgcattc	cctgacaacg	cgactcccaa	tcgagtcggg
287041	cccttggtcg	caggctggga	atccaagggt	gaacacgggc	gtctgttctg	ccgaggccct
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287161	ggttggtctg	atcacggcga	cttggttgag	attcacgacg	acggtcaatt	tcaaatcttc
287221	ggtcgccgcg	acgatgtgat	cgatgtggac	aacggcttca	aagtcttccc	cgccaccatc
287281	gaacggcaac	tactgcagct	agagggaatc	gaacaagccg	tcttgcctca	tcaccaaggc
287341	cagctttgtc	tgctgctctc	acacagccaa	ccccaaagta	ccgcgcgacg	tccaaccggc
287401	cgcgatccaa	ttgaatcatg	cttgggccgat	agccttccgc	cgggaacaag	cgtgaagcga
287461	ctcaaacctg	ccgaaccatt	gtccatcaag	tcaggagaac	tcaccgccaa	gggaaccctt
287521	cgcgcgacaa	tcattcgctc	tgcccgactc	tctagcccc	cggatagtcg	cccaaacccac
287581	tctcgcgatc	cataacggcc	tggtatccgg	aaacaattcg	tagcaagacc	gttcgccatc
287641	tgctcgacgg	aagcatctac	cgacattggg	cctcaaaccg	aagcctgaag	aagctcggtc
287701	aaattcggga	tgcacggaca	acaagcaagt	gctgctgggt	tcctaggcac	gttcgcgact
287761	ctcgatacgg	catcctccct	gaacaaacga	actcggtcgc	atcgtttgta	tcaagcctca
287821	aaaaaaccgc	tctcgtctgc	gggggaccgc	aactcccata	gaccagcaa	cgggactctg

287941	at tt t g g c t t t t	c g a g t t g c g a	g a g g g a t g a a	a t g a g a a t c a	g g c c g t c g a g	a t t c g c t c g a
288001	t c t t g a a g c a	t t t g c a c g a a	c c t g t g g a c g	c c a g a t t c c a	a a g a c t g t t c	a t a g c a a a t t
288061	c t t g a c t c a t	t c a a t g a a a c	c a a c t g a a g g	a c t c t c a t g c	c c a a c t a c t g	t c g c g a t g t t
288121	a a c a a g a a t c	g g a a a g c a t t	c a c g c t t g t t	g a a c t c c t c g	t g g t a a t c g c	a a t a a t t g g c
288181	g t a t t g g t g g	g a t t a t t g c t	g c c a g c c g t g	c a a t c c g c t c	g c g a a g c a g c	a c a c g c a t g
288241	a g t t g c t t c a	a c a a c a t g a a	g c a g c t t g g t	c t t g c a a t g c	a c a a c t a t c a	c g a c g c t t t
288301	c g a a g c t t t c	c c t a t g g t c a	c c t c a a a t c a	g g a c t t t c c g	t g a c c c a c a a	a c g g g a t t c c
288361	t g g t a c c a a a	a c a t c c t c c c	t t t t g t t g a a	c a a c a g g c a t	a c g c c g a a a a	a t a t c g a a a c
288421	g c t g c c a c g a	t c t a c a g t g t	c t a c g a a g c g	g a a t g g a t t c	a t c g c a t g c c	c c t g g a a c t c
288481	g c a g g g g t c g	c c g t c c c c a c	g t t c a t g t g t	c c g t c c g a a c	c c t c c g g c c c	a g c t c t c g g t
288541	g g c g g c g g g t	c c g a c a a t g g	t t t c c a a g g t	a g t t a c g g t g	t t t c c g c t g g	t g g a g g c a c t
288601	t t g c c t c a a g	a t c t t c t a g g	a g g g a t c a c t	c c g g a t g a g a	t c a a c a t c a t	t a a a c c g g a t
288661	c c g g g a g g g a	t g t t c g g t g a	g a c g a g g a c c	t a t a a g t t c a	g a g a t t g t c t	c g a t g g a a c g
288721	t c t a a c a c c c	t a c t c g c c a g	c g a g a c g a t c	a t t c g c g g c g	c g a g c g g c g g	a a g t t g g g g a
288781	g g c a t g g g a g	g c t a t t g g g g	t g g t t c t c c t	c a c g g a t c c t	t c g g t t t c t c	t t c a g c a g a g
288841	c c c c c a a a c a	c a t c c g t t t c c	c g a t c g t g t g	t a t t c c t g c a	a a a g c a c a a a	t t t c c c g a a a
288901	t c a c c t t g c g	a a a a c g g g a a	c g c t g a c g g t	c t c a c g g g c c	g a t g g a a c t t	c g c c c g c a g c
288961	c a t c a c a c c g	g t g g t g t a t t	a a c g g c t t t c	t g t g a t g g a t	c c g t t c g g t t	t g t t a c c g a t
289021	t c g a t c g a a c	g t c a g a t c t g	g a g a g a c t t a	g g c a a c c g t g	c c g a c g g t c a	c g t c c t g g g t
289081	g a g t t t t a g g	g g g g c a t a a g	g g a g t c t t c a	g a t a t g t g a g	c c g c c t a g c g	t t c g c c a a g g
289141	t c t c t a c a c g	a a a a c g g g g c	t a a c g c c c a a	a c g g c t c g c a	t t c t t g c c c c	c a a t c a t t c c
289201	a g c c a a a c g g	t t t g a g a t a c	g t c t a c c t g a	c g a a c a g g a g	c t t c g t t t c t c	a a a t c g t g a a
289261	a c c t t c c c a c	g c c g t a c a c a	t c a a a t t t t g	t t g a g a t t c a	c g t c a a t g t a	a a g a a t g c a
289321	g t t t g t t c t a	t c g g g c t c t t	t a t c a c g c c g	t t g a t a c t a a	c t g g t t g c c c	a g c g c c g a g c
289381	g g t c t c g a g t	t g t a t c c g g t	g a c t g g t a c t	g t g a c a t t c g	a g g g c a a g c c	g a t c g a t a c c
289441	g g c c g a a t t c	a a t t c c g c a c	t g c c t c g g a a	g a g a g g c g a a	g t t t c a g t g c	t g c a a t c g a g
289501	a a t g g c a a t t	a c g a g a t g g a	a a c c c t c a c c	g g t c c g a t g a	c a g t t g a a g t	c c g g g c c t c c
289561	c g g t t g a t t g	a a g g c a a g t t	t g a c a a g t c c	a a c c c c g a c g	a a c t c a c c c c	a g c g g g c g a a
289621	a t g t a c a t t c	c t c a a a a a t a	c a a t t c t c g c	a c t g a a c t a a	c c g c g g a c g t	g c c a g c g g g c
289681	g g c g a c a c a a	t c g a c t t c a a	c t t g c t t g g t	t c c t a a a c a g	c c c g t a a t t	c a g t t g t g c t
289741	c t g c c a a t c a	c g g c a g c a g a	a c c a t a c c c a	a c a a a t g c a a	g c a a g t t c c g	c c t t g a g a t c
289801	a c t t g c t t g c	g t a t g t t g a a	a t t a c g t t g t	t t g t c a t t c g	g g g g t g a c g a	c a g c g t a a a t
289861	c c a g t a g g g a	t t g t g t t a c t	g a g c a a c g g c	c c a a g c c a g g	c c c g g g a a t a	t c a a g c c g g a
289921	t c g t a a g c t t	c g c t g c c t a g	t c c c c t g c c c	c g t g g c a t g t	a c g c g c a c a t	c a c g a t g c c g
289981	a g g a a g t a c a	g g a a t a a c a g	c g g a a c t g c c	a g a g c a c c a c	t g c t a g t c a c	g t c g g c c g g t
290041	g t g a a c a t c a	t c g a t a t g a c	g a a g a t t a c c	a a c a c c g c g a	c t c g c c a a c t	t t g t a t g t a g
290101	t c c t g c g t t t	g a a t c a a a t c	a a t g c g t t g c	a g g a a c a g c a	t c a c c a a t g g	c a a t t g g a a g
290161	g c g a c g c c g a	a t c c c a a t g g	c a a c a t c a a c	a c a a a g t t g a	c g t a a t a g g t	c a g c c g a g g c
290221	t c c a c c g c g a	c g t c c a t c g a	t c c a t t g a a t	t g c a a c a a g a	a c g t c a g c a c	g t a g t g c a g c
290281	a c c a a c c c a a	a c g c g a g c a c	g a c g c c c g a g	a c a a a c a g c a	c c a c g c t g a a	c g g t a g g t a a
290341	a c g t a g a c a t	a a c g t c g t t c	g t g a c t a t g c	a a a c a g c g g	c c a c a a a c g a	c c a c a g g t g a
290401	t a g a a g a t c a	t g g g g g a g g c	a a g c a c c g c g	c c a a c a a t c a	a a c c c g c t t t	c a c c c a a a t c
290461	a t g a a c g g c t	c t t c g a t c t t	c a a t g a a c t c	a g c c c g c g t t	c a c t g c g a c g	g a g c t g a a t c
290521	a t g g g c a c c a	a t t c a t c g g g	g t t g g g g a t c	g t c c c c a t c g	a t t t c a t c a a	t t c c g c g g t g
290581	g t g a t c c t c t	c t g g a a t g t c	c a g c g c a g c c	g a c t c g c c t g	c t t c g g c t t c	g a c a t c g g g a
290641	c t g t t c t t t t	c a t c c g g t t c	a g a t t c g a c g	g c c g t g c c a g	t g g c c t c c g g	c g g t t c c a c c
290701	a t g t c t c c g g	t c g c c a c t g c	g a c g t c c c c c	g a c t g g c a g c g	t g t a c a c c a c	t g t c g c g a c c
290761	a g a g a a t t g g	a c g t c a a g a a	t t c g t a g a a c	c g a c t g a c c t	g c g g a t c t t c	c t t g c g g t c g
290821	g g t a g c c c c a	t c t c t t t c a g	g t c g c g a t c g	g c g t t g t a t t	c g a t g a t c g c	c t g t t t g a g c
290881	g g c t c c t g g a	t g a a t c g c a c	c a c t c g g t t g	g c g a a c a t c a	a t c c a a c c g c	c a a t c c g a t c
290941	a a c a a c c a a a	t g a t t g c t t t	g a c c a g a g a g	c c a c g g a g t t	c t t c g a g a t g	c t c c c c g a a c
291001	g t c a t c g t c g	a a t t g t c g a a	c a a a t c g t c t	t t g g g t c g c g	t c a g t g c t t c	c a c g a g t t t c
291061	a a t c c a c c a g	g g g a g g g a g g	g t a c c a t t g t	g t g a a c t a c	t c t g c a c c g a	a c t a c t c g a t
291121	g c c a a c t a c t	c g g c g t c g a g	c c a t t c t a a c	t g a c c a t t c c	a a t c t c g c a c	g g t g c c a t t c
291181	a t g a c c g a t c	c a a c t t c c t c	t t c c a a t c c c	g c g a c c g c c g	t t t c c g t c g a	t t c g g t t t c g
291241	c c t c a g a c a c	t c g t g g g a a a	a c g a g t t c t g	t c g t t t g t g g	g c g a a a t t t a	c g a g g a c t t g
291301	g a g c t t t g g t	a c c c c a a a c t	a c g c c t g a t c	g a g g c g g g a g	c a g a a t t t t t	t g t c g c g g g c
291361	c c a a a a g c g g	g c g a a a a a t a	c g a c g g c a a a	c t g g g c t a c c	c c t g t g t a a g	c g a c c t t g c c
291421	a t c g a c g c t t	g t g a g g t g a	t t c c t t t g a c	g g g t t g c t g g	t t c c c g g c g g	g t t c a t g c c g
291481	g a c a a a c t g a	g g c g a g a c c c	g a a g g t a t t g	c a a c t c g t c c	g t g a c t t t g a	c g c g g c t a a a
291541	a a g c c g a t c g	c c g c g a t t t g	t c a c g g c g g c	t g g a t t c c c a	t c t c a g c a g g	c g t c t a c c g c
291601	g g c g t t c g c g	t g a c c g g a t c	c c c g g g c a t c	a a g g a c g a c c	t c g t g a a c g c	g g g a g c a a t c
291661	t t c g a a g a c g	c t t c g g t c g t	g g t c g a c g g g	c a c c a c g t c a	g c a g t c g c c g	c c c t g a c g a c
291721	c t g c c c g a t t	t c t g c c g c c a	c t t c a t c g c c	c t g c t c g c g t	a a t c c c a a c c	t g t a g c t c g g
291781	t g c t c c c c c a	c t g a g a c g a g	c a t g g a c c a g	c c g t c t t c a a	c c g t t t g c g t	c g c a g g g g g g
291841	a c t t g c c t c a	a a c g g t c g c a	c g a a c g a c g c	g a g c c t g t g a	g a c g a t g g a t	c g t g c t t g g
291901	c g g c t g a g c g	c g g c g a g a c g	g a a c a a t t a g	g g a c a a t g g t	t c t a c t c t g g	t g c a a t c a c c
291961	g a a c c c c a a c	a t c t c a c g g c	g g g g a c c g c c	g t g c t a c a g g	t t t t t g g t g g	c t g t g a c a t t
292021	t t g t g a a a c t	g a a g c g t c g t	g a t t c c t t g g	c g g a g t t g a c	t t g a c a t c g a	t t g t c g c g g a
292081	t t c g t a g g g t	c g g c t c g a t g	g a t g a t t c c a	a g g t t c t t t c	c g a t t t g g t t	g g a c g g c g t t
292141	c c c g c g t g t a	t t t t c g t t c c	c a c g a a c g a a	t g a c t c t c t c	g g c a c c g a t g	c g g t g t t g g t
292201	g g g c a a c c t g	c g c g c t g g c a	a t t g t g a t g c	t t g g t t c a g g	a t g c t c g c t g	t t t c g a a a c g
292261	g t g t t t g g t c	c g a t g g a t c g	t c c g g c g a a t	t g a a t t c g g g	g t c g a a t c a c	a c a c a a g t t t
292321	c a a a g c t c a c	c c a c a a g a g c	c g a a a g a c g a	t t t c g t t g c a	g g c g g a t t t t	c g t c a c g t c g
292381	g c a c c c a a g a	c c t g g a c g a a	t c g c t g t g g c	a g c a c g t t g a	t g a a a c c g c t	t t t c c g c c a a

292501	cċttgċċgā	aācggċāgāā	ġagaatġttg	cctċgggċgā	tgaċccaātċ	aatcgċttgċ
292561	tttcaaccgċ	cggggtgttg	ggacgcagtc	catcggtat	cgaaaccatt	ccgttgcgtc
292621	catcgagcg	acacgaactt	ccgatctcca	cggtgctgga	tgggtctcat	gtcgactgg
292681	ctcaagagaa	cggcaagctc	accggccgct	cattggattc	gccccagatg	tcgctgtcgt
292741	tgacaccaac	gttgggcccc	ggacctgggc	aagtcacctt	ggagatccgt	cccgaatcc
292801	agcatgttct	ggtccagcaa	cgtttcatca	gcagcgaagc	ggcgacacgt	ttggcgaccg
292861	gacgctccac	ttgggaactg	ccggaatga	atctttcgtg	ggccgccaat	ccgcatctga
292921	cgttgctgat	cgctccggtg	catcaaccag	acgaaaacga	accaacgttt	ggattggcca
292981	ggcaaatgct	tcgcgacgċċ	gatcacatgc	aagacgacca	acatgtgatg	ttgctgctgc
293041	gaatcaacga	tttgccgtct	tcctgatctc	cggaaaaatt	ctgctgggtg	gattcgctgc
293101	cgtgcaaacg	aggcggtag	ctcatgtctt	tcacacgagc	gagattttcg	cgatccacgc
293161	atgccccgc	gaaggtttgc	caccatttgc	taaacttctt	ttttcgatga	ctgctgatcg
293221	catctgtacc	ggttggaaactt	cgtttcatgaa	agacgctcac	tttggtgac	actccctctc
293281	ccgatcccgċ	gċcgaccgctc	aacgcaccac	cggtctcgċċ	acccggcca	gċgctgtcga
293341	tggacgaagt	gaccgtgċgċ	caatccacċċ	cgctagacgċ	ccaggccatt	cacgctttga
293401	tċgċtċcggtt	tgtttcċgċag	catctgctgċ	tgtċgċggac	cgaagccgaa	atcatcgagt
293461	tgaccċgcca	cgggttċgctc	gċgatggtcċ	gtċċacgctg	catcgċcttt	tcċgċcatcg
293521	aggtċtaċag	tcċcaagctg	gċċgaactgċ	aatgtċttggċ	cggtgacċċċ	gaagcccaac
293581	gtttgggact	gggacgcaaa	ttggtcgggċ	actgċatcga	aagagccċgċ	acgctcggtg
293641	tċgatggaaat	cċtċgċgatc	agctcċtċċg	aagacttċct	caaatcatgċ	ggcttċgatt
293701	actċgttgċċ	cgaccagaag	aaagcċttgt	tċtgċċaact	ccgtċċtċgċ	aacttċgatg
293761	accactgaaa	tċgaaccgċt	cgaatttttċ	aagcaatcca	ttċtgacgċċ	cagċċcttċg
293821	ggttacgaag	aaccgatcca	aaaactgatc	ggcgaatacc	tgaaacċgca	cagcgacgaa
293881	gtċtċgatċg	acgtgċacgċ	aaaactgacċ	gtċċgggtċg	gċgaagcggċ	tggccccaaċ
293941	ctgatgttgg	ctggtċactg	tċaccaaatc	ggcatgċtga	tttċacacat	cgacgatcaa
294001	ggattċttgt	acċcccaaac	gatċgggggt	tgggacċċac	agcaactgat	cggtcaatcc
294061	atgacggtgt	ggaccgacga	cggtċċċgċt	tċċgċggtċa	tċagtċgcaa	gċċaatċċac
294121	ttgttgtċtċ	aacaggaacg	cgċgċaggtg	gtċaaċgtgċ	aacaaatgtg	gċtggacatċ
294181	ggagccaaag	atggtgacga	agċcaaatac	aaagtċċgċa	tċgggċactg	ggtagċttg
294241	aacċttgċct	accgagaact	gtgtggċgac	atggtċagċg	gtċċgggċat	cgtaacaaa
294301	acgggċatgt	ggacggtċat	tgaaacċgċċ	cgċtċgċtċg	cċtċgtċċga	tċaagċgttg
294361	cagtċgċaac	tċcacagċgt	cgċgactgtċ	caagaggaga	tċgggtċtċg	tggagccaaċ
294421	accċgtgċċg	gtċgċatċaa	ċċċagatgtg	gċċatċgċgċ	tggatgtċac	gċatgċatċa
294481	gactgċċċga	cgatċgacaa	acaacaacaa	ggċgatatac	agatċggtgg	cgċċċċggtg
294541	atċttċċgċg	gċċċaaċat	caacgċċaaa	gtċgċaaagċ	gactgatgċa	actggċgac
294601	gacaacgaca	tċgċgtatċa	acċtċgċgċg	cċtċgċċgċg	cċgċgċċgaa	tgattċċaac
294661	gtgttgċagċ	tttċtċggttċ	aggċgttgċċ	acaggacttg	tċgċgattċċ	caaccgċtac
294721	atgċactċag	ċċgtċgaaac	gatċagċċtċ	ggtgacatċg	aagċgattgċ	gaaactgċtċ
294781	acċgtgttċg	ċtċaatċgċt	gacaccagaa	tċgċatttċa	tċċċċggttg	atċgagċtċg
294841	gċtgaggaag	ċtċgtgacċat	tċgggttċggt	ggattċgċagt	gagagagaga	gatċtċacċgċ
294901	cgċagacċċg	cgċgtċtaċag	gttgacċatċ	atċċċagċċt	gtagċtċggt	ggtċċċċac
294961	cgagċċagċt	gtċaaacċċt	tċaaactttg	tċċċacċgtt	ċtaattċċggċ	aacċgċċtċa
295021	atċċaagaag	catċtċċgċt	ċtċtċċggaca	gċggtttgtt	tċċċagċtċa	caatċggtgt
295081	gċtċagaaag	ttgttċacaa	acaagċċtgt	agaccċċttg	ċċgatċċtċg	ċtċgtgtċċa
295141	gttċaacgċa	ċċgattċtċgċ	ċttttgaaċa	actċgacċgt	cgċgaacċgtt	tċċtttttga
295201	aggatċċaaa	ċċċgċacttċ	aagċtċacċa	agttgtċgċt	ttgtċgtċċg	gtgtactttg
295261	ċtċgagċċag	aacċgċtttċ	tċcagaacċg	ċatacggaca	ttċaaċagac	gtgactttgċ
295321	gċaactċċgt	gtċtttċgċċa	aacacċgtċt	accacċċtċ	caagtttgac	tċċgacċgċt
295381	ggaacċċatċ	gagcaagaaa	ttċċggttċg	cggtttċċgċ	agtċatċttċ	tċċatċgċat
295441	ċċċgaagċaa	ċttċaccacċg	atċgtactċgċ	gaactaaatt	tċċtċċċgċa	atċatċtċtt
295501	caatggċċgċ	cgċgtgċggt	ċċattċgċtt	cgċgttċcagċ	tċgċaataaa	tċgċċggtċg
295561	acaaatggac	ċċagċċċagċ	tgggattċċg	ċċaactċgċa	catċgttċċċ	ttċċċċgċac
295621	cgċgacċċċ	aagcacaac	accaggttċg	gttċgggċga	tggċaatċgċ	tgatċggagt
295681	gatgaactċac	aacċttċgggt	gaaggagċċa	gċċtċttċtċ	gtagacatgċ	caacċtċgat
295741	ċċgtgggagċ	aagċtċgtċt	tċgċaggtga	tgtċataagċ	gagatggċċa	tċċagċċgac
295801	aaatċċtċċa	tċagċgatac	gtatttċgaa	acgacagċċg	aggacttċtċ	gċtgatttċċ
295861	catċċgċacċg	atċċċaagċċ	atċttgċċgt	tċċaataaċċ	tggactggaa	acggtgċċċg
295921	attċċgactċ	cgċagċċgċg	gċagtċagag	gaacaaagag	ċċċatċċact	tċgggaaċtċ
295981	ċċgċaccċgat	ċacċtċgatg	tagaaggtat	tgggagtċag	ċtċgttċgat	tċagċtċatċa
296041	ggaggagaaċ	ċttċtċacatt	cgttgggċga	cgċggtċagċ	ttċaggċgag	caaaaggaat
296101	gċtċtċagċċ	cagċttttċg	gtċatċgttt	cgċgagċttg	ċtggagtċgt	tċaggċaact
296161	tċgtggċgċtċ	tttċċċgċċg	gċttgagċċa	tatċċgċċċg	gċċacċgċċg	ċtċċacċċga
296221	ċċacċttċggċ	cgċċgċacċċg	acċċagċtċac	cgċtċttċċaa	accacċgatċa	accagatċtċ
296281	ggċtċagċtċċ	acċgacċaaċ	atċactttgt	cgċttċatċga	cgaagċċaac	agċactċgċg
296341	ttggċgtċtċ	gċtċttċtċg	cgaatttċgat	cgatċċaaċċ	tċgċatċatg	ttggggttċg
296401	cacċgċċgċt	ttċagċaaċg	atċagċaaċg	gtċgċċċgac	ċttggttċċa	tċtċgċatċa
296461	agtċatċċċgċ	ggaaatċtta	ċċgċċċgċg	tċacċtċgtt	gagtċgtċtċg	accagċttċg
296521	atċgatċgċċ	caacagċgaa	tċċaagċgac	tċagċacatċ	gggtatċgċa	acgtċċaaac
296581	ggċgagtċaa	acċgċgaacċ	gċċgċacċga	cgċċgttċgta	atċċgtċatg	tċggtċgttt
296641	ċċgċttċtċgċ	agċċttċggċa	tċaaagacaa	attċagċgċg	atagtċċgċa	gċtttċgċtt
296701	acgacaattċ	tttċttċagċ	cgċċgaactt	ċtċċgatċaa	cgċċacċgtg	cgċgċagċag
296761	ċċacċgaagċ	atċgċaaattċ	agtttċċċgt	ċċacċtċgtt	cagċaaċċċt	tċgċtttċgt
296821	cgċggtċtċċ	tttċggċacċg	tċgċċċgtċa	atċgttċċgat	ċċggċgagtt	ċċċgtggaaa
296881	cgċtttċtċtċ	gacċacċgacċ	tċaaacċgaac	cgacttċgtt	gggttċgtċtċ	agggtagttċ
296941	cacċgċacag	ttċacċgactg	aacgttċċċa	tċgaaacċat	gċgacatggg	tċgggatact



297061	agcgaatttc	atcgcttttg	ccgaccatgc	caaagcagtc	ttgttctgatc	ttgaccaaag
297121	tctcgtcgtc	gatggctttg	gggttggtga	aatcaaaccg	caagcgatcc	ggttcaacct
297181	tgtcgccttg	ttgttcggcg	tgcggtccaa	catgagtgtg	taatgcgtgg	tgcaaatgt
297241	gagtcgcact	atgggctcgt	gccaacgcgc	tgcggttttc	gacatcaacc	tttgccgtgc
297301	atgtttcgcc	ttcgttgatc	ttcccacgaa	tcaactcgacc	gtgatgaacg	atcatcgacg
297361	cgtgcgcgtg	agtgtcgatg	acctcgaact	caaagtgtgc	gttgggaatc	acaccgatgt
297421	cgccaacttg	gccaccggat	tcaccgtaga	acggcgaatg	atccagaacc	aatcgcagga
297481	cagcatcttc	ggggcgatca	agatgactga	gcagttgccc	gtcgtcgcct	ttgcctttgc
297541	catcgccggg	gatgatgcct	ttgacgaccg	cggttgcttc	cgtttggttcg	taaccaacaa
297601	atgggggtttc	tcgcagagcc	tctttcaacg	tttccagtgg	tccagttttg	aacagcacac
297661	gttgctccgcc	gtcgttttcg	tcagcgtgtt	tgtccatcgc	ttcccgaaaa	ccagaccaat
297721	cgaaggtgaa	gttctgttcg	gcggcgaggg	tttgaaccaa	ctcgggcggc	acgccatagg
297781	tggtcagcaa	atcagcggct	tctgcaccgg	gcaccatcac	ggatgcttcg	tcgttcatct
297841	cttcgaacaa	acgatggatg	cgtttcatcc	caccgtcgat	cgttgagaag	aaagccttct
297901	cttccgattc	aatcgcttcg	ctgacacgct	gagtcgtttg	gccgagctct	ggataagcgg
297961	ccttgagggc	gtccgcaact	gcttcgacca	acttgtagag	gaagggctca	cgcagattca
298021	tttgatagcc	gtccagcacc	gcgcgacgaa	tcaaacggcg	gatgaccgac	cgagcgtctt
298081	tggggcgggg	atacacattt	tcataaacgg	cgaaaacgct	ggctcgcgcg	tggtcgggtga
298141	tccggcgcaa	cgctcggcca	ttgtcacttt	cgatattcgta	cttcacgcgcg	cagacttccg
298201	acgcgggcttc	gacgatcggg	aacagactgt	cgatgtggaa	gttcgttggc	actccctgca
298261	ggacgctggc	ggttcgttcc	agtcccatgc	cggtgtcgat	gttcttgctg	ggcaacggat
298321	gcaagttgtc	cgggggcggtg	ccgacgcgat	tgaactgggt	gaacaccaag	ttccaaattt
298381	cgacgtcgtc	gccgtcttcc	agttggtaat	agatctcgct	gcagggagcc	cagactccgt
298441	ccgggcttcc	gctgggtgcc	gacgcggggc	agaagttttc	gtcctcgctc	attcgcgaaa
298501	tgcgttgggt	cggtcaatccg	atcttgcgtg	gccaaatgcc	aaacgcttcg	tcgtcatctt
298561	tgtagaccgt	gaccgtcaga	cgctcgcggg	ggatgcccag	ccactttttg	tcggtcagga
298621	attcccacgc	ccagtggatg	gcttcttctt	tgaataaatc	gccgaacgaa	aagttgccca
298681	gcatttcgaa	gaacgtgtgg	tggaaacggg	tccggccccc	attgtcgatg	tcaccggttc
298741	gcaagcattt	ctggcacgtg	gtcgcgcgag	tgaattccag	tttgaccttt	ccaaggaagt
298801	ggtctttgaa	ctggttcatc	cccgcgggag	tgaacaaaac	cgatggatcc	caagccggaa
298861	cgagcacgtc	gctgggttgg	cggaacgcaac	ctttggtctc	aaagaacgcc	aagtattttt
298921	cgcgaggttc	gtcagttttc	atcaggatgt	gcgggtggat	tcaacaagga	aaagatcggg
298981	gattgagcca	cgggggctcg	cgttccatcg	tcggcatgat	atcagtcgat	gcccaacggg
299041	tgacaggtgc	cgaatttcgg	cccacaatgc	cgggccgccc	acgggtgctg	cgatgctttt
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310981 accgacacgg gcaggatcaa ccaatcgcaa aagatgaatg catcaagctt ggcgacggca  
311041 aattagccgt cgacgttggg cgaaccagtg actttgtcac tgtacatcgc cagtttgccg  
311101 agcacttgat cgatggcatg tgacgagacg ttgtttgctt ccaacgcac tggcctcagg  
311161 ccacagaatt tggagaaatg aactccggtg attccacgtc cggcatgaac cttcgtcagg  
311221 tccgcaccgg tgtactggat atctccggaa gtgatcgaag cgatgaactc ggtttgcac  
311281 cgagccagct tttcgatcgg gactccatca aagaagtggg tcaactctgg atccgcaaga  
311341 acccgaacgt acatctcgtc gacaacacga cggacgccat ccattcctcc gagctgggtc  
311401 agtaagtcgg attcagattg actcatgatg gaatatctcc agtcagatta cataggggtc  
311461 ggttcgtaag gaatgtcttc gatcaaatcc atgggcaatg gagccacggt catgccggt  
311521 tccctgcaga ttccatcgat cgcttctctg gacttctgca ccaagaattc tcgagtctgt  
311581 cccttgtact gagacgtcga tgccgttggg ctcacatcggc cgctgaaatt ggtttcgttc  
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311821 tcccaggtat cgatgacata gccgacgttg tcttgcctt ccaaaagctc agcaccggca  
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311941 cggaaaccaa tcccaagttt gatgtcgcgt gaactcgttg aatggcaagc gattcgttgc agcaggaaca  
312001 cggttgcgtt ggacatcgaa cacgtcggc acccaattg tgagcgattt cgccgagcgg gtgcagttga  
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312301 agttcgatca gctcgttttg gatttgcttg gattgttttg gatgttttga cggttgggac  
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313021 gaatcttctt gtgatcgctt ggagtctcga tcagcaacgg gctcatcgac  
313081 tcgacgaaca agtccgcccg gaaggaatcg tcgctggatt ccagatcgga  
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313201 gatcgatctg aaccagatcg atctgaatcc cttcgatctg ccttggggcg  
313261 ccgcatcgcg aatccgaacg ttcgccacgt cgtccaccgc gacgtcgac  
313321 gtttcggatg aatcggaatc agattcttcg cggtcaccgc gaggcgatt  
313381 tctacgacga cgtccgaatc ggacattttt tgcgttgac caccgacggc  
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313621 atttccaccg tgtctgatgc gatgagatcg gactcatcat cgaaggcttc  
313681 gcatcctcgt cgtcgaaatc atcattggcg agcaaaccgc tagcgaatcc  
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313861 ttgttttcag ccacgcccga tccagatggg acgtcatctg agtcacgtc  
313921 ccaaaaccag gcaacttcgg cgggtggttg acggcgcgga gtgcctgcaa  
313981 gcaccttcgt catcgctcga gaaagcggag gctttcgcg gtgcggtttc  
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314101 tcaggttcag cagcaggttt ttcaggttcg actttggcag cggggcgatc  
314161 ggtgtcccca acaaactcgc gaggatattc caattgtctg gcatgtggt  
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314281 cgacaaaaag tgtgcaatga tctgaactgg cttcaatcgc ggcgtggact  
314341 gcaggaaacc ggttcgtggg ccgaccgaca tcgattgatc gggcttcgct  
314401 gacacccttt tctctacaag agtgtccctg tggtaaccga attttctcga

L3 ANSWER 84 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AR268952 GenBank (R)  
GenBank ACC. NO. (GBN): AR268952  
GenBank VERSION (VER): AR268952.1 GI:29699689  
CAS REGISTRY NO. (RN): 504700-37-2  
SEQUENCE LENGTH (SQL): 27  
MOLECULE TYPE (CI): DNA; linear  
DIVISION CODE (CI): Patent  
DATE (DATE): 10 Apr 2003  
DEFINITION (DEF): Sequence 6 from patent US 6500643.  
SOURCE: Unknown.

Unclassified  
 NUCLEIC ACID COUNT (NA): 5 a 6 c 5 g 10 t 1 others  
 REFERENCE: 1 (bases 1 to 27)  
 AUTHOR (AU): Wu, D.-H.; Gu, Y.; Millard, W.J.; He, Y.-J.  
 TITLE (TI): \*\*\*Human\*\*\* \*\*\*high\*\*\* \*\*\*affinity\*\*\*  
 \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 JOURNAL (SO): Patent: US 6500643-A 6 31-DEC-2002;

FEATURES (FEAT):  

Feature Key	Location	Qualifier
source	1..27	/organism="unknown"

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L3 ANSWER 85 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AR268951 GenBank (R)  
 GenBank ACC. NO. (GBN): AR268951  
 GenBank VERSION (VER): AR268951.1 GI:29699688  
 CAS REGISTRY NO. (RN): 504700-36-1  
 SEQUENCE LENGTH (SQL): 25  
 MOLECULE TYPE (CI): DNA; linear  
 DIVISION CODE (CI): Patent  
 DATE (DATE): 10 Apr 2003  
 DEFINITION (DEF): Sequence 5 from patent US 6500643.  
 SOURCE: Unknown.  
 ORGANISM (ORGN): Unknown.

Unclassified  
 NUCLEIC ACID COUNT (NA): 5 a 7 c 8 g 5 t  
 REFERENCE: 1 (bases 1 to 25)  
 AUTHOR (AU): Wu, D.-H.; Gu, Y.; Millard, W.J.; He, Y.-J.  
 TITLE (TI): \*\*\*Human\*\*\* \*\*\*high\*\*\* \*\*\*affinity\*\*\*  
 \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 JOURNAL (SO): Patent: US 6500643-A 5 31-DEC-2002;

FEATURES (FEAT):  

Feature Key	Location	Qualifier
source	1..25	/organism="unknown"

SEQUENCE (SEQ):  
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L3 ANSWER 86 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AR268950 GenBank (R)  
 GenBank ACC. NO. (GBN): AR268950  
 GenBank VERSION (VER): AR268950.1 GI:29699687  
 CAS REGISTRY NO. (RN): 504700-35-0  
 SEQUENCE LENGTH (SQL): 1893  
 MOLECULE TYPE (CI): DNA; linear  
 DIVISION CODE (CI): Patent  
 DATE (DATE): 10 Apr 2003  
 DEFINITION (DEF): Sequence 3 from patent US 6500643.  
 SOURCE: Unknown.  
 ORGANISM (ORGN): Unknown.

Unclassified  
 NUCLEIC ACID COUNT (NA): 430 a 570 c 516 g 377 t  
 REFERENCE: 1 (bases 1 to 1893)  
 AUTHOR (AU): Wu, D.-H.; Gu, Y.; Millard, W.J.; He, Y.-J.  
 TITLE (TI): \*\*\*Human\*\*\* \*\*\*high\*\*\* \*\*\*affinity\*\*\*  
 \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 JOURNAL (SO): Patent: US 6500643-A 3 31-DEC-2002;

FEATURES (FEAT):  

Feature Key	Location	Qualifier
source	1..1893	/organism="unknown"

SEQUENCE (SEQ):  
 1 atggcagcaa aaactcccag cagtgcaggag tctgggctgc ccaaactgcc cgtgcccccg  
 61 ctgcagcaga ccctggccac gtacctgcag tgcattgcag acttggtgtc tgaggagcag  
 121 ttcaggaaga gccaggccat tgtgcagcag tttggggccc ctggtggcct cggcgagacc

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241 ctgaaatgaaca tgtatctcāa cāācgcgctg gcctctgctg tcaāctcāag cctgcccgtg
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361 atctctgggtg tactcagcta caaggccctg ctggacagcc actccattcc cactgactgt
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481 tccctaccggc tccccggcca taccaggagc acgtttgggtg ctgagaacag cagcatcatg
541 ccggagcctg agcacgtcat cgtagcctgc tgcaatcagt tctttgtctt ggatgttggtc
601 attaatcttcc gccgtctcag tgagggggat ctgttcactc agttgagaaa gatagtcaaa
661 atggcttcca acgaggacga gcgtttgcct ccaattggcc tgctgacgtc tgacgggagg
721 agcgagtggg ccgaggccag gacggtcctc gtgaaagact ccaccaaccg ggactcgtg
781 gacatgattg agcgctgcat ctgccttgta tgcctggacg cgccaggagg gctggagctc
841 agcgacaccc acagggcact ccagctcctt cagggcggag gctacagcaa gaacggggcc
901 aatcgctggg acgacaagt cctgcagttt gtgggtgggc gagacggcac ctgcggtgtg
961 gtgtgcaaac actccccatt cgatggcatc gtcctgggtg agtgactga gcatctgctc
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1741 tgcaaagaga cttcttctag caagtttgca aaagctgtgg aagaaagcct cattgacatg
1801 agagacctct gcagtctgct gccgcctact gagagcaagc cattggcaac aaaggaaaaa
1861 gccacgaggg ccagccaggg acaccaacct tga

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L3 ANSWER 87 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

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LOCUS (LOC): AR268949 GenBank (R)
GenBank ACC. NO. (GBN): AR268949
GenBank VERSION (VER): AR268949.1 GI:29699686
CAS REGISTRY NO. (RN): 504700-34-9
SEQUENCE LENGTH (SQL): 1743
MOLECULE TYPE (CI): DNA; linear
DIVISION CODE (CI): Patent
DATE (DATE): 10 Apr 2003
DEFINITION (DEF): Sequence 1 from patent US 6500643.
SOURCE: Unknown.
ORGANISM (ORGN): Unknown.
NUCLEIC ACID COUNT (NA): 411 a 395 c 405 g 532 t
REFERENCE: 1 (bases 1 to 1743)
AUTHOR (AU): Wu,D.-H.; Gu,Y.; Millard,W.J.; He,Y.-J.
TITLE (TI): ***Human*** ***high*** ***affinity***
***choline*** ***transporter***
JOURNAL (SO): Patent: US 6500643-A 1 31-DEC-2002;

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FEATURES (FEAT):
Feature Key Location Qualifier
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source 1..1743 /organism="unknown"

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121 gccatcatag ttggtggccg agatattggt ttattgggtg gtggatttac catgacagct
181 acctgggtcg gaggagggtg tatcaatggc acagctgaag cagtttatgt accaggttat
241 ggcctagctt gggctcaggc accaattgga tattctctta gtctgatttt aggtggcctg
301 ttctttgcaa aacctatgcg ttcaaagggg tatgtgacca tgttagacce gtttcagcaa
361 atctatggaa aacgcacatg cggactcctg tttattcctg cactgatggg agaaatgttc
421 tgggctgcag caattttctc tgctttggga gccaccatca gcgtgatcat cgatgtggat
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541 ctctattctg ttggcctacac tgatgtcggt cagctctttt gcatttttgt agggctgtgg
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661 catgccaaat accaaaagcc gtggctggga actgttgact catctgaagt ctactcttgg
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781 gttctctctt ctctctcagc cacctatgct caagtgtgtt ccttcctggc agctttcggg
841 tgccctggta tggccatccc agccatactc attggggcca ttggagcttc cacagactgg
901 aaccagactg catatgggct tccagatccc aagactacag aagaggcaga catgatttta
961 ccaattgttc tgcagtatct ctgccctgtg tatatttctt tctttgggtc tgggtgcagtt
1021 tctgctgctg ttatgtcatc agcagattct tccatcttgt cagcaagttc catgtttgca
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1561 cacagtgaag aaaacatgga taagacaatt cttgtcaaaa atgaaaatat taaattagat
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1741 tga

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L3 ANSWER 88 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): E49871 GenBank (R)  
 GenBank ACC. NO. (GBN): E49871  
 GenBank VERSION (VER): E49871.1 GI:22554902  
 CAS REGISTRY NO. (RN): 450667-38-6  
 SEQUENCE LENGTH (SQL): 1743  
 MOLECULE TYPE (CI): DNA; linear  
 DIVISION CODE (CI): Patent  
 DATE (DATE): 27 Aug 2002  
 DEFINITION (DEF): \*\*\*High\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\*  
 SOURCE: Homo sapiens.  
 ORGANISM (ORGN): Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;  
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;  
 Hominidae; Homo

NUCLEIC ACID COUNT (NA): 412 a 393 c 406 g 532 t

#### COMMENT:

OS Homo sapiens ( \*\*\*human\*\*\* )  
 PN JP 2001136976-A/3  
 PD 22-MAY-2001  
 PF 27-DEC-1999 JP 1999368991  
 PI TATSUYA HAGA,TAKASHI OKUDA  
 PC C12N15/09,A01K67/027,A61K38/00,C07K14/47,C07K16/18,C07K19/00,  
 PC C12N5/10,  
 PC C12P21/02,C12P21/08,C12Q1/00,C12N15/00,A61K37/02,C12N5/00 CC  
 FH Key Location/Qualifiers  
 FT CDS (1)..(1743).

#### REFERENCE:

1 (bases 1 to 1743)  
 AUTHOR (AU): Haga,T.; Okuda,T.  
 TITLE (TI): \*\*\*High\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\*  
 JOURNAL (SO): Patent: JP 2001136976-A 3 22-MAY-2001; SCIENCE & TECH  
 AGENCY

#### FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1743	/organism="Homo sapiens" /db-xref="taxon:9606"

#### SEQUENCE (SEQ):

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121 gccatcatag ttggtggccg agatattggt ttattggttg gtggatttac catgacagct
181 acctgggtcg gaggagggtg tatcaatggc acagctgaag cagtttatgt accaggttat
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361 atctatggaa aacgcatggg cggactcctg tttattcctg cactgatggg agaaatgttc
421 tgggctgcag caattttctc tgctttggga gccaccatca gcgtgatcat cgatgtggat
481 atgcacattt ctgtcatcat ctctgcactc attgccactc tgtacacact ggtgggaggg
541 ctctattctg tggcctacac tgatgtcgtt cagctctttt gcatttttgt agggctgtgg
601 atcagcgtcc cctttgcatt gtcacatcct gcagtcgcag acatcgggtt cactgctgtg
661 catgccaaat accaaaagcc ttggctggga actggtgact catctgaagt ctactcttgg
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 1741 tga

L3 ANSWER 89 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AB084377 GenBank (R)  
 GenBank ACC. NO. (GBN): AB084377  
 GenBank VERSION (VER): AB084377.1 GI:22506641  
 CAS REGISTRY NO. (RN): 450515-00-1  
 SEQUENCE LENGTH (SQL): 291  
 MOLECULE TYPE (CI): mRNA; linear  
 DIVISION CODE (CI): Primates  
 DATE (DATE): 21 Nov 2002  
 DEFINITION (DEF): Homo sapiens mRNA for \*\*\*high\*\*\* - \*\*\*affinity\*\*\*  
 \*\*\*choline\*\*\* \*\*\*transporter\*\*\* CHT1, 5'UTR.  
 SOURCE: Homo sapiens ( \*\*\*human\*\*\* )  
 ORGANISM (ORGN): Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;  
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;  
 Hominidae; Homo  
 NUCLEIC ACID COUNT (NA): 51 a 123 c 74 g 43 t  
 REFERENCE: 1  
 AUTHOR (AU): Okuda,T.; Okamura,M.; Kaitsuka,C.; Haga,T.; Gurwitz,D.  
 TITLE (TI): Single Nucleotide Polymorphism of the \*\*\*Human\*\*\*  
 \*\*\*High\*\*\* \*\*\*Affinity\*\*\* \*\*\*Choline\*\*\*  
 \*\*\*Transporter\*\*\* Alters Transport Rate  
 J. Biol. Chem., 277 (47), 45315-45322 (2002)  
 OTHER SOURCE (OS): CA 138:252025  
 REFERENCE: 2 (bases 1 to 291)  
 AUTHOR (AU): Okuda,T.  
 TITLE (TI): Direct Submission  
 JOURNAL (SO): Submitted (26-APR-2002) Takashi Okuda, University of  
 Tokyo, Faculty of Medicine, Department of  
 Neurochemistry; 7-3-1 Hongo, Bunkyo-ku, Tokyo 1130033,  
 Japan (E-mail:okuda@m.u-tokyo.ac.jp,  
 Tel:81-3-5841-3560, Fax:81-3-3814-8154)

FEATURES (FEAT):	Feature Key	Location	Qualifier
source	1..291		/organism="Homo sapiens" /db-xref="taxon:9606" /tissue-type="spinal cord"
gene	1..291		/gene="CHT1"
5'UTR	1..291		/gene="CHT1" /note="high-affinity choline transporter CHT1"

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 61 gcgctcccag gttcttggag acgccgagtg aggagccgcc ctgaccgccc ggccccgctc  
 121 cgcaactgcac cccgaccac cccgcacctt ccttttctgc accctcgcac ccacaccctt  
 181 cgcggttcca gggggcgggc gcccggggcg gacgccttgc gcgtgcagcc accactccag  
 241 aagacttaat gaagtagcca gctgcagaag aatctggatc attagataaa a

L3 ANSWER 90 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BD012719 GenBank (R)  
 GenBank ACC. NO. (GBN): BD012719  
 GenBank VERSION (VER): BD012719.1 GI:22092908  
 CAS REGISTRY NO. (RN): 445761-48-8  
 SEQUENCE LENGTH (SQL): 1743  
 MOLECULE TYPE (CI): DNA; linear  
 DIVISION CODE (CI): Patent  
 DATE (DATE): 2 Aug 2002  
 DEFINITION (DEF): \*\*\*High\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\*  
 SOURCE: Homo sapiens.  
 ORGANISM (ORGN): Homo sapiens

Eutelēostomi; Mammalia; Eutheria; Primates; Catarrhini;  
Hominidae; Homo

NUCLEIC ACID COUNT (NA): 412 a 393 c 406 g 532 t

COMMENT:

OS Homo sapiens ( \*\*\*human\*\*\* )  
PN WO 0116315-A/3  
PD 08-MAR-2001  
PF 18-AUG-2000 WO 2000JP005545  
PR 27-AUG-1999 JP 99P 240642, 27-DEC-1999 JP 99P 368991 PI  
TATSUYA HAGA, TAKASHI OKUDA  
PC C12N15/12, C07K14/47, C12Q1/68, C07K19/00, C07K16/18, C12N5/10, PC  
A61K38/17,  
PC A61K45/00, A61P25/28, G01N33/53, A01K67/027  
CC

FH Key Location/Qualifiers  
FT CDS (1)..(1743).

REFERENCE: 1 (bases 1 to 1743)  
AUTHOR (AU): Haga, T.; Okuda, T.  
TITLE (TI): \*\*\*High\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
\*\*\*transporter\*\*\*  
JOURNAL (SO): Patent: WO 0116315-A 3 08-MAR-2001; JAPAN SCIENCE AND  
TECHNOLOGY CORP, TATSUYA HAGA, TAKASHI OKUDA

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1743	/organism="Homo sapiens" /db-xref="taxon:9606"

SEQUENCE (SEQ):

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1 atggctttcc atgtggaagg actgatatgt atcatcgtgt tctaccttct aattttgctg
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121 gccatcatag ttggtggccg agatattggt ttattggttg gtggatttac catgacagct
181 acctgggtcg gaggagggtg tatcaatggc acagctgaag cagtttatgt accagggtat
241 ggcctagctt gggctcaggg accaattgga tattctctta gtctgatttt aggtggcctg
301 ttctttgcaa aacctatgcy ttcaaagggg tatgtgacca tgtagaccc gtttcagcaa
361 atctatggaa aacgcatggg cggactcctg tttattcctg cactgatggg agaaatgttc
421 tgggctgcag caattttctc tgctttggga gccaccatca gcgtgatcat cgatgtggat
481 atgcacattt ctgtcatcat ctctgcactc attgccactc tgtagacact ggtgggaggg
541 ctctattctg tggcctacac tgatgtcgtt cagctctttt gcattttttg agggctgtgg
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661 catgccaaat accaaaagcc ttggctggga actgttgact catctgaagt ctactcttgg
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901 aacagactg catatgggtt tccagatccc aagactacag aagaggcaga catgatttta
961 ccaattgttc tgcagtatct ctgcctgtg tatatttctt tctttggtct tgggtcagtt
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1381 ttctaccctg gctattaccc tgatgataat ggtatatata atcagaaatt tccatttaaa
1441 acacttgcca tggttacatc attcttaacc aacatttgca tctcctatct agccaagtat
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1741 tga
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L3 ANSWER 91 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BD005267 GenBank (R)  
GenBank ACC. NO. (GBN): BD005267  
GenBank VERSION (VER): BD005267.1 GI:18633228  
CAS REGISTRY NO. (RN): 392945-96-9  
SEQUENCE LENGTH (SQL): 1743  
MOLECULE TYPE (CI): DNA; linear  
DIVISION CODE (CI): Patent  
DATE (DATE): 31 Jan 2002  
DEFINITION (DEF): \*\*\*High\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
\*\*\*transporter\*\*\*  
SOURCE: Homo sapiens.  
ORGANISM (ORGN): Homo sapiens



Eutelēostomi; Mammalia; Eutheria; Primates; Catarrhini;  
Hominidae; Homo

NUCLEIC ACID COUNT (NA): 412 a 393 c 406 g 532 t

COMMENT:

OS Homo sapiens ( \*\*\*human\*\*\* )  
PN JP 03074455-T/3  
PD 19-JAN-2001  
PF 18-AUG-2000 JP 2000005545  
PR 27-AUG-1999 JP 99P 240642, 27-DEC-1999 JP 99P 368991 PI  
TATSUYA HAGA, TAKASHI OKUDA  
PC C12N15/12, C07K14/47, C12Q1/68, C07K19/00, C07K16/18, C12N5/10, PC  
A61K38/17,  
PC A61K45/00, A61P25/28, G01N33/53, A01K67/027  
CC  
FH Key Location/Qualifiers  
FT CDS (1)..(1743).

REFERENCE:

1 (bases 1 to 1743)  
AUTHOR (AU): Haga, T.; Okuda, T.  
TITLE (TI): \*\*\*High\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
\*\*\*transporter\*\*\*  
JOURNAL (SO): Patent: JP 03074455-T 3 19-JAN-2001; JAPAN SCIENCE AND  
TECHNOLOGY CORP, TATSUYA HAGA, TAKASHI OKUDA

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1743	/organism="Homo sapiens" /db-xref="taxon:9606"

SEQUENCE (SEQ):

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121 gccatcatag ttggtggccg agatattggt ttattgggtg gtggatttac catgacagct
181 acctgggtcg gaggagggtat tatcaatggc acagctgaag cagtttatgt accaggttat
241 ggcctagctt gggctcaggg accaattgga tattctctta gtctgatttt aggtggcctg
301 ttctttgcaa aacctatgcg ttcaaagggt tatgtgacca tgtagaccc gtttcagcaa
361 atctatggaa aacgcattggg cggactcctg tttattcctg cactgatggg agaatgttc
421 tgggctgcag caattttctc tgctttggga gccaccatca gcgtgatcat cgatgtggat
481 atgcacattt ctgtcatcat ctctgcactc attgccactc tgtacacact ggtgggaggg
541 ctctattctg tggcctacac tgatgtcgtt cagctctttt gcatttttgt agggctgtg
601 atcagcgtcc cctttgcatt gtcacatcct gcagtcgcag acatcgggtt cactgctgtg
661 catgccaagt accaaaagcc gtggctggga actggtgact catctgaagt ctactcttgg
721 cttgatagtt ttctgttgtt gatgctgggt ggaatcccat ggcaagcata ctttcagagg
781 gttctctctt cttcctcagc cacctatgct caagtgtgtt ccttcctggc agctttcggg
841 tgcttggtga tggccatccc agccatactc attggggcca ttggagcatc aacagactgg
901 aaccagactg catatggggt tccagatccc aagactacag aagaggcaga catgatttta
961 ccaattgttc tgcagtatct ctgccctgtg tatatttctt tctttggtct tgggtgcagt
1021 tctgctgctg ttatgtcatc agcagattct tccatcttgt cagcaagttc catgtttgca
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1741 tga
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L3 ANSWER 92 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC):

GenBank ACC. NO. (GBN): HSA308377 GenBank (R)

GenBank VERSION (VER): AJ308377.1 GI:18375495

CAS REGISTRY NO. (RN): 388546-92-7

SEQUENCE LENGTH (SQL): 610

MOLECULE TYPE (CI): DNA; linear

DIVISION CODE (CI): Primates

DATE (DATE): 23 Jan 2002

DEFINITION (DEF): Homo sapiens partial CHT1 gene for \*\*\*high\*\*\*  
\*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
, exon 1 and joined mRNA.  
\*\*\*human\*\*\*

SOURCE:



Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;  
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;  
Hominidae; Homo

NUCLEIC ACID COUNT (NA): 102 a 200 c 197 g 111 t

REFERENCE: 1 (sites)

AUTHOR (AU): Wieland, A.; Bonisch, H.; Brüss, M.

TITLE (TI): Molecular cloning of the \*\*\*human\*\*\* and murine  
high affinity choline transporters and  
characterization of the \*\*\*human\*\*\* gene structure

JOURNAL (SO): Unpublished

REFERENCE: 2 (bases 1 to 610)

AUTHOR (AU): Brüss, M.

TITLE (TI): Direct Submission

JOURNAL (SO): Submitted (23-JAN-2001) Brüss M., University of Bonn,  
Pharmacology and Toxicology, Reuterstr. 2b, D-53113  
Bonn, GERMANY

#### FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..610	/organism="Homo sapiens" /db-xref="taxon:9606" /chromosome="2" /map="2q11-13"
exon	<1..196	/gene="CHT1" /number=1
mRNA	join(<1..196, AJ308378.1:183..411, AJ308379.1:879..992, AJ308379.1:1745..1900, AJ308380.1:579..727, AJ308381.1:35..178, AJ308382.1:663..816, AJ308383.1:887..1104, AJ308384.1:792..>2239)	/gene="CHT1"
gene	join(1..610, AJ308378.1:183..411, AJ308379.1:879..1900, AJ308380.1:579..727, AJ308381.1:35..178, AJ308382.1:663..816, AJ308383.1:887..1104, AJ308384.1:792..2239)	/label=CHT1-mRNA /gene="CHT1"
intron	197..>610	/gene="CHT1" /number=1

#### SEQUENCE (SEQ):

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121  tcgcacccac acccctcgcg gttccagggg gcggcgggcc cgggcggagc gctttcgcgt
181  gcagccacca ctccaggtag gacggacggt tcattcctgc gcctacgggc ccgcaccctc
241  ggaaacgcct tgggcaccga ccccgggcgg ttttagaggg gagggacgcg gcgtttttcc
301  ctctcggtgg gatgcgaggg cgggtttgct gtctggcacc gttgctgtca ggggtgaaga
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421  cgggagagca tcgggctgct gcggagagga acttgccctg ttgggttgct acaaaggtag
481  agaagaacaa gcccgcgggc gcttcctttt cctcctttta attccggaga ggctgattct
541  ttcccccaac gtctctttac ccacctgcac gcacaaatgt gagagtttcc ccagaaact
601  tgtgtgtgag
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L3 ANSWER 93 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): HSA308378 GenBank (R)

GenBank ACC. NO. (GBN): AJ308378

GenBank VERSION (VER): AJ308378.1 GI:18375493

CAS REGISTRY NO. (RN): 388546-91-6

SEQUENCE LENGTH (SQL): 1178

MOLECULE TYPE (CI): DNA; linear

DIVISION CODE (CI): Primates

DATE (DATE): 23 Jan 2002

DEFINITION (DEF): Homo sapiens partial CHT1 gene for \*\*\*high\*\*\*  
\*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
, exon 2 and joined CDS.

SOURCE: \*\*\*human\*\*\*

ORGANISM (ORGN): Homo sapiens

Eutelēostomi; Mammalia; Eutheria; Primates; Catarrhini;  
Hominidae; Homo

NUCLEIC ACID COUNT (NA): 329 a 210 c 262 g 377 t

REFERENCE: 1 (sites)

AUTHOR (AU): Wieland, A.; Bonisch, H.; Bruss, M.

TITLE (TI): Molecular cloning of the \*\*\*human\*\*\* and murine  
high affinity choline transporters and  
characterization of the \*\*\*human\*\*\* gene structure

JOURNAL (SO): Unpublished

REFERENCE: 2 (bases 1 to 1178)

AUTHOR (AU): Bruess, M.

TITLE (TI): Direct Submission

JOURNAL (SO): Submitted (23-JAN-2001) Bruess M., University of Bonn,  
Pharmacology and Toxicology, Reuterstr. 2b, D-53113  
Bonn, GERMANY

#### FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1178	/organism="Homo sapiens" /db-xref="taxon:9606" /chromosome="2" /map="2q11-13" /gene="CHT1"
gene	join(1..1178, AJ308379.1:879..1900, AJ308380.1:579..727, AJ308381.1:35..178, AJ308382.1:663..816, AJ308383.1:887..1104, AJ308384.1:792..1421)	/gene="CHT1"
intron	<1..182	/gene="CHT1" /number=1
exon	183..411	/gene="CHT1" /number=2 /usedin=AJ308377:CHT1-mRNA
CDS	join(234..411, AJ308379.1:879..992, AJ308379.1:1745..1900, AJ308380.1:579..727, AJ308381.1:35..178, AJ308382.1:663..816, AJ308383.1:887..1104, AJ308384.1:792..1421)	/function="re-uptake of choline" /codon-start=1 /label=CHT1-CDS /product="high affinity choline transporter" /protein-id="CAC88115.1" /db-xref="GI:18375494" /translation="MAFHVEGLIAIIVFYLLILL VGIWAAWRTKNSGSAERSEAIIV GGRDIGLLVGGFTMTATWVGGGYINGTAEAVYVP GYGLAWAQAPIGYSLSLILGGLFF AKPMRSKGYVTMLDPFQOIYGKRMGGLLFIPALM GEMFWAAAIFSAIGATISVIIDVD MHISVIISALITLYTLVGGLYSVAYTDVVQLFC IFVGLWISVPFALSHPAVADIGFT AVHAKYQKPWLGTVDSEVYSWLDSEFLLMLGGI PWQAYFQRLSSSSATYAQVLSFL AAFGCLVMAIPAILIGAISTDWNQTAYGLPDP KTTEEADMILPIVLQYLCPVYISF FGLGAVSAAVMSSADSSILSASSMFARNIYQLSF RQNASDKEIVVMRITVFVFGASA TAMALLTKTVYGLWYLSDDLVIYVIFPQLLCVLF VKGTNTYGAVAGYVSGFLRLITGG EPYLYLQPLIFYPGYPPDDNGIYNQKFPFKTLAM VTSFLTNICISYLAKYLFESGTLF PKLDVFDVAVARHSEENMDKTLVKNENIKLDEL ALVKPRQSMTLSSSTFTNKEAFLDV DSSPEGSGTEDNLQ"
intron	412..>1178	/gene="CHT1" /number=2

SEQUENCE (SEQ):

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181 agaagactta atgaagtagc cagctgcaga agaactctgga tcattagata aaaatggcct
241 tccatgtgga aggactgata gctatcatcg tgttctacct tctaattttg ctggttgga
301 tatgggctgc ctggagaacc aaaaacagtg gcagcgcaga agagcgcagc gaagccatca
361 tagttggtgg ccgagatatt ggtttattgg ttggtggatt taccatgaca ggttcagacg
421 ccgccggctc catgcagtc tcccttcctt ggcattctgt agtgtgcagc gtgtggcttc
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601 gtagtacttg aacaaaaatg atttttataa aaatcactgg actgaacagt cacgaaacaa
661 atcttggttc cctgggctat tgagtgggtg gaaacagagt aaaaacaaag aggtggggga
721 atgggaagct gtcctagtat tacaagctat gtatctgcta attaattgtg taggcagcat
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841 tgaataccat ctagtgatgg tttttaatct gcataaataa atttgggggt gatgatattc
901 ccaattgagt gattccctgt tttgaaacct aattctttca ttaataact aattcctcac
961 aggaagacaa tcacatgtta tgagtccaca gcactaataa agagatttca tgaacctgtt
1021 tataaaaggg aaaagctagg gtgtgtcttc ataggaatcc ccaggccacc atctgcagtc
1081 atctctcatt caaaccttct ttgtgttagc aggaactgat attcttttct tactttgcac
1141 taaagtgggt ctgttttaaag ggtgatttgt ttcttttt

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L3 ANSWER 94 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): HSA308384 GenBank (R)  
 GenBank ACC. NO. (GBN): AJ308384  
 GenBank VERSION (VER): AJ308384.1 GI:18369775  
 CAS REGISTRY NO. (RN): 387812-77-3  
 SEQUENCE LENGTH (SQL): 2239  
 MOLECULE TYPE (CI): DNA; linear  
 DIVISION CODE (CI): Primates  
 DATE (DATE): 23 Jan 2002  
 DEFINITION (DEF): Homo sapiens partial CHT1 gene for \*\*\*high\*\*\*  
 \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 , exon 9.  
 \*\*\*human\*\*\*

SOURCE:  
 ORGANISM (ORGN): Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;  
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;  
 Hominidae; Homo

NUCLEIC ACID COUNT (NA): 664 a 442 c 440 g 693 t

REFERENCE:  
 1 (sites)  
 AUTHOR (AU): Wieland,A.; Bonisch,H.; Bruss,M.  
 TITLE (TI): Molecular cloning of the \*\*\*human\*\*\* and murine  
 high affinity choline transporters and  
 characterization of the \*\*\*human\*\*\* gene structure

JOURNAL (SO): Unpublished  
 REFERENCE:  
 2 (bases 1 to 2239)  
 AUTHOR (AU): Bruess,M.  
 TITLE (TI): Direct Submission  
 JOURNAL (SO): Submitted (23-JAN-2001) Bruess M., University of Bonn,  
 Pharmacology and Toxicology, Reuterstr. 2b, D-53113  
 Bonn, GERMANY

Feature Key	Location	Qualifier
source	1..2239	/organism="Homo sapiens" /db-xref="taxon:9606" /chromosome="2" /map="2q11-13"
intron	<1..791	/gene="CHT1" /number=8
gene	1..2239	/gene="CHT1"
exon	792..>2239	/gene="CHT1" /number=9 /usedin=AJ308378:CHT1-CDS /usedin=AJ308377:CHT1-mRNA

SEQUENCE (SEQ):

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601 gtccaccagc gaagtcacct tgattgtttg ctttgggtgc tgtagctgta gttgggtttt
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1321 gacagagcat gaccctcagc tcaactttca ccaataaaga ggccttcctt gatgttgatt
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1441 tgccttttga aacagaacac tgtaatatgg tagttcttga gagatggat gcagcataca
1501 aaaatatatt aaaaatataa acaatgttca ggagagtaaa aattcatata aagtgcattt
1561 gcacaaatac aagccaagct agaaggaagc acctatgaaa gcaacaactt tgtttctcat
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1861 ccttgaaatg tgcaatgaat taaccagctg atttttctta gtgtgatgat taacccttc
1921 tttcatgttc tgagctataa catttgctga atatgcaatt tgttattctt ttattaatgg
1981 catgtaatat tctgagcacg ggcaaagaaa acacacaaaa aattatgtat tggcatttat
2041 ttatgtgcaa ggtgatagga aaactgaatc catctttgta gaagagcact gggctaattt
2101 gtatgtttcc atagctacta tatgcataaa caacagtacc tgaaggatta ttaagcaacc
2161 ttaaagcaat aagttcatta aacagaaggt aataggaaga acagtacatt tttgtcttta
2221 tctcaagtat ataaagttt

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L3     ANSWER 95 OF 111            GENBANK.RTM.    COPYRIGHT 2004 on STN

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LOCUS (LOC):                HSA308383          GenBank (R)
GenBank ACC. NO. (GBN):    AJ308383
GenBank VERSION (VER):     AJ308383.1  GI:18369774
CAS REGISTRY NO. (RN):     387812-76-2
SEQUENCE LENGTH (SQL):     1657
MOLECULE TYPE (CI):        DNA; linear
DIVISION CODE (CI):        Primates
DATE (DATE):               23 Jan 2002
DEFINITION (DEF):          Homo sapiens partial CHT1 gene for ***high***
                             ***affinity***      ***choline***      ***transporter***
                             , exon 8.
SOURCE:                     ***human***
ORGANISM (ORGN):            Homo sapiens
                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                             Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                             Hominidae; Homo
NUCLEIC ACID COUNT (NA):   529 a   304 c   287 g   537 t
REFERENCE:                   1 (sites)
AUTHOR (AU):                Wieland,A.; Bonisch,H.; Bruss,M.
TITLE (TI):                 Molecular cloning of the ***human*** and murine
                             high affinity choline transporters and
                             characterization of the ***human*** gene structure
JOURNAL (SO):               Unpublished
REFERENCE:                   2 (bases 1 to 1657)
AUTHOR (AU):                Bruess,M.
TITLE (TI):                 Direct Submission
JOURNAL (SO):               Submitted (23-JAN-2001) Bruess M., University of Bonn,
                             Pharmacology and Toxicology, Reuterstr. 2b, D-53113
                             Bonn, GERMANY

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FEATURES (FEAT):
Feature Key      Location      Qualifier
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source           1..1657      /organism="Homo sapiens"
                             /db-xref="taxon:9606"
                             /chromosome="2"
                             /map="2q11-13"
gene             1..1657      /gene="CHT1"
intron           <1..886      /gene="CHT1"
                             /number=7
exon             887..1104    /gene="CHT1"
                             /number=8

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intron 1105..>1657

/usedin=AJ308377:CHT1-mRNA  
/gene="CHT1"  
/number=8

SEQUENCE (SEQ):

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1 tagatacaca ttcttgtttg gtatttctgt atcataaatc tcagtaaggc cacaaagtgc
61 tgcattgtaag caggctttgt gacaattgta atagaaaatg agggagaagaa aaatggtagg
121 atccaaagag aacaattcct atttggtcca atgatcatga tattaaaaaa gttcagcaaa
181 taaaaagccg actatgctaa tgaacattta aggattccat agttcttcaa cacatgctac
241 aactaaccag taaagaagct atgtattcaa agataaatct gtgtttcaag tcttcttacc
301 ctaccacaca ccaaaacttc ctgaaaattt cagccacatg actgtaattt ttattcaata
361 aaaagggaact gttctttaacc tagtgaaatt ctatgcaatg tggaaatagg agaaaagtaa
421 tgctgaggca gcttcaaaac caagtattatg tacagagaga tgatggctga gaatagccct
481 actattgtct ttcttcaatt acacatgaat aactgagcct taaagaagaa acagtgagt
541 tcccaccaca ttccaagtgt gttgaaggaa tactctagaa ttctgtttat gagagtgtgt
601 tttctatgat tctaggcaat gtaacaccat cattgcagaa aggaaatata tatcttacca
661 ccagtgtctg tgcaggcatt gtgaataaca ctaactataa ccaataacct ttagaagcca
721 agagatataa gacatttcca cttgaccagc acatggactt cacaccagac taatgtatat
781 gattctgagt ttatttcaaa acaacctagt aaataggatg accccagatg gataaagaac
841 atttggttcc ttggtggtta taatggttgt tgattctgtt caacagactg gaaccagact
901 gcatatgggc ttccagatcc caagactaca gaagaggcag acatgatttt accaattgtt
961 ctgcagtatc tctgcctctg gtatatattt ttctttgggtc ttggtgcagt ttctgctgct
1021 gttatgtcat cagcagattc ttccatcttg tcagcaagtt ccatgtttgc acggaacatc
1081 taccagcttt ccttcagaca aaatgtaaga acagtcttct tcaacctgat catttactag
1141 cattgctctt gcatgcttct gatgttgtat ttggtgtata tacagtatta tatatttatt
1201 aatattctat gttaaactct actgtacttt aagcatacga gattaaataa caaattatac
1261 ctatgctgaa tggatgctat cagtacctgt tcttattcat gtcaatacta aagggacaac
1321 atcaatataa ttatttccca agaggtagag tcacagggct atcatttaac ctttttgtct
1381 ttctgatgaa agagtaatga aacctaaact attcagcaaa acttttagta taattaaatt
1441 ctctatgaca ctggaataatc ttggtggaag cagggcagtg taagttgttc gacacgtatt
1501 tttgtaactt ctgaactgtt ttatacttgc actccaaagt ccacctttgc aggaagatat
1561 cctctcaatt tgattttctt tattgaatca aagtggctgc aaaacagcat gcttctttgg
1621 ttgattaaag cttttcctct ctctagggtt tagttac
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L3 ANSWER 96 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): HSA308382 GenBank (R)  
GenBank ACC. NO. (GBN): AJ308382  
GenBank VERSION (VER): AJ308382.1 GI:18369773  
CAS REGISTRY NO. (RN): 387812-75-1  
SEQUENCE LENGTH (SQL): 1467  
MOLECULE TYPE (CI): DNA; linear  
DIVISION CODE (CI): Primates  
DATE (DATE): 23 Jan 2002  
DEFINITION (DEF): Homo sapiens partial CHT1 gene for \*\*\*high\*\*\*  
\*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
, exon 7.  
\*\*\*human\*\*\*  
SOURCE:  
ORGANISM (ORGN): Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;  
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;  
Hominidae; Homo  
NUCLEIC ACID COUNT (NA): 398 a 326 c 284 g 459 t  
REFERENCE:  
1 (sites)  
AUTHOR (AU): Wieland,A.; Bonisch,H.; Bruss,M.  
TITLE (TI): Molecular cloning of the \*\*\*human\*\*\* and murine  
high affinity choline transporters and  
characterization of the \*\*\*human\*\*\* gene structure  
JOURNAL (SO): Unpublished  
REFERENCE:  
2 (bases 1 to 1467)  
AUTHOR (AU): Bruess,M.  
TITLE (TI): Direct Submission  
JOURNAL (SO): Submitted (23-JAN-2001) Bruess M., University of Bonn,  
Pharmacology and Toxicology, Reuterstr. 2b, D-53113  
Bonn, GERMANY

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1467	/organism="Homo sapiens" /db-xref="taxon:9606" /chromosome="2" /map="2q11-13"
gene	1..1467	/gene="CHT1"
intron	<1..662	/gene="CHT1"

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exon          663..816          /gene="CHT1"
                                   /number=7
                                   /usedin=AJ308378:CHT1-CDS
                                   /usedin=AJ308377:CHT1-mRNA
intron        817..>1467      /gene="CHT1"
                                   /number=7

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# SEQUENCE (SEQ):

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1  tgagaatatt ttatgatggt tagaccacc agatgataac aaattgaagg cctctggggg
61 agttttaaata cagttcaaaa taggtaaatt aatgaaaaga aataattgct gtatgtaatt
121 atagagaaaa cttcaggaaa ttctgcataa ttgaaagtgt atgatacatt gtcttagttc
181 agttgggttaa caaagcatca taaacggagt ggcttataaa caacacagat ttatttttca
241 cagttttttca catggctggg aagtccaaga tcaaggtgcc ggcagattca ctgcctgggt
301 aggattcgca tcctcataga aggcaccttc ttgctgcctc ctcacatggt ggaaggaaaa
361 aaactccttt gactctcttt tataaggact ccaccctcat gggctaatac tctcccaaag
421 ttgccaactt gatacctaata accatcacct tggggatcaa aatttcagtg tatgaattta
481 gggggaacat aaacatcaga tcatagcaaa cataattgata ctaattgata ttgtgggcta
541 catgccacat tttttttact acttctaagt tgtacttagg cctattctaa atgtgattgc
601 aataaaaactc tttaaaaaaa tgaatagatg tttgcctctc catccttggt tttcccgcac
661 agatgctggg tggaaatcca tggcaagcat actttcagag ggttctctct tcttctcag
721 ccacctatgc tcaagtgtgt tccttcctgg cagctttcgg gtgcctgggt atggccatcc
781 cagccatact cattgggggc attggagcat caacaggtaa atctcttgca gcttcaccac
841 atgtgccagt tagtttacca atccccaccc agacaccctt ctgtcccact cccctctttc
901 ctccacatag tgaattcttt ctcaccacat tcatatctat agatttgta tagcattcag
961 taaatcgtat tatagttcag cggcctccat tttttttttt tttttttttt tagtagagac
1021 ggggtttcat catgttggtc aggtctggtc caaactcctg acctcaggtg atccatctgc
1081 ctcggtctcc caaagtgtgt gaattatagg tgtgagctac tgcgccagc ctccaatttt
1141 tttgattgct cactccacta tgaacattgt gtgagcacac cctcctccca gttttgggtat
1201 atttatccat tgtttatatg cactcctgtc agcagtggat ctcaaccaag gtgcatgtcg
1261 acatcatctg gggaaatggt gggagatctt ttaaaaatac ggatatgtgg cctacttcac
1321 aggaatttta ttttaataac tgaagataga gatgggcact agtggtcttt taaaaccctt
1381 aggtgagttg agagccagag ttgagagtca caggcttaga gacgtttacc tgtcatcctc
1441 atgacctccc taaagatcac tttgaac

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L3 ANSWER 97 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

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LOCUS (LOC):          HSA308381      GenBank (R)
GenBank ACC. NO. (GBN): AJ308381
GenBank VERSION (VER): AJ308381.1  GI:18369772
CAS REGISTRY NO. (RN): 387812-74-0
SEQUENCE LENGTH (SQL): 736
MOLECULE TYPE (CI):   DNA; linear
DIVISION CODE (CI):   Primates
DATE (DATE):          23 Jan 2002
DEFINITION (DEF):     Homo sapiens partial CHT1 gene for ***high***
                      ***affinity*** ***choline*** ***transporter***
                      , exon 6.
                      ***human***
SOURCE:
  ORGANISM (ORGN):     Homo sapiens
                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                      Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                      Hominidae; Homo
NUCLEIC ACID COUNT (NA): 191 a 148 c 197 g 200 t
REFERENCE:
  1 (sites)
  AUTHOR (AU):         Wieland,A.; Bonisch,H.; Bruss,M.
  TITLE (TI):          Molecular cloning of the ***human*** and murine
                      high affinity choline transporters and
                      characterization of the ***human*** gene structure
  JOURNAL (SO):        Unpublished
REFERENCE:
  2 (bases 1 to 736)
  AUTHOR (AU):         Bruess,M.
  TITLE (TI):          Direct Submission
  JOURNAL (SO):        Submitted (23-JAN-2001) Bruess M., University of Bonn,
                      Pharmacology and Toxicology, Reuterstr. 2b, D-53113
                      Bonn, GERMANY

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## FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..736	/organism="Homo sapiens" /db-xref="taxon:9606" /chromosome="2" /map="2q11-13"
gene	1..736	/gene="CHT1"
intron	<1..34	/gene="CHT1"

exon 35..178 /gene="CHT1"  
 /number=6  
 /usedin=AJ308378:CHT1-CDS  
 /usedin=AJ308377:CHT1-mRNA  
 intron 179..>736 /gene="CHT1"  
 /number=6

SEQUENCE (SEQ):

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1  tcgcctaggg ctccagtgtc actttctgtt gcagtggatc agcgtcccct ttgcattgtc
61 acatcctgca gtcgcagaca tcgggttcac tgctgtgcat gccaaatacc aaaagccgtg
121 gctgggaact gttgactcat ctgaagtcta ctcttggcct gatagttttc tgttgttggg
181 aagtaatgct cttacctgaa gaatgtgatt taattgttcc tgaaatcaaa tttgttttca
241 cgatttttcat attcatagta aaaaaatgtg cttgtgggct catggccatt tctgaattga
301 ggactctcta tcgggagggg ggagccaggg ccggactatc gtggctggca gtgtcagggg
361 ggagaacaaa tgaggccctg aggggacagc ataaggtgtt ctgggtgggt ggctcctcatt
421 tccgtttgtga tgtaagtcaa ggaataacat gccctacccc caggactttc cccaacctga
481 aggcaaaacc ttgtaaaggc tttattttgt gttttgaatt aaggcatgaa acccaactta
541 tgaataaagt ctctcattca ctcttgaatt acagagtaag tgaattagta gtgctagagg
601 ccctaagtga ggcaggttgg aaagggacat gtcactcagg aaagatgcca agagagaggc
661 cctcaggagc cagaggaagc ttgaaaacag gcagaacttt gggcaaaagg tgcaggcact
721 ttgcaggagg acatgg
  
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L3 ANSWER 98 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): HSA308380 GenBank (R)  
 GenBank ACC. NO. (GBN): AJ308380  
 GenBank VERSION (VER): AJ308380.1 GI:18369771  
 CAS REGISTRY NO. (RN): 387812-73-9  
 SEQUENCE LENGTH (SQL): 1308  
 MOLECULE TYPE (CI): DNA; linear  
 DIVISION CODE (CI): Primates  
 DATE (DATE): 23 Jan 2002  
 DEFINITION (DEF): Homo sapiens partial CHT1 gene for \*\*\*high\*\*\*  
 \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 , exon 5.  
 \*\*\*human\*\*\*  
 SOURCE:  
 ORGANISM (ORGN): Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;  
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;  
 Hominidae; Homo  
 NUCLEIC ACID COUNT (NA): 415 a 234 c 224 g 435 t  
 REFERENCE:  
 1 (sites)  
 AUTHOR (AU): Wieland,A.; Bonisch,H.; Bruss,M.  
 TITLE (TI): Molecular cloning of the \*\*\*human\*\*\* and murine  
 high affinity choline transporters and  
 characterization of the \*\*\*human\*\*\* gene structure  
 JOURNAL (SO): Unpublished  
 REFERENCE:  
 2 (bases 1 to 1308)  
 AUTHOR (AU): Bruess,M.  
 TITLE (TI): Direct Submission  
 JOURNAL (SO): Submitted (23-JAN-2001) Bruess M., University of Bonn,  
 Pharmacology and Toxicology, Reuterstr. 2b, D-53113  
 Bonn, GERMANY

Feature Key	Location	Qualifier
source	1..1308	/organism="Homo sapiens" /db-xref="taxon:9606" /chromosome="2" /map="2q11-13"
gene	1..1308	/gene="CHT1"
intron	<1..578	/gene="CHT1"
exon	579..727	/number=4 /gene="CHT1" /number=5 /usedin=AJ308378:CHT1-CDS /usedin=AJ308377:CHT1-mRNA
intron	728..>1308	/gene="CHT1" /number=5

SEQUENCE (SEQ):

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1  ttcaaatagt taccatcatg ttacacttgc ctacagtgtt tagtacggta acaatctgca
61 cgaatttgta gcccaggagc aataggccat accatgtagc ctagggtgtg agtagttaca
121 ccatcaagat ttgtgagtga gtacatactg tgaagtgcac aacagtgaaa tcacctaaca
  
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```

241 tcagaggttcc agatagtga attattttga gtctctgtga tgtattttaa tttctcaggt
301 aattcagggt cttctataac cataccatgg atctgtgtgt cctccaaata aataagttag
361 caaaccagta atttcagaaa gaaaaagtat gtatctcact gaatttatta agatatacaa
421 atttcaatat aaaaattaac tttagggtgt ttcattccact gcatttcata tgacagagag
481 aaaaatgttg tttatcactg aacttttcatt atgtcccttat acaaagagca gaatctgtct
541 gggcaccttg accacagaac tctcttggtt gtttgcagga gccaccatca gcgtgatcat
601 cgatgtggat atgcacattt ctgtcatcat ctctgcactc attgccactc tgtacacact
661 ggtgggaggg ctctattctg tggcctacac tgatgtcgtt cagctctttt gcatttttgt
721 agggctggta agtgggagca cccaagattc tcctcctttt tttctgtaaa aggtaatgta
781 ttttatacta actcattaaa aatgagtaga aatattattt tccctcatga gtaatacata
841 ctaagtcaca tacatgaaat ttcaaatttc tccataaatt aattagatga aaaactcgtc
901 attttgataa aatttgacag aaaagtgtgc tctccattgg actgttagaa aggtctaggt
961 cttgctttcc ttaatgccta gatttgatgg aaacttatgc atgatctcct tttagtattt
1021 aaggcaatcc atttccctcg gcagagataa caaaattcaa accttagtgg taacttgtag
1081 aagtctccct ttacgttagt tgggtgaatcc taagaatgct cataagacat agaaatgatc
1141 ccattggaaa actgtggatt tcaaatatta atcatcacta tttgtggtct aaaaacaaag
1201 aaaattctta attatataag gcaccagaaa gatttattat ctattgtttt tattataatt
1261 atgagacatg agtatttatt agtattatta gcactatatt aagagcac

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L3 ANSWER 99 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): HSA308379 GenBank (R)  
GenBank ACC. NO. (GBN): AJ308379  
GenBank VERSION (VER): AJ308379.1 GI:18369728  
CAS REGISTRY NO. (RN): 387812-40-0  
SEQUENCE LENGTH (SQL): 2326  
MOLECULE TYPE (CI): DNA; linear  
DIVISION CODE (CI): Primates  
DATE (DATE): 23 Jan 2002  
DEFINITION (DEF): Homo sapiens partial CHT1 gene for \*\*\*high\*\*\*  
\*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
, exons 3-4.  
\*\*\*human\*\*\*

SOURCE:  
ORGANISM (ORGN): Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;  
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;  
Hominidae; Homo

NUCLEIC ACID COUNT (NA): 785 a 405 c 397 g 739 t  
REFERENCE: 1 (sites)

AUTHOR (AU): Wieland,A.; Bonisch,H.; Bruss,M.  
TITLE (TI): Molecular cloning of the \*\*\*human\*\*\* and murine  
high affinity choline transporters and  
characterization of the \*\*\*human\*\*\* gene structure

JOURNAL (SO): Unpublished  
REFERENCE: 2 (bases 1 to 2326)  
AUTHOR (AU): Bruess,M.  
TITLE (TI): Direct Submission  
JOURNAL (SO): Submitted (23-JAN-2001) Bruess M., University of Bonn,  
Pharmacology and Toxicology, Reuterstr. 2b, D-53113  
Bonn, GERMANY

FEATURES (FEAT):	Location	Qualifier
Feature Key		
source	1..2326	/organism="Homo sapiens" /db-xref="taxon:9606" /chromosome="2" /map="2q11-13"
intron	<1..878	/gene="CHT1" /number=2
gene	1..2326	/gene="CHT1"
exon	879..992	/gene="CHT1" /number=3 /usedin=AJ308378:CHT1-CDS /usedin=AJ308377:CHT1-mRNA
intron	993..1744	/gene="CHT1" /number=3
exon	1745..1900	/gene="CHT1" /number=4 /usedin=AJ308378:CHT1-CDS /usedin=AJ308377:CHT1-mRNA
intron	1901..>2326	/gene="CHT1" /number=4

SEQUENCE (SEQ):

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61 atagtāāata tcttactaaa agatccataā ataaatāatag aattgcaagt atgtaāgcag
121 ttcacattttt accttcttct gagtgctagg tagtctaggc cttāaggtaa acatttāaac
181 tcacttttgga caccttgtag tagaagtgtc atctcgatcc tctcttctact cctaataact
241 taaggtagta agtacaactt agtggtgatg gagataagat ttgcaagctc tgatatcccc
301 agagtgttca agaaaagact ctattagtga aaagcacatt tctacaaaca tacactcacc
361 tacatagata catgtgtaca cacatgcacg tacacatgca caccactccg tgaggacagt
421 ataaaaaacat caatacaagt aaaatggaag ggcctcgaaa taaagaaaat ttacccttg
481 acctcagact atattacata taatatcatg aaaatgctgc tgactcaatg catttagaaa
541 acatctaggg cagcactatc caatagaaat ataatatgag ccacaaacat aatgttacat
601 tttctacaaa cctctaaaaa caaaaagaaa taggtāaatt aatgttaata gtataactta
661 tgtaactcaa ttcattcaac atgttttcat ttcaacatgt gattaatgaa agaaaaaaca
721 tttgaaatct ggtgtttatt ttatatctct aaaacaactc aatctaggct cgtcacattt
781 caggtgctca gtaacttcta gtagccactg gtttggcagg cagatgtagg tataacaggt
841 aagacagtat cactccctca cttttcattc tgtttcagct acctgggtcg gaggagggtg
901 tatcaatggc acagctgaag cagtttatgt accaggttat ggcctagctt gggctcaggc
961 accaattgga tattctctta gtctgatttt aggtāagtga aagtgcaaat ctcaagtact
1021 cactcagtaa agtatacaga acaagagtat aaataacaag tggagtaaca agtcaaacac
1081 tctgaataac cattgtāaaa aaatgtcccc agagatcttt aaggagtcat taccagaaac
1141 tggtaagtag cagaacacta atgcttāaat tatttgatct cttgggtggg aatatattta
1201 aaatcctctg gacctgtggc tgtcagcaca gtgaatttct taacataatc atgttttatt
1261 tctttcaaaa caagtatgga tatatcatta aaaatgaatc aacttgaaat gtacctgtgt
1321 ttcttttagc aagtcaaatg aataagaggt caaaagtatt atataacaga aggtacctca
1381 tttttggggc actcaaaagg cttttattga atctgtgctt attcaaaacc tctaaatgct
1441 atgttgagag atagaaatgc attgaggcat ttaagtgcgc aatgtgctgg ttcacgtttt
1501 tcaattcaca tacctcaaca tgaccactt atcctttgga cacatacaat ggtaagtgtg
1561 ctāāataaat tatattagat tgctāaacct aatatttata gtaggttggt actgtgtgca
1621 gacttgttcc tcaatccata caggtgttct ggāaatgca ttttcttga taaatggcag
1681 catagtaaaa gactattata ttacattctt tttattttct cctāaacagt tgcttāattt
1741 ttagggtggc tgttctttgc aaacctatg cgttcaaaagg ggtatgtgac catgttagac
1801 ccgtttcagc aaatctatgg aaacgcgatg ggcgactcc tgtttattcc tgactgatg
1861 ggagaaatgt tctgggctgc agcaattttc tctgctttgg gtaaggacca gctaagttgt
1921 ctagctgcat ctttgtagtt aactaaacat cagatacgca accttacttt cctcagcctt
1981 ggcttctgag gacattttta tcaaaaccat atgctgaacc atatttatat gcataaaagc
2041 ttaatggāaa ttctacgttt acttgcaata tgggtggcaga ggtaaataa aacctcagct
2101 acactttcca tacttgaatt gcctcattag accaataact atgaattata atgactcaatt
2161 tgcttttatg agtcataat atgtttgaac aaagaataat gaattaagca tagctāaaaa
2221 gtgcagttta cttaacataa atgtttāaaa caaggattca tgaaccaggg gttagtgaga
2281 atactaatac atatttttgg tgttgaataa atttāāataa atgatt

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L3 ANSWER 100 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AJ414146 GenBank (R)  
 GenBank ACC. NO. (GBN): AJ414146 AL590842  
 GenBank VERSION (VER): AJ414146.1 GI:15979072  
 CAS REGISTRY NO. (RN): 361328-59-8  
 SEQUENCE LENGTH (SQL): 210050  
 MOLECULE TYPE (CI): DNA; linear  
 DIVISION CODE (CI): Bacteria  
 DATE (DATE): 21 Nov 2002  
 DEFINITION (DEF): *Yersinia pestis* strain C092 complete genome; segment 6/20.

SOURCE: *Yersinia pestis* C092  
 ORGANISM (ORGN): *Yersinia pestis* C092  
 Bacteria; Proteobacteria; Gammaproteobacteria;  
 Enterobacteriaceae; *Yersinia*

NUCLEIC ACID COUNT (NA): 53724 a 46781 c 53011 g 56534 t

COMMENT:

Notes:

Details of *Y. pestis* sequencing at the Sanger Centre are available on the World Wide Web.

(URL, [http://www.sanger.ac.uk/Projects/Y\\_pestis/](http://www.sanger.ac.uk/Projects/Y_pestis/)).

REFERENCE: 1 (bases 1 to 210050)  
 AUTHOR (AU): Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; Sebaihia, M.; James, K.D.; Churcher, C.; Mungall, K.L.; Baker, S.; Basham, D.; Bentley, S.D.; Brooks, K.; Cerdeno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Feltwell, T.; Hamlin, N.; Holroyd, S.; Jagels, K.; Leather, S.; Karlyshev, A.V.; Moule, S.; Oyston, P.C.F.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.G.  
 TITLE (TI): Genome sequence of *Yersinia pestis*, the causative agent of plague  
 JOURNAL (SO): Nature, 413 (6855), 523-527 (2001)  
 OTHER SOURCE (OS): CA 135:314279

AUTHOR (AU): Parkhill, J.  
 TITLE (TI): Direct Submission  
 JOURNAL (SO): Submitted (04-OCT-2001) Submitted on behalf of the  
 Yersinia sequencing team, Sanger Centre, Wellcome Trust  
 Genome Campus, Hinxton, Cambridge CB10 1SA E-mail:  
 parkhill@sanger.ac.uk

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..210050	/organism="Yersinia pestis C092" /strain="C092" /db-xref="taxon:214092" /note="biovar: Orientalis"
gene	829..11946	/gene="yapH" /note="synonym: YPO1004"
CDS	829..11946	/gene="yapH" /note="Previously sequenced as Yersinia pestis YapH protein TR:CAC14227 (EMBL:AJ277631) (3705 aa) fasta scores: E(): 0, 99.6% id in 3705 aa. Similar in regions to Escherichia coli YchA protein TR:Q9JMS3 (EMBL:AP001918) (1371 aa) fasta scores: E(): 0, 39.1% id in 1405 aa, and to Escherichia coli adhesin Aida-I precursor SW:AIDA-ECOLI (Q03155) (1286 aa) fasta scores: E(): 0, 29.2% id in 1286 aa. Contains a possible N-terminal signal sequence." /codon-start=1 /transl-table=11 /product="putative autotransporter protein" /protein-id="CAC89847.1" /db-xref="GI:15979073" /db-xref="SPTREMBL:Q8ZHA1" /translation="MNTIFKVIWNASLNVVVVS ELAKGRIKTKSSRNLISEGVLPKF EQSMVSKLFRKNLLALLSLGSI VFLSTGPVFAADI TVSTQAELSAALSNGTYDKIILGA DITLIGSLTVNMTSNQVVIDGQKFGLTVNNTTN YGLVVSSSGSTLTTLQNMSKIDSAN YYSMVVLNGANTAVNVIYNNIDFLGSSQLIYMGA YGAATNSIMTFGDILNDVVVNDRA QEIGE VNKLAFTGRFHVHTGTGSSVTSFVSTGGAN NTSTMDFASGADV KIDRTGSTGDL TSTGVNAFAYTFADGASFELIANQNVFSGTTTNR GLEIGSYNSIDGFGSGVKIVLQSR SDGSIISGNGIDNATTNAAGINNNSAGDANVIYN LGTGSILKATNTGILATKNANNAS DIYIRSAGDITAATGISATHNGTGTVKIKNDGTI TSTTAGIAISSASIKEISVDNTDG TITATAGTGVNVLASAILNLFGGTINTSATANGI TFAGTEGGHTLTDLTINLLGTGIA LSNVAGVNLTLNVTNLNTLNGTALNSLTGLTLVD SLNGRNTINIEGAGIGIAATNTEL NTFDAEALDINVNGAGIGIQATGGGVNLSASNLI INVANTLGTALQITDGIDNTTTIG NEIQLNAENATAINFLGSSSKTLNNGTIKGSVI FAGVADHI INNNGTLDGTLTTGAG NDTLVLDSSSQSNDVINLGDGNNSVTIQNGATVS SIITGNGNDTFTINGMSVGSSTYL SLDAGTGLNTLNFNASTDELAATSLQGFTNINL VDSHITLVSDDNIGSGMVNIDSSS ELLFGSTFDGILHATLGAGTGSAIVNNSANVSLE QASMFAGTWQVNQGGALTASNSNQ LGSAKIGLDGTLNLDNIALFNHVLGTNGTLNVAK NLATTA FDFGSTVGGAFSGIVNLT KTTFALSADNAAALASATLKLSDDSVTTVGTDDR TLHGLDLSGGT LIFDGAVPQSQTS GVVTVTDLALNSGTVNITGSGSWDNTDPLATNVS ILEQDRAGSTLELINATNVTGDID ALDLLVNGTAITSGTQGVQSAIQGGSTVANAIH

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gene      complement(12049..13929 /gene="YPO1005"
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CDS       complement(12049..13929 /gene="YPO1005"
)
/Note="Similar to neighbouring
CDSs YPO1007 and YPO1006. Similar
to Salmonella typhimurium
leucine-rich repeat protein SlrP
TR:Q9XCV2 (EMBL:AF127079) (765 aa)
fasta scores: E(): 0, 39.0% id in
644 aa, and to Shigella flexneri
65.4 kDa antigen IpaH 4.5
SW:IPA4-SHIFL (P18009) (574 aa)
fasta scores: E(): 0, 40.4% id in
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17.30, E-value 0.36"
/ gene="YPO1005"

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12.90, E-value 7.8"
/ gene="YPO1006"

CDS complement(14492..15367) /gene="YPO1006"

/ note="Similar to neighbouring
CDSs YPO1005 and YPO1007. Similar
to regions of Salmonella
typhimurium secreted protein h2
TR:Q9RPH0 (EMBL:AF160727) (788 aa)
fasta scores: E(): 2.5e-24, 41.9%
id in 272 aa, and to regions of
Yersinia pestis outer membrane
protein YopM TR:O68701
(EMBL:AF053946) (409 aa) fasta
scores: E(): 7e-23, 40.5% id in
259 aa"
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/ transl-table=11
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/ protein-id="CAC89849.1"
/ db-xref="GI:15979075"
/ db-xref="SPTREMBL:Q8ZH99"
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9.30, E-value 43"
/ gene="YPO1006"

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LRR, Leucine Rich Repeat, score
9.40, E-value 43"
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CDS complement(15575..17392) /gene="YPO1007"

/ note="Similar to neighbouring
CDSs YPO1005 and YPO1006. Similar
to Salmonella typhimurium
leucine-rich repeat protein SlrP
TR:Q9XCV2 (EMBL:AF127079) (765 aa)
fasta scores: E(): 0, 36.9% id in
642 aa, and to Shigella flexneri
65.4 kDa antigen IpaH
SW:IPA4-SHIFL (P18009) (574 aa)

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569 aa, and to Salmonella typhimurium secreted protein H2  
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misc-feature	complement(17006..17065 )	/gene="YPO1007"  /note="Pfam match to entry PF00560 LRR, Leucine Rich Repeat, score 9.90, E-value 36"
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CDS	18111..19667	/gene="YPO1008"

/note="Similar to Vibrio cholerae  
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 gonorrhoeae putative efflux pump  
 component MtrF TR:Q9RNX2  
 (EMBL:AF176820) (522 aa) fasta  
 scores: E(): 0, 37.2% id in 524  
 aa, and to Escherichia coli  
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		HVASDSAYVILMPVAAMMFYASGR
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		SHSNIGTLMATSGADFLRTLAMPA
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gene 19745..20977  
CDS 19745..20977

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fasta scores: E(): 0, 39.6% id in  
396 aa, and to Escherichia coli  
Peptidase T PepT SW:PEPT-ECOLI  
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IDIIGVTAHPMSAKNVLINPIRVAYDIISEFSPQ  
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FVKSYQLTRTICLSAACA"

misc-feature 19781..20011

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/gene="YPO1009"  
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misc-feature 20549..20818

/gene="YPO1009"  
/note="Pfam match to entry PF01546  
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gene 21365..23437  
CDS 21365..23437

/gene="YPO1011"  
/gene="YPO1011"  
/note="Similar to Azospirillum  
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salicin receptor salC TR:Q9LAE4  
(EMBL:AF143227) (726 aa) fasta  
scores: E(): 0, 25.3% id in 730  
aa, and to Escherichia coli  
probable TonB-dependent receptor  
YncD SW:YncD-ECOLI (P76115) (700  
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MEGIQSVGFFIDGVYANTFDTELLDVDRIEVLRG  
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SPEYKIGLSYGNYNRTQVTTVLGGSINDSEQFSY  
RAALKYLYGNGYFKRDYDGKNNVD  
NLNDFSGRFKLRWQPMDDGWDVMTTFDIQNRNG

		SDVDAYKGQVNAVYTFDDIDFTSVSAYVDERKVD NQDLDFTRLISISELLMNRKTKQFS QEFRLNSKYSQPFNLIGSYFYQDDENEIDFRY LPYNLAQLRKSDIKTNNYAVFGNV NYYLLNDVELVAGARYDYEKKKLNFLMDNGFNPY QPYSHDNNSNSFGAFLPKVGLNYY ITGDAMLYTSIARGYKSGGFNTLGPQSSRAYNAE YMTTYEAGVKTEWFDRTVRWNTSL FWNDMKDQQVEVAYYPISSVNSGKSLSRGLESE LAWRITRGLTVSANVGYTDAYFKN FPTEIKVDNNYIPVNYKGNRPANSPGYTYSIGAD YNFLNGYFVNATYNVKGSTYLDNA NSKKQPAYGLLDLTAGYENKDYGVNVWIKNILDE TYVTRAFKMDDGIWYGRAGEPINF GVNFNVKF"
misc-feature	21365..21487	/gene="YPO1011" /note="PS00430 TonB-dependent receptor proteins signature 1."
misc-feature	23117..23434	/gene="YPO1011" /note="Pfam match to entry PF00593 TonB-boxC, TonB dependent receptor C-terminal region, score 28.70, E-value 1.3e-06"
gene	23618..26928	/gene="YPO1012"
CDS	23618..26928	/pseudo /gene="YPO1012" /note="This CDS is disrupted by the insertion of IS100 element. Similar to regions of polyketide synthases/peptide synthetases eg. Bacillus subtilis MycA TR:Q9R9J1 (EMBL:AF184956) (3971 aa) fasta scores: E(): 0, 29.5% id in 1112 aa, Streptomyces coelicolor polyketide synthase SC3f7.12 TR:O54155 (EMBL:AL021409) (2297 aa) fasta scores: E(): 0, 31.1% id in 1199 aa and Sorangium cellulosum polyketide synthase EpoC TR:Q9L8C7 (EMBL:AF210843) (7257 aa) fasta scores: E(): 0, 39.3% id in 499 aa." /pseudo /codon-start=1 /transl-table=11 /product="putative peptide/polyketide synthase subunit (pseudogene)"
misc-feature	23705..25051	/gene="YPO1012" /note="Pfam match to entry PF00501 AMP-binding, AMP-binding enzyme, score -62.80, E-value 6.5e-12"
misc-feature	25382..25576	/pseudo /gene="YPO1012" /note="Pfam match to entry PF00550 pp-binding, Phosphopantetheine attachment site, score 29.50, E-value 1.5e-06"
misc-feature	25637..26854	/pseudo /gene="YPO1012" /note="Pfam match to entry PF00109 ketoacyl-synt, Beta-ketoacyl synthase, score 419.00, E-value 4.3e-122"
misc-feature	26081..26131	/pseudo /gene="YPO1012" /note="PS00606 Beta-ketoacyl synthases active site."
misc-feature	26929..28882	/pseudo /note="insertion sequence, IS100"
misc-feature	26929..26956	/note="IS100 inverted repeat"
gene	27015..28037	/gene="YPO1013" /note="synonyms: y1093, ypmt1"
CDS	27015..28037	/gene="YPO1013" /note="Similar to Escherichia coli transposase for insertion sequence"

		(P15025) (390 aa) fasta scores: E(): 3e-27, 33.1% id in 329 aa. Identical to the previously sequenced Yersinia pestis, Yersinia pseudotuberculosis, and Escherichia coli pesticin plasmid insertion sequence transposase Y1055 TR:P74993 (EMBL:U59875) (340 aa) fasta scores: E(): 0, 100.0% id in 340 aa" /codon-start=1 /transl-table=11 /product="transposase for insertion sequence IS100" /protein-id="CAC89855.1" /db-xref="GI:15979080" /db-xref="SPTREMBL:P74993" /translation="MVTFTVMEIKILHKQGMSS RAIARELGISRNTVKRYLQAKSEP PKYTTPRPAVASLLDEYRDYIRQRIADAHYPKIPA TVIAREIRDQGYRGGMTILRAFIR SLSVPQEQEPAVRFETEPGRQMQVDWGTMRNGRS PLHVFVAVLGYSRMLYIEFTDNMR YDTLETCHRNAFRFFGGVPREVLVDNMKTIVLQR DAYQTGQHRFHPSLWQFGKEMGFS PRLCRPFRAQTKGKVERMVQYTRNSFYIPLMTRL RPMGITVDVETANRHGLRWLHDVA NQRKHETIQARPCDRWLEEQQSMLALPPEKKEYD VHLDENLVNFDKHPHPLHSIYDS FCRGVA" /gene="YPO1013" /note="Pfam match to entry PF00239 recombinase, Site-specific recombinases, score 25.70, E-value 4.7e-06"
misc-feature	27039..27122	/gene="YPO1013" /note="Predicted helix-turn-helix motif with score 2147 (+6.50 SD) at aa 18-39, sequence MSSRAIARELGISRNTVKRYLQ"
misc-feature	27066..27131	/gene="YPO1013" /note="Pfam match to entry PF00665 rve, Integrase core domain, score 81.90, E-value 1.6e-22"
misc-feature	27360..27893	/gene="YPO1014" /note="synonym: ypmt1.57c"
gene	28034..28816	/gene="YPO1014" /note="Similar to Escherichia coli insertion sequence IS21 putative ATP-binding protein, IstB SW:ISTB-ECOLI (P15026) (265 aa) fasta scores: E(): 0, 47.4% id in 249 aa. Also almost identical to Yersinia pestis and Escherichia coli putative IS100 transposase ypmt1.57c TR:Q9R3L5 (EMBL:AL117211) (260 aa) fasta scores: E(): 0, 99.6% id in 260 aa." /codon-start=1 /transl-table=11 /product="insertion sequence IS100, ATP-binding protein" /protein-id="CAC89856.1" /db-xref="GI:15979081" /db-xref="SPTREMBL:Q9R3L5" /translation="MMELQHQRMLALAGQLQLE SLISAAPALSQQAVDQEWSYMDFL EHLLHEEKLARHQRKQAMYTRMAAFPAVKTFEEY DFTFATGAPQKQLQSLRSLSFIER NENIVLLGPSGVGKTHLAIAMGYEAVRAGIKVRF TTAADLLLQLSTAQRQGRYKTTLO RGVMAPRLLIIDEIGYLPFSQEEAKLFFQVIAKR YEKSAMILTSNLPFGQWDQTFAGD AALTSAMLDRILHSHVVIKGESYRLRQKRKAG VIAEANPE"
CDS	28034..28816	

		/note="Pfam match to entry PF01695 IstB, IstB-like ATP binding protein, score 367.20, E-value 1.7e-106"
misc-feature	28361..28384	/gene="YPO1014" /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
misc-feature	complement(28855..28882)	/note="IS100 inverted repeat"
gene	28881..29060	/gene="YPO1014a"
CDS	28881..29060	/partial /gene="YPO1014a" /note="Similar to the C-terminal regions of Escherichia coli prepilin peptidase dependent protein A PpdA SW:PPDA-ECOLI (P33554) (156 aa) fasta scores: E(): 0.00089, 41.304% id in 46 aa, and Escherichia coli O157:H7 prepilin peptidase dependent protein A ECS3683 TR:BAB37106 (EMBL:AP002563) (156 aa) fasta scores: E(): 0.00089, 41.304% id in 46 aa. Probable gene remnant resulting from insertion of the upstream IS element and recombination." /codon-start=1 /transl-table=11 /product="prepilin peptidase (partial)" /protein-id="CAC89857.1" /db-xref="GI:15979082" /db-xref="SPTREMBL:Q8ZH94" /translation="QITLPLQKEMGFYGVNRTAQ AGNIILSSPAGRIRLVISSRGRIR LCSEQQSMAGIHLCL"
gene	29051..29659	/gene="YPO1015"
CDS	29051..29659	/gene="YPO1015" /note="Similar to Escherichia coli prepilin peptidase dependent protein B SW:PPDB-ECOLI (P08371) (187 aa) fasta scores: E(): 5e-17, 30.4% id in 191 aa, and N-terminus of Pseudomonas aeruginosa general secretion pathway protein J precursor SW:GSPJ-PSEAE (Q00517) (237 aa) fasta scores: E(): 0.19, 39.3% id in 61 aa" /codon-start=1 /transl-table=11 /product="putative prepilin peptidase dependent protein" /protein-id="CAC89858.1" /db-xref="GI:15979083" /db-xref="SPTREMBL:Q8ZH93" /translation="MPLVVNVLSTPLNAQPTRTA GFTLPPEMMLALSFGSLIALSTAQV LPKLSQQISVLQOHYRLELVMNQAMGAMEKDLRR AGFCHGKCGEAITIEHYLGETAH SCLIVAYDLNCNGRWEGAKHQESEYFGYRLRNKA LESQRGELNCHGRGWEEKLFDPRDV TVTHFSVTPLSGQLFKLRLVGHKTGNPAIHHQVT YLIRGNV"
misc-feature	29108..29170	/gene="YPO1015" /note="PS00409 Prokaryotic N-terminal methylation site."
gene	29656..30126	/gene="YPO1016"
CDS	29656..30126	/gene="YPO1016" /note="No significant database matches" /codon-start=1 /transl-table=11 /product="putative membrane protein"

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misc-feature	29683..29742	/gene="YPO1016"
		/note="1 probable transmembrane helix predicted for YPO1016 by TMHMM2.0"
gene	30114..30524	/gene="YPO1017"
CDS	30114..30524	/gene="YPO1017"
		/note="Weakly similar to Escherichia coli prepilin peptidase dependent protein C precursor PpdC SW:PPDC-ECOLI (P08372) (107 aa) fasta scores: E(): 0.42, 23.7% id in 114 aa, and to Pseudomonas aeruginosa PilV TR:Q57003 (EMBL:L36117) (185 aa) fasta scores: E(): 0.91, 32.8% id in 58 aa"
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misc-feature	30192..30254	/gene="YPO1017"
		/note="PS00409 Prokaryotic N-terminal methylation site."
misc-feature	30198..30266	/gene="YPO1017"
		/note="1 probable transmembrane helix predicted for YPO1017 by TMHMM2.0"
gene	30659..34030	/gene="recC"
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CDS	30659..34030	/gene="recC"
		/EC-number="3.1.11.5"
		/note="Similar to Escherichia coli exodeoxyribonuclease V gamma chain RecC SW:EX5C-ECOLI (P07648) (1122 aa) fasta scores: E(): 0, 63.5% id in 1123 aa, and to Vibrio cholerae exodeoxyribonuclease V, 125 kDa subunit VC2322 TR:Q9KPP4 (EMBL:AE004302) (1148 aa) fasta scores: E(): 0, 45.8% id in 1130 aa"
		/codon-start=1
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MLMHL SQWRQQLGQPRELSEWLPICRQLLDTFFD  
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INFCTLMPMRSIPFKVVCLLGMND  
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947 aa, and to Vibrio cholerae  
peptidase, insulinase family  
VC2072 TR:Q9KQC8 (EMBL:AE004281)  
(939 aa) fasta scores: E(): 0,  
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gene 34112..37000  
CDS 34112..37000



misc-feature 34274..34693

misc-feature 34340..34411

gene 36997..40659

CDS 36997..40659

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Peptidase-M16, Insulinase  
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166.30, E-value 5e-46"  
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zinc-binding region signature."  
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/note="synonyms: rorA, YPO1020"  
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RecB SW:EX5B-ECOLI (P08394) (1180  
aa) fasta scores: E(): 0, 62.0% id  
in 1190 aa, and to Vibrio cholerae  
exodeoxyribonuclease V, 135 kDa  
subunit VC2320 TR:Q9KPP6  
(EMBL:AE004302) (1208 aa) fasta  
scores: E(): 0, 48.0% id in 1203  
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PMLREMMARRHLAENLLATPGGER  
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misc-feature	37006..39120	PEOKLIEEMDRLFSGTIGSNATAS DKSGSNVIHSGERASR" /gene="recB" /note="Pfam match to entry PF00580 UvrD-helicase, UvrD/REP helicase, score 367.30, E-value 1.6e-106"
misc-feature	37066..37089	/gene="recB" /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
gene	40656..42614	/gene="recD" /note="synonym: YPO1021"
CDS	40656..42614	/gene="recD" /EC-number="3.1.11.5" /note="Similar to Escherichia coli exodeoxyribonuclease V alpha chain RecD SW:EX5A-ECOLI (P04993) (608 aa) fasta scores: E(): 0, 56.7% id in 638 aa, and to Vibrio cholerae exodeoxyribonuclease V, 67 kDa subunit VC2319 TR:Q9KPP7 (EMBL:AE004302) (706 aa) fasta scores: E(): 0, 45.3% id in 727 aa" /codon-start=1 /transl-table=11 /product="exodeoxyribonuclease V alpha chain" /protein-id="CAC89864.1" /db-xref="GI:15979089" /db-xref="SPTREMBL:Q8ZH87" /translation="MMTLLAQAAARDLLRPLDVQ FSRMIAGDDDDPRLQLAAAILSAEV GAGHVCLPLRYLQPELLFGGRQPDLSLALWQAAG SPDKAQWLQALQNAPVVS DGSQPT PLVLQOERLYLQRMWQYEGDVVQFIASDSVFINR DSDFMTSKGIATSVDESLLRETLD ALFGCAGSEVDWQKVAAAVAATRRISVISGGPGT GKTTTVAKLLTALIRLSQGQRLRI KLAAPTGKAAARLTESLGKAIHQFFLTDDERKLF PDQASTLHRLLGVPNSQRLRYHR GNPLNLDVLVVDEASMDLPMMARLIAALPAKAK VIFLGDRDQLASVEAGAVLGDICR FAELGYSEQRAQQLTQLTGYLLTNNALTSNVLTN KALANKAQPDETYSDSANVRDSL LLRKSYPFDEKSGIGQLALAVNAGEYRQALSVLN SAYS DVERFPLADEEDYQVLL EAC AVGYQH YLERVAALAPAAEVLA AFGRYQLLCALR SGPFGVSGLNERIEQVLHRKGFII RPSGPSGRWYVGRPVMIELNDSALGLFNGDIGIA LHDNEGELRVYFQLPDGNIKSVQP SRLPSHETAYAMTVHKSQGFSEFEHTALVLPNTFM PVLTR ELVYTAITRARQHLTL YCS DAVLSHAIRTPTLRLSGLVDRLNTLNRQ"
misc-feature	41223..41246	/gene="recD" /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
misc-feature	42384..42524	/gene="recD" /note="Pfam match to entry PF01443 Viral-helicase1, Viral (Superfamily 1) RNA helicase, score 29.70, E-value 6.5e-08"
gene	complement(42769..44094 )	/gene="argA"
CDS	complement(42769..44094 )	/note="synonym: YPO1022" /gene="argA" /EC-number="2.3.1.1" /note="Similar to Escherichia coli amino-acid acetyltransferase ArgA SW:ARGA-ECOLI (P08205) (443 aa) fasta scores: E(): 0, 87.3% id in 441 aa, and to Vibrio cholerae N-acetylglutamate synthase VC2316 TR:Q9KPQ0 (EMBL:AE004301) (456 aa) fasta scores: E(): 0, 65.8% id in

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acetyltransferase"
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(GNAT) family, score 42.00,
E-value 1.3e-08"
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)
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aakinase, Amino acid kinase
family, score 65.00, E-value
1.6e-15"
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CDS               44330..45580 /gene="YPO1023"
)
/EC-number="3.5.1.28"
/note="Similar to Escherichia coli
N-acetylmuramoyl-L-alanine amidase
AmiC precursor SW:AMIC-ECOLI
(Q46929) (417 aa) fasta scores:
E(): 0, 70.4% id in 419 aa, and to
Neisseria meningitidis
N-acetylmuramoyl-L-alanine amidase
AmiC or NMA2028 TR:Q9JT18
(EMBL:AL162757) (416 aa) fasta
scores: E(): 0, 49.9% id in 421
aa"
/codon-start=1
/transl-table=11
/product="N-acetylmuramoyl-L-alani
ne amidase AmiC precursor"
/protein-id="CAC89866.1"
/db-xref="GI:15979091"
/db-xref="SPTREMBL:Q8ZH85"
/translation="MADSNHNSGRRRL LQGAAAA
WMLSISRVGFAASSHIVAVRVWPS
STYTRVTLESNTPLKYRQFAL THPDRI VVDIEGV
QLNSVLKEISRQVQSADPYLKQAR
VGQFDKNTVRLVLELKQSI SPQLFTLKPFAEFRN
RLVVDLYPAEGGTS AEDDPLLALL
EDYNKGNVDRTLPPETPKAGKAGRDRPIIIMLDP
GHGGEDPGAIGKNKTKEKDIVLQI
ARRLRALIQKEANMRVFMTRNEDVFIPLKVRVAK
ARKLRADLFISIHADAFTNRAASG
SSVFALSTKGATSTAARFLAQTONEADQIGGVSK
SGDPYLDHTIIDLLQTATINDSLK
FGKEVLSRMSKINKLHKNRVDQAGFAVLKAPDIP
SILVETAFISNLEEERKLRTSRFQ
QQIAESIFAGIKAYFANGGAMARL"
misc-feature      45077..45553 /gene="YPO1023"
)
/note="Pfam match to entry PF01520
Amidase-3,
N-acetylmuramoyl-L-alanine

```

tRNA	complement (45810..45886)	1.4e-67" /product="tRNA-Met"  /note="tRNA Met anticodon CAT, Cove score 86.07"
tRNA	complement (46010..46086)	/product="tRNA-Met"  /note="tRNA Met anticodon CAT, Cove score 86.07"
gene CDS	46302..47474 46302..47474	/gene="YPO1025" /gene="YPO1025" /EC-number="3.2.1.-" /note="Similar to Escherichia coli membrane-bound lytic murein transglycosylase A precursor SW:MLTA-ECOLI (P46885) (365 aa) fasta scores: E(): 0, 69.9% id in 366 aa, and to Vibrio cholerae membrane-bound lytic murein transglycosylase A precursor TR:Q9KPQ4 (EMBL:AE004301) (368 aa) fasta scores: E(): 0, 46.0% id in 359 aa" /codon-start=1 /transl-table=11 /product="membrane-bound lytic murein transglycosylase A precursor" /protein-id="CAC89867.1" /db-xref="GI:15979092" /db-xref="SPTREMBL:Q8ZH84" /translation="MTSRWGKYLLSGIMIAVLG CQSRPTDRGQQYKDGRLQSLLELV NEPNAAGKPVNAKDYSQVKVINQSSPGLYNRNS DTFNAVQNWMLAGADTSKLSLFLG NAYQMEGVNDFGNVQFTGYYPVLQARYTPQGEF RHPLYRMPAKGKRRLPDRAAIYAG ALDNRNLI IAYTNSLVDNFMMEVQSGSYVDYGDG RPLTFFGYAGKNGHAYRSIGKVLI DRGEVARADMSMQAIRQWAENHSEAEVRELLEQN PSFVFFKPVMYAPVKGASAVPLIA KASVASDKSLIPPGTTLLAEVPLLDQGKFTGKY QMRLMVALDVGGAIKGQHFDIYQG IGHEAGQAAGFYNHYGRVWVLKNAQSSGPLFTAY KGGTQSEPTSNDSSLLVNNQDR" /gene="YPO1025" /note="PS00013 Prokaryotic membrane lipoprotein lipid attachment site."
misc-feature	46332..46364	
gene CDS	47617..48444 47617..48444	/gene="YPO1026" /gene="YPO1026" /note="Similar to Escherichia coli hypothetical protein YgdL SW:YGDLE-ECOLI (Q46927) (268 aa) fasta scores: E(): 0, 80.5% id in 267 aa, and to Vibrio cholerae HesA/MoeB/ThiF family protein VC2311 TR:Q9KPQ5 (EMBL:AE004301) (273 aa) fasta scores: E(): 0, 65.8% id in 263 aa" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAC89868.1" /db-xref="GI:15979093" /db-xref="SPTREMBL:Q8ZH83" /translation="MSTAYSEAYQQRFGGIARLY GQALALFSQAHVCVIGIGGVGSW AAEALARTGIGAITLIDMDVVCVTNTNRQIHALLR HNIGQAKTEVMAERILAINPECHV TCIDDFITADNVAELLNKNFSYVIDAIDSVRPKA ALLSYCRRYKIPVVTGGAGGQID PTRIAVVDLAKTIQDPLAAKLRLKSDFNVVKN SKGKLGIDCVFSSEPLVYPQADGS

misc-feature 47701..48114 VSHVLKKMMAKAAARQHESAATAS"  
/gene="YPO1026"  
/note="Pfam match to entry PF00899  
ThiF-family, ThiF family, score  
183.20, E-value 4.2e-51"

misc-feature 48319..48387 /gene="YPO1026"  
/note="1 probable transmembrane  
helix predicted for YPO1026 by  
TMHMM2.0"

gene complement(48480..48923 /gene="YPO1027"  
)

CDS complement(48480..48923 /gene="YPO1027"  
)  
/note="Similar to Escherichia coli  
hypothetical protein YgdK  
SW:YGDK-ECOLI (Q46926) (147 aa)  
fasta scores: E(): 5.7e-30, 59.0%  
id in 139 aa, and to Vibrio  
cholerae hypothetical protein  
VC2310 TR:Q9KPQ6 (EMBL:AE004301)  
(144 aa) fasta scores: E():  
3.5e-19, 43.1% id in 144 aa"  
/codon-start=1  
/transl-table=11  
/product="conserved hypothetical  
protein"  
/protein-id="CAC89869.1"  
/db-xref="GI:15979094"  
/db-xref="SPTREMBL:Q8ZH82"  
/translation="MMIAPHFPFGHDITATDLIEK  
FSAHKQWEDRYRQLILLAKQLPPL  
QEAWKKNELELTGCENRVWLGHQHLPGDGLHFY  
DSEGRIVRGLLAVILTAVEGKTPQ  
QVLAADPLALFEQLGLRQQLSTSRANGLQALAQG  
VQTIAAKYAER"

gene complement(49058..50377 /gene="YPO1028"  
)

CDS complement(49058..50377 /gene="YPO1028"  
)  
/note="Similar to Escherichia coli  
ORF-O401 TR:Q46925 (EMBL:U29581)  
(401 aa) fasta scores: E(): 0,  
67.1% id in 401 aa, and to Vibrio  
cholerae aminotransferase, class V  
VC2309 TR:Q9KPQ7 (EMBL:AE004301)  
(404 aa) fasta scores: E(): 0,  
51.5% id in 396 aa"  
/codon-start=1  
/transl-table=11  
/product="putative  
aminotransferase class V"  
/protein-id="CAC89870.1"  
/db-xref="GI:15979095"  
/db-xref="SPTREMBL:Q8ZH81"  
/translation="MRPSLMCITSICITSLLKHA  
TMIKAKKFRGHSQDANNSMKVFNP  
MDFRREFPALSDKLTLYLDSAATALKPRAMIDATQ  
QFYQQDSATVHRSQHQSALSLTVR  
FENTRQQVADFINSSAENIIWTRGTTEAINLIA  
QSYARPRLOPEDEIIVSEAEHHAN  
LIPWLMVAEQTGAKIVKLPLGLDHLPLDQLPQL  
LNEKTRILALGQMSNVTGGSPDLA  
QAIRLAHQYDCVVVDGAQGIVHYPADVQALDID  
FYAFSSHKLYGPTGIGVLYGKTEL  
LEEMPAWQGGGKMLTHASFGGFTPEVPHYRFEAG  
TPNIAGVIGLSAVLKWLEHIDLEE  
AEVYSQGLATMAENKLAQLPGFHSYRCQQSSLLA  
FTFDGVHHSDDLVALLAEQGIALRA  
GQHCAPLMAALGVNGSLRASFAFYNTPDVEML  
CSALGKALELLRD"

misc-feature complement(49100..50176 /gene="YPO1028"  
)  
/note="Pfam match to entry PF00266  
aminotran-5, Aminotransferases  
class-V, score 5.20, E-value

misc-feature complement(49568..49627 /gene="YPO1028"  
 )  
 /note="PS00595 Aminotransferases  
 class-V pyridoxal-phosphate  
 attachment site."  
 gene 50923..51840 /gene="gcvA"  
 /note="synonym: YPO1029"  
 CDS 50923..51840 /gene="gcvA"  
 /note="Similar to Escherichia coli  
 glycine cleavage system  
 transcriptional activator GcvA  
 SW:GCVA-ECOLI (P32064) (305 aa)  
 fasta scores: E(): 0, 88.2% id in  
 304 aa, and to Vibrio cholerae  
 transcriptional regulator, LysR  
 family VC0896 TR:Q9KTK6  
 (EMBL:AE004173) (306 aa) fasta  
 scores: E(): 0, 69.3% id in 296  
 aa"  
 /codon-start=1  
 /transl-table=11  
 /product="glycine cleavage system  
 transcriptional activator"  
 /protein-id="CAC89871.1"  
 /db-xref="GI:15979096"  
 /db-xref="SPTREMBL:Q8ZH80"  
 /translation="MSKRLPPLNALRAFDAAARH  
 LSFTKAAEELFVTQAAVSHQIKSL  
 EDLGLGLKLFRRNRNRSLLLTEEGQSYLDIKEIFT  
 SINEATRKLQARSAGALTVSLPP  
 SFAIQWLVPRLSGFNAAYPGIDVRIQAVDREEDK  
 LADDVDVAIFYGRGNWSGLRTERL  
 YAEFLLPVCAPSLLTGENGLKVPSDLNHTLLHD  
 TSRRDWLAYTRQLGVPOINVQOGP  
 IFSHSAMVVQAAVHGOALVNNVMAQSEIEAGR  
 LVCPFNDVLVSKNAFYLVCHDSQA  
 ELGKIAAFRQWILARAASEQEKLRFYEN"  
 misc-feature 50944..51357 /gene="gcvA"  
 /note="Pfam match to entry PF00126  
 HTH-1, Bacterial regulatory  
 helix-turn-helix protein, lysR  
 family, score 185.90, E-value  
 6.3e-52"  
 misc-feature 50983..51048 /gene="gcvA"  
 /note="Predicted helix-turn-helix  
 motif with score 1894 (+5.64 SD)  
 at aa 21-42, sequence  
 LSFTKAAEELFVTQAAVSHQIK"  
 misc-feature 50986..51078 /gene="gcvA"  
 /note="PS00044 Bacterial  
 regulatory proteins, lysR family  
 signature."  
 gene 52006..52401 /gene="YPO1030"  
 CDS 52006..52401 /gene="YPO1030"  
 /note="Similar to Escherichia coli  
 hypothetical protein YgdD  
 SW:YGDD-ECOLI (P32065) (131 aa)  
 fasta scores: E(): 0, 71.8% id in  
 131 aa"  
 /codon-start=1  
 /transl-table=11  
 /product="conserved hypothetical  
 protein"  
 /protein-id="CAC89872.1"  
 /db-xref="GI:15979097"  
 /db-xref="SPTREMBL:Q8ZH79"  
 /translation="MNSRLMLIFSALSGFFYVAF  
 GAFGAHVLSTSLGLNEMAWIRTGL  
 EYQGFHTLVILILAVAMQRQVSLWFWYWSGALLAL  
 GTLLFSGSLYCLALSHLRLWIYIT  
 PVGGVCFLAGWILMLIGALRLRKRAERHE"  
 misc-feature 52018..52086 /gene="YPO1030"  
 /note="one of 4 probable  
 transmembrane helices predicted  
 for YPO1030 by TMHMM2.0"

misc-feature	52201..52269	/note="one of 4 probable transmembrane helices predicted for YPO1030 by TMHMM2.0" /gene="YPO1030"
misc-feature	52297..52365	/note="one of 4 probable transmembrane helices predicted for YPO1030 by TMHMM2.0" /gene="YPO1030"
gene CDS	52394..53500 52394..53500	/note="one of 4 probable transmembrane helices predicted for YPO1030 by TMHMM2.0" /gene="YPO1031" /gene="YPO1031" /note="Similar to Escherichia coli hypothetical protein YgdE SW:YGDE-ECOLI (P32066) (366 aa) fasta scores: E(): 0, 78.1% id in 365 aa, and to Haemophilus influenzae hypothetical protein HI1195 SW:YGDE-HAEIN (P45100) (363 aa) fasta scores: E(): 0, 60.9% id in 358 aa" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAC89873.1" /db-xref="GI:15979098" /db-xref="SPTREMBL:Q8ZH78" /translation="MNNKIALYCRSGFEKECAAE ITEKAAQLEIFGFARVKENSGYVL FECYQLEDADRLIREIPREFIFARQMMVVGELL KDLPPEDRVSPIVGMLVGVIKAG ELRVEVADTNESKELLKFCRKLTVPLRSALREQK ILSARENAHRPVVHVFFIAPGCCY VGYSYSNNNSPFYMGIPRLKFPDAPSRSTLKE EAFHVFIPADEWEERLASGMHAVD LGACPGGWTYQLVQSRMMIQAVDNGLMAQSLMDT GOVTHHRADGFKYEPTRSNIYWL CDMVEKPTKVTQLITKWLNVNGWCREAIFNLKLPM KKRYEEVVQNLA MMDEQLKENGIN ADIIHAKQLYHDREEVTVHVRRRIWSGAPGRRDERY " /gene="xni"
gene	complement(53751..54506)	/note="synonyms: exo, YPO1032"
CDS	complement(53751..54506)	/gene="xni"  /EC-number="3.1.11.-" /note="Similar to Escherichia coli exodeoxyribonuclease IX Xni or Exo SW:EX9-ECOLI (P38506) (281 aa) fasta scores: E(): 0, 71.7% id in 247 aa, and to Vibrio cholerae exodeoxyribonuclease IX VC0898 TR:Q9KTK4 (EMBL:AE004173) (283 aa) fasta scores: E(): 0, 53.9% id in 254 aa" /codon-start=1 /transl-table=11 /product="exodeoxyribonuclease IX" /protein-id="CAC89874.1" /db-xref="GI:15979099" /db-xref="SPTREMBL:Q8ZH77" /translation="MQIHLIVDALNLIRRIHAV QGSPCVKACQHALQQLIQHSQPSH AVAVFDEDDRSDSWRHQCLPDYKAGRSPMPDNLQ QEMPLIRQAFNELGVACWHS PGNE ADDLAATLVVKVAGAGHQVTIVSTDKGYCQLLAP NIQIRDYFQKRWLDMPFVKQEFV LPRQLPDYWGLAGISSSKIPGVAGVGAKTATLLL QQADTLEVLYQNLESIPEKWRKKL QQHQQMAFTCKQIATLKTDLLLSGNLQQLRLKK" /gene="xni"
misc-feature	complement(53754..54500)	



```

5-3-exonuclease, 5'-3'
exonuclease, score 123.20, E-value
4.9e-33"
gene      complement(54766..56130 /gene="YPO1033"
)
CDS      complement(54766..56130 /gene="YPO1033"
)
/note="Similar to Escherichia coli
hypothetical protein YgdH
SW:YGDH-ECOLI (P37350) (454 aa)
fasta scores: E(): 0, 82.6% id in
454 aa, and to Vibrio cholerae
hypothetical protein VC0899
TR:Q9KTK3 (EMBL:AE004173) (457 aa)
fasta scores: E(): 0, 69.9% id in
455 aa"
/codon-start=1
/transl-table=11
/product="conserved hypothetical
protein"
/protein-id="CAC89875.1"
/db-xref="GI:15979100"
/db-xref="SPTREMBL:Q8ZH76"
/translation="MITHVSPLGSMDLLSQLEVD
MLKRTASSDLYRLFRNCSLAVLNS
GSLTDNSKELLSRNETFDINVLRERGVKLELVN
PPEHAFVDGKIIRSLQANLFAVLR
DILFVNGQIVSASNFQHLNMESSHLTNLVFSIL
RNARALHIDEEPNMVVCWGGHSIN
ETEYLYARKVGSQGLRELNICTGCGPGAMEAPM
KGAAVGHAQQHYKKGRFIGMTEPS
IIAAEPPNPLVNELVIMPDIEKRLEAFVRIAHGI
IIFPGGVGTAEELLYLLGILMNPE
NSEQVLPLILTGPKEADYFKVVDEFIMNTLGDG
ARKYYQIIIDDPDEVARQMKKAMP
LVKEYRRNTGDAYSFNWSIRIEPDLQHPFEPNHE
NMANLDLSHNQPPEKLAAALRRAF
SGIVAGNVKEVGIQAIEAHGPFKLHGDPQLMKQM
DRLLQDFIAQHRMKLPGSVYTPCY EICS"
gene      complement(56283..57128 /gene="YPO1034"
)
CDS      complement(56283..57128 /gene="YPO1034"
)
/note="Similar to Escherichia coli
hypothetical protein Yqcd
SW:YQCD-ECOLI (Q46920) (282 aa)
fasta scores: E(): 0, 75.9% id in
282 aa, and to Vibrio cholerae
hypothetical protein VC0902
TR:Q9KTK0 (EMBL:AE004174) (287 aa)
fasta scores: E(): 0, 64.2% id in
282 aa"
/codon-start=1
/transl-table=11
/product="conserved hypothetical
protein"
/protein-id="CAC89876.1"
/db-xref="GI:15979101"
/db-xref="SPTREMBL:Q8ZH75"
/translation="MSSYQNHKALAEITLTKPTA
YCDYYDATLLQAVPRSMNREPLGL
YPDNLFPFHGADIWTLYELSWLNSNGLPQVAVGEI
SLNADSINLIESKSFKLYLNSFNQ
TIFADKESVRMTLQRDLAACAQGNVSVALYDLDE
ITGQPISNFNGECLDKQDIRIDSY
EFNADYLQGAAGKDHVEESLVSHLLKSNCLITHQ
PDWGSVQIHYRGPQIDHEALLRYL
VSFRHHNEFHEQCVERIFNDIMRFCQPETLTVYA
RYTRRGGLDINPWRSTDFVPLTG RLARQ"
/gene="syd"
/note="synonyms: ydr, YPO1035"
/gene="syd"
/note="Similar to Escherichia coli
Syd protein SW:SYDP-ECOLI (P43526)
(181 aa) fasta scores: E(): 0,

```

		cholerae Syd protein VC0903 TR:Q9KTJ9 (EMBL:AE004174) (198 aa) fasta scores: E(): 0, 50.0% id in 176 aa" /codon-start=1 /transl-table=11 /product="Syd protein" /protein-id="CAC89877.1" /db-xref="GI:15979102" /db-xref="SPTREMBL:Q8ZH74" /translation="MNISTALRSFTQRYIDLWQQ QTGHLPAASKELYGVSPSPCIVETGE DQVFWQPQAFLEATLTNIERALEIQLHPDIHDF YTQQYAGDMMADLGNHRFTLLQVW SEDDFIRLQENLIGHLVTQKRLKLSPTLFLATTS SEMTMASLCNVSGNVVLEQFGSDK RTLLASTLSHFLDALRPVLPE"
gene	58074..58355	/gene="csrB"
misc-RNA	58074..58355	/gene="csrB"
		/note="Similar to Escherichia coli regulatory RNA csrB, 62% identity in 283 nt overlap"
misc-feature	58356..59067	/note="IS200-like insertion sequence: IS1541. Contains a 'G' at nucleotide position 315"
gene	58501..58959	/gene="tnp"
		/note="synonym: YPO1036"
CDS	58501..58959	/gene="tnp"
		/note="Similar to Salmonella typhimurium, and Salmonella typhi transposase for insertion sequence IS200 TnpA SW:T200-SALTY (Q57334) (152 aa) fasta scores: E(): 0, 94.1% id in 152 aa. Identical to the Yersinia pseudotuberculosis IS1541 element transposase Tnp TR:Q9X9F5 (EMBL:AJ238014) (152 aa) fasta scores: E(): 0, 100.0% id in 152 aa" /codon-start=1 /transl-table=11 /product="transposase for the IS1541 insertion element" /protein-id="CAC89878.1" /db-xref="GI:15979103" /db-xref="SPTREMBL:Q9X9F5" /translation="MRDEKSLAHTRWNCKYHIVF APKYRRQVFYREKRRRAIGSILRKL CEWKNVNILEAECCVDHIHMLLEIPPKMSVSGFM GYLKKGKSSMLLYEQFGDLKFKYRN REFWCRGYVVDTVGKNTARIQEYIKHQLEEDKMG EQLSIPYPGSPFTGRK"
misc-feature	58555..58866	/gene="tnp"
		/note="Pfam match to entry PF01797 Transposase-17, Transposase IS200 like, score 236.10, E-value 5.1e-67"
gene	59213..59545	/gene="YPO1037"
CDS	59213..59545	/gene="YPO1037"
		/note="Similar to Escherichia coli hypothetical protein YqcC SW:YQCC-ECOLI (Q46919) (109 aa) fasta scores: E(): 1.3e-15, 41.3% id in 109 aa, and to the N-terminal region of Erwinia carotovora exoenzyme regulation regulon ORF1 SW:YQCB-ERWCA (Q47417) (376 aa) fasta scores: E(): 1.8e-16, 67.1% id in 70 aa. Note that the Erwinia carotovora paralogue is fused to the downstream gene" /codon-start=1 /transl-table=11 /product="conserved hypothetical

gene 59545..60318  
CDS 59545..60318

/protein-id="CAC89879.1"  
/db-xref="GI:15979104"  
/db-xref="SPTREMBL:Q8ZH73"  
/translation="MSTENKVRQSLQDIEFAMRE  
TDLWQTVPPPEAEAFESNEPFSIDT  
MAAEQWLQWVFLPRMYALLELNGPFPTRFAITPY  
FEEALS GDGRPDYSALLAQLRCLD·DLLNKESE"  
/gene="YPO1038"  
/gene="YPO1038"  
/note="Similar to Escherichia coli  
hypothetical protein YqcB  
SW:YQCB-ECOLI (Q46918) (260 aa)  
fasta scores: E(): 0, 69.3% id in  
257 aa, and to the C-terminal  
region of Erwinia carotovora  
exoenzyme regulation regulon ORF1  
SW:YQCB-ERWCA (Q47417) (376 aa)  
fasta scores: E(): 0, 76.3% id in  
257 aa. Note that the Erwinia  
carotovora paralogue is fused to  
the upstream gene"  
/codon-start=1  
/transl-table=11  
/product="Conserved hypothetical  
protein"

misc-feature 59572..60054

/protein-id="CAC89880.1"  
/db-xref="GI:15979105"  
/db-xref="SPTREMBL:Q8ZH72"  
/translation="MLEIIYQDEHIVAVNKPAGW  
LVHRSWLDNRNETVFVMQTVRDQIG  
QHVVTVHRLDRPTSGVLLMALSSDVARMLSLQFE  
QHQQIKTYHAVVRGYVLEGGTVDY  
AMAEELDKIADKFAKSDKAPQPSVSHYEALAQVE  
VPLAIGRYETARYSLVALKPETGR  
KHQLRRHMAHIRHPPIIGDSTHGDLRQNRGVAQHF  
GCSRLMLHASHLHLNHPVTGEALT  
LTARWDEPWQGLMSQFGWSGIAPHLERVEFPLTA  
SQDNE"  
/gene="YPO1038"  
/note="Pfam match to entry PF00849  
PseudoU-synth-2, RNA  
pseudouridylate synthase, score  
176.90, E-value 3.4e-49"

misc-feature 59692..59736

gene 60346..60795  
CDS 60346..60795

/gene="YPO1038"  
/note="PS01129 Rlu family of  
pseudouridine synthase signature."  
/gene="YPO1039"  
/gene="YPO1039"  
/note="Similar to Escherichia coli  
hypothetical protein TR:Q46917  
(EMBL:U29581) (149 aa) fasta  
scores: E(): 0, 66.2% id in 148  
aa, and to Erwinia carotovora  
SCRI193 TR:Q47418 (EMBL:X79474)  
(151 aa) fasta scores: E(): 0,  
68.9% id in 148 aa"  
/codon-start=1  
/transl-table=11  
/product="conserved hypothetical  
protein"

gene complement(60885..61274 )  
CDS complement(60885..61274 )  
)

/protein-id="CAC89881.1"  
/db-xref="GI:15979106"  
/db-xref="SPTREMBL:Q8ZH71"  
/translation="MAQVGIFVGTIVYGNALLVAE  
EAENILKDQGHEVKLFDEGTLTDW  
QHRYRQHYVLVITSTTGQGDFFDSIASLFAVARDQ  
VGFQPELRYGVIALGDSSYDNFCG  
AGRTFDELLQEQGATRIGERLEIDAIEHSEPEAI  
SAPWVEQWGRLLQ"  
/gene="YPO1040"  
/gene="YPO1040"  
/note="Similar to Escherichia coli  
hypothetical protein YaeH"

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gene      complement(61398..62222)
CDS       complement(61398..62222)
misc-feature complement(61575..61628)
misc-feature complement(61629..61682)
misc-feature complement(61725..61778)
misc-feature complement(61737..61823)

fasta scores: E(): 0, 85.7% id in
126 aa, and to Vibrio cholerae
hypothetical protein VC2264
TR:Q9KPU8 (EMBL:AE004298) (137 aa)
fasta scores: E(): 1.9e-27, 64.3%
id in 126 aa"
/codon-start=1
/transl-table=11
/product="conserved hypothetical
protein"
/protein-id="CAC89882.1"
/db-xref="GI:15979107"
/db-xref="SPTREMBL:Q8ZH70"
/translation="MYDNLKSLGITQPEDVDRYS
LRQEANNDILKIYFRKDKGEFFAK
SVKFKYPRQRKTVVSDNASHGYKEINEINPNLRY
VIDELDQLCKRDQIEVDLKRKILD
DLRHLESVVTNKIAEIEADLEKLTNGR"
/gene="dapD"

/note="synonym: YPO1041"
/gene="dapD"

/EC-number="2.3.1.117"
/note="Similar to Escherichia coli
2,3,4,5-tetrahydropyridine-2-carbo
xylate N-succinyltransferase dapD
SW:DAPD-ECOLI (P03948) (274 aa)
fasta scores: E(): 0, 92.3% id in
274 aa, and to Mycobacterium bovis
2,3,4,5-tetrahydropyridine-2-carbo
xylate N-succinyltransferase dapD
SW:DAPD-MYCBO (P56220) (274 aa)
fasta scores: E(): 0, 93.8% id in
274 aa"
/codon-start=1
/transl-table=11
/product="2,3,4,5-tetrahydropyridi
ne-2-carboxylate
N-succinyltransferase"
/protein-id="CAC89883.1"
/db-xref="GI:15979108"
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/translation="MQQLQNVIETAFERRADITP
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ETRYYDKVPMKFAGYDEARFQREG
FRVVPATVRKGAFIARNTVLMPSYVNIGAFVDE
GTMVDTWATVGSCAQIGKNVHLSG
GVGIGGVLEPLQANPTIIEDNCFVGARSEVVEGV
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VKKVDAKTRSKVGINELLRTID"
/gene="dapD"

/note="Pfam match to entry PF00132
hexapep, Bacterial transferase
hexapeptide (four repeats), score
11.30, E-value 23"
/gene="dapD"

/note="Pfam match to entry PF00132
hexapep, Bacterial transferase
hexapeptide (four repeats), score
10.60, E-value 28"
/gene="dapD"

/note="Pfam match to entry PF00132
hexapep, Bacterial transferase
hexapeptide (four repeats), score
13.30, E-value 6"
/gene="dapD"

/note="PS00101 Hexapeptide-repeat
containing-transferases"

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misc-feature complement(61779..61832 /gene="dapD"  
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 hexapeptide (four repeats), score  
 5.50, E-value 1.4e+02"

misc-feature complement(61848..61901 /gene="dapD"  
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 /note="Pfam match to entry PF00132  
 hexapep, Bacterial transferase  
 hexapeptide (four repeats), score  
 3.20, E-value 2.8e+02"

gene complement(62397..65135 /gene="glnD"  
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 /note="synonym: YPO1042"

CDS complement(62397..65135 /gene="glnD"  
 )  
 /EC-number="2.7.7.59"  
 /note="Similar to Escherichia coli  
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 GlnD SW:GLND-ECOLI (P27249) (890  
 aa) fasta scores: E(): 0, 76.5% id  
 in 880 aa"  
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 LNDEQAQRVGQLITLLWDLKLEVG  
 HSVRTLEECLLEGLADLTATNMIESRLICGDVA  
 LFLQMQKHIFSDSFWSPQFFHAK  
 VVEQQERHCRYHGTSYNLEPDIKSSPGGLRDIHT  
 LLWVARRHFGATSLSEMVDGFLT  
 NAERNELNESQSFLWRIRFALHLVLTRYDNRLLF  
 DRQLSVAQLLRYEGEGNEPVEHMM  
 KDFYRMTRRVSELNNMLLQLFDEAILALDANEKP  
 RPLDEEFQLRGDLIDLRLDENLFVR  
 QPEAIMRMFYLMVRNQDIKGIYSTTVRRLRHARR  
 HLKAPLCHIPEARLKFMAILRHGP  
 AVSRALLPMHRHSVLWAYMPQWGSIVGQMQFDLF  
 HAYTVDEHTIRVLLKIESFADEDT  
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 GDHSILGAHDAVEFAEQHGLNSRE  
 SQLVAWLVRCHLLMSVTAQRRDIQDPAVIQQFSA  
 EVQSETRLRYLVSLTVADICATNE  
 NLWNSWKQSLRLRELYFATEKQLRRGMQNSPDLRE  
 RVRHHRLQALALLRMDNIDEEALH  
 RIWSRCRADYFLRHSPNQLAWHARHLLHEDSTKP  
 LVLVSROATRGGTEIFIWSPDRPS  
 LFAAVVGELDRRNLVHDAQIFTNRDGMAMDTFI  
 VLEPDGSPLAQDRHPIISHALQQA  
 INRSDYQHPPRVRLSPKLRHFSVPTEANFLPTH  
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misc-feature complement(63267..63671 /gene="glnD"  
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 /note="Pfam match to entry PF01966  
 HD, HD domain, score 75.50,  
 E-value 1.1e-18"

misc-feature complement(64566..64883 /gene="glnD"  
 )  
 /note="Pfam match to entry PF01909"

gene complement(65138..65929) Nucleotidyltransferase domain, score 39.90, E-value 5.8e-08 /gene="ampM"

CDS complement(65138..65929) /note="synonyms: b0168, map, YPO1043" /gene="ampM"

/EC-number="3.4.11.18"  
 /note="Similar to Escherichia coli methionine aminopeptidase  
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 fasta scores: E(): 0, 84.0% id in 263 aa"  
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 /db-xref="SPTREMBL:Q8ZH67"  
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 HGIPSDEKVLKEGDIVNIDVTVIK  
 DGFHGDTSKMFIVGKPTILGERLCRVTQESLYLA  
 IKMVKPGIRLRTLKAIQKFVEAE  
 NFSVVREYCGHGIGEGFHEEPQVLHYDADDGGVV  
 LQAGMAFTIEPMVNAGDYRIRRTMK  
 DGWTVKTKDRNLSAQYEHTIVVTDNGCEIMTLRK  
 DDTIPNIITHE"

misc-feature complement(65192..65920) /gene="ampM"

misc-feature complement(65372..65428) /note="Pfam match to entry PF00557 Peptidase-M24, metallopeptidase family M24, score 336.80, E-value 2.4e-97" /gene="ampM"

gene 66364..67089 /note="PS00680 Methionine aminopeptidase subfamily 1 signature." /gene="rpsB"

CDS 66364..67089 /note="synonym: YPO1044" /gene="rpsB"

/note="Similar to Escherichia coli 30S ribosomal protein S2 RpsB  
 SW:RS2-ECOLI (P02351) (240 aa)  
 fasta scores: E(): 0, 93.8% id in 240 aa"  
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 /db-xref="SWISS-PROT:Q8ZH66"  
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 AVKEAANNCDQFFVNRWLGGMLT  
 NWKTVRQSIKRLKDLEIQSQDGTDFDKLTKEALM  
 RTRELNKLENSLGGIKDMGGLPDA  
 LFVVDADHEHIAIKEANNLGIPVFSIVDTNSDPD  
 GVDFIIPGNDDAIRAVKLYLGAVA  
 TAVREGRSQDLAVQAEESFVEAE"

misc-feature 66379..66414 /gene="rpsB"

misc-feature 66388..67038 /note="PS00962 Ribosomal protein S2 signature 1." /gene="rpsB"

misc-feature 66835..66909 /note="Pfam match to entry PF00318 Ribosomal-S2, Ribosomal protein S2, score 435.90, E-value 3.5e-127" /gene="rpsB"

gene	67217..68074	S2 signature 2."
CDS	67217..68074	/gene="tsf" /note="synonym: YPO1045" /gene="tsf" /note="Similar to Escherichia coli elongation factor Ts Tsf SW:EFTS-ECOLI (P02997) (282 aa) fasta scores: E(): 0, 78.4% id in 282 aa" /codon-start=1 /transl-table=11 /product="elongation factor Ts" /protein-id="CAC89887.1" /db-xref="GI:15979112" /db-xref="SWISS-PROT:Q8ZH65" /translation="MVAITAALVKELRERTAAGM MECKKALVEANGDIELAIDNMRKS GQAKAAKKAGRIAAEGIILAKVSADGKYGVILEL NCETDFVAKDAGFKAFGEVINAA LAEKIADIDVLKAKFEEQRANLVAKIGENINIRR VAVLEGDILGTYLHGARIGVMVAA TGADDEELVKHIAMHIAASKPEYVKPDDVPAEVVA REHQIQLDIAIESGKPREIAEKMV EGRMRKFTGEVSLTGQNFVMDPSKTVGDLLKENN ADVNNFIRFEVGEIEKVETDFAA EVAAMSKQS"
misc-feature	67223..67342	/gene="tsf" /note="Pfam match to entry PF02094 TS-N, TS-N domain, score 71.00, E-value 2.6e-17"
misc-feature	67385..68011	/gene="tsf" /note="Pfam match to entry PF00889 EF-TS, Elongation factor TS, score 356.30, E-value 3.2e-103"
misc-feature	67445..67477	/gene="tsf" /note="PS01127 Elongation factor Ts signature 2."
gene	68283..69008	/gene="pyrH"
CDS	68283..69008	/note="synonyms: smbA, YPO1046" /gene="pyrH" /EC-number="2.7.4.-" /note="Similar to Escherichia coli uridylate kinase PyrH SW:PYRH-ECOLI (P29464) (240 aa) fasta scores: E(): 0, 90.8% id in 240 aa" /codon-start=1 /transl-table=11 /product="uridylate kinase" /protein-id="CAC89888.1" /db-xref="GI:15979113" /db-xref="SWISS-PROT:Q8ZH64" /translation="MATNAKPVYQRIILLKLSGEA LQGAEGFGIDASVLDMAQEVKEL VELGIQVGVVIGGNLFRGAGLAQAGMNRVVGHD MGMLATVMNGLAMRDALHRAVYVNA RLMSAIPLNGVCDNYSWAEAISLLRHNRRVVF GTGNPFFTTDSAACLRGIEIEADV VLKATKVDGVYSADPVKNPDATLYEQLTYQDVLE QELKVMDLAAFTLARDHNLPIRVF NMNKP GALRRVVMGENEGTLIAK"
misc-feature	68310..68861	/gene="pyrH" /note="Pfam match to entry PF00696 aakinase, Amino acid kinase family, score 148.00, E-value 1.7e-40"
gene	69144..69701	/gene="frr"
CDS	69144..69701	/note="synonyms: b0172, rrf, YPO1047" /gene="frr" /note="Similar to Escherichia coli ribosome recycling factor SW:RRF-ECOLI (P16174) (185 aa) fasta scores: E(): 0, 80.5% id in 185 aa"



		<pre> /transl-table=11 /product="ribosome recycling factor" /protein-id="CAC89889.1" /db-xref="GI:15979114" /db-xref="SWISS-PROT:Q8ZH63" /translation="MINEIRKDAEVRMEKCLEAF QNHISKIRTGRASPSILDGIQVEY YGTATPLRQLANIVVEDSRTLALTVFDRSLSAAV EKAIMTSDLGLNPSSAGTVIRVPL PALTEERRKDLIKVVRAEAEQGRVSIRNVRRDAN DKVKALLKDKEISEDEDRRSQDDV QKLTDAYIKKVDAALAVKEAELMDF" </pre>
misc-feature	69198..69692	<pre> /gene="frr" /note="Pfam match to entry PF01765 RRF, Ribosome recycling factor, score 336.80, E-value 2.4e-97" </pre>
gene	69915..71111	<pre> /gene="dxr" /note="synonyms: b0173, YPO1048" </pre>
CDS	69915..71111	<pre> /gene="dxr" /EC-number="1.1.1.-" /note="Similar to Escherichia coli 1-deoxy-D-xylulose 5-phosphate reductoisomerase SW:DXR-ECOLI (P45568) (398 aa) fasta scores: E(): 0, 72.2% id in 396 aa" /codon-start=1 /transl-table=11 /product="1-deoxy-D-xylulose 5-phosphate reductoisomerase" /protein-id="CAC89890.1" /db-xref="GI:15979115" /db-xref="SWISS-PROT:Q8ZH62" /translation="MKQLTILGSTGSIGNSTLSV VRANPELFKVTALVAGRNVREMAQ QCLEFSPRYAAMSDEHSAKSLRLLLAEQGSDTEV YSGETAACELAALDDVDQVMAAIV GIAGLPSTLAAIRAGKQVLLANKESLITCGKLFM DEVKRSRAQLLPIDSEHNAIFQSL PERIQRQLGYSSLNENGVSRIILTGSGGPFRETP LSQFSDVTPDQACAHPNWSMGRKI SVDSATMMNKGLEYIEARWLFNASAEQIEVVLHP QSVIHSMVRYHDGSILAQMGTDPDM RTPIAHAMAYPMRVSSGVAPLDFCKVGALTFTTP DYQRYPCCLKLAIDACNAGQAATTA LNAANEISVMAFLDSKIRFTDIEVINRTVVEGLL LSEPTSVEEVLVIDRKARDVAAQV IAKLNN" </pre>
gene	71335..72093	<pre> /gene="upps" /note="synonyms: rth, YPO1049" </pre>
CDS	71335..72093	<pre> /gene="upps" /EC-number="2.5.1.31" /note="Similar to Escherichia coli undecaprenyl pyrophosphate synthetase SW:UPPS-ECOLI (Q47675) (253 aa) fasta scores: E(): 0, 78.8% id in 245 aa" /codon-start=1 /transl-table=11 /product="undecaprenyl pyrophosphate synthetase" /protein-id="CAC89891.1" /db-xref="GI:15979116" /db-xref="SPTREMBL:Q8ZH61" /translation="MSPVKEDRANLSRSPRHVA IIMDGNGRWAKNKGKLRVFGHKAG VKSVRRRAVSFAAKHNLDALTLYAFSSSENWNRPDQ EVTALMELFVRALDSEVKSLHKHN VRLSIIGDISRFSGRQLQERIRRSEKLTANNDGLK LNIAANYGGRWDIIQGVRLAEQV QKGELQPTDISEESLNSYICLHEQSQVDLVIRTG GEHRISNFWLLWQIAYAELYFTDVL WPDFDENVFEGALNAFAQRERRFGGTTPIDATAS " </pre>
misc-feature	71398..72063	<pre> /gene="upps" /note="Pfam match to entry PF01255" </pre>

misc-feature	71896..71949	undecaprenyl diphosphate synthase, score 454.70, E-value 8e-133" /gene="uppS" /note="PS01066 Undecaprenyl pyrophosphate synthetase family signature."
gene	72103..72951	/gene="cdsA"
CDS	72103..72951	/note="synonyms: cds, YPO1050" /gene="cdsA" /EC-number="2.7.7.41" /note="Similar to Escherichia coli phosphatidate cytidylyltransferase cdsA or cds SW:CDSA-ECOLI (P06466) (249 aa) fasta scores: E(): 0, 75.2% id in 246 aa" /codon-start=1 /transl-table=11 /product="phosphatidate cytidylyltransferase" /protein-id="CAC89892.1" /db-xref="GI:15979117" /db-xref="SPTREMBL:Q8ZH60" /translation="MLKYRLITALILIPVVIGAL FLLPPVGFAIVTLVVCMLAAWEWG QLAGFASRTQRIWLAILCGFLLVAMLLSLPEYQH SPHLLLVSTPLWLSMGWWVAALML VLTYPRSAVSWRNSRLRLRIIFGILTIIPFFWGMF ALRQYGYEQNHNTGAWWLLYVMLL VWGADSGAYMFGKLFQKHLAPKVSFGKTWEGLI GGLLTSALISLLFGRYAPLDIVPE KLLICSVVAALASVLGDLTESMFKREAGIKDSGH LIPGHGGILDRIDSLTAAVPVFAC LMLLVF"
misc-feature	72106..72945	/gene="cdsA" /note="Pfam match to entry PF01148 Cytidylyltrans, Phosphatidate cytidylyltransferase, score 155.80, E-value 7.5e-43"
misc-feature	72121..72225	/gene="cdsA" /note="one of 6 probable transmembrane helices predicted for YPO1050 by TMHMM2.0"
misc-feature	72268..72324	/gene="cdsA" /note="one of 6 probable transmembrane helices predicted for YPO1050 by TMHMM2.0"
misc-feature	72343..72411	/gene="cdsA" /note="one of 6 probable transmembrane helices predicted for YPO1050 by TMHMM2.0"
misc-feature	72454..72513	/gene="cdsA" /note="one of 6 probable transmembrane helices predicted for YPO1050 by TMHMM2.0"
misc-feature	72550..72618	/gene="cdsA" /note="one of 6 probable transmembrane helices predicted for YPO1050 by TMHMM2.0"
misc-feature	72676..72735	/gene="cdsA" /note="one of 6 probable transmembrane helices predicted for YPO1050 by TMHMM2.0"
misc-feature	72817..72897	/gene="cdsA" /note="PS01315 Phosphatidate cytidylyltransferase signature."
gene	72980..74335	/gene="YPO1051"
CDS	72980..74335	/gene="YPO1051" /note="Similar to Escherichia coli hypothetical 49.1 kDa protein in cdsA-hlpA intergenic region SW:YAEI-ECOLI (P37764) (450 aa) fasta scores: E(): 0, 77.6% id in 451 aa, and to Neisseria meningitidis putative integral membrane protein NMA0084 TR:Q9JX32 (EMBL:AL162752) (446 aa) fasta

		aa" /codon-start=1 /transl-table=11 /product="putative membrane protein" /protein-id="CAC89893.1" /db-xref="GI:15979118" /db-xref="SWISS-PROT:Q8ZH59" /translation="MMSILWSLAAFIVALGILIT VHEFGHFWVARRCGVRVERFSIGF GKALWRRTRDROGTEYVIALIPLGGYVKMLDERVE AVAPELRHQSFNNKTVLQRAAIVS AGPIANFLFAIVAYWLVIIGVPSVRPVIGDISP QSIAAQANISSGMELKSVDGIETP DWDSVRLALISRIGDKQMQVGVPFGSDNVVEKT LDLRQWQFEPDKQDPVVALGIIPR GPQIESVLAEVQPGSAAQKAGLQAGDRIVKVNGQ LLDRWQTFVLQVRDNPQGPLVLDI ERESTPLSLTLIPDTKSVGENRSEGFAGVVPKVI PLPDEYKTIRQYGPFTAVYQAGDK TWQLMRLTVSMLGKLITGDVKLNNLSGPISIAQG AGLSAEYGLVYYLMFLALISVNLG IINLFLPLVLDGGHLLFLAIEKLGKGPVSERVQD FSYRIGSILLVLLMGLALFNDFSR L"
misc-feature	72992..73060	/gene="YPO1051" /note="one of 4 probable transmembrane helices predicted for YPO1051 by TMHMM2.0"
misc-feature	73034..73063	/gene="YPO1051" /note="PS00142 Neutral zinc metallopeptidases, zinc-binding region signature."
misc-feature	73271..73339	/gene="YPO1051" /note="one of 4 probable transmembrane helices predicted for YPO1051 by TMHMM2.0"
misc-feature	73574..73816	/gene="YPO1051" /note="Pfam match to entry PF00595 PDZ, PDZ domain (Also known as DHR or GLGF)., score 46.40, E-value 6.2e-10"
misc-feature	74108..74176	/gene="YPO1051" /note="one of 4 probable transmembrane helices predicted for YPO1051 by TMHMM2.0"
misc-feature	74258..74317	/gene="YPO1051" /note="one of 4 probable transmembrane helices predicted for YPO1051 by TMHMM2.0 one of 4 probable transmembrane helices predicted for YPO1051 by TMHMM2.0"
gene CDS	74372..76759 74372..76759	/gene="YPO1052" /gene="YPO1052" /note="Similar to Photorhabdus luminescens outer membrane antigen Oma TR:Q9S341 (EMBL:AJ236920) (797 aa) fasta scores: E(): 0, 80.4% id in 797 aa, and to Haemophilus influenzae protective surface antigen D15 precursor SW:D151-HAEIN (P46024) (797 aa) fasta scores: E(): 0, 44.3% id in 804 aa" /codon-start=1 /transl-table=11 /product="putative surface antigen" /protein-id="CAC89894.1" /db-xref="GI:15979119" /db-xref="SPTREMBL:Q8ZH58" /translation="MAMKKLLIASLLFGSATVYG ADGFVVDNIHFEGLRVAVGAALL NMPVRVGDTVSDDDIGKTIRALFATGNFEDVRVL RDGNTLIVQVKERPTIASITFSGN KAVKEDMLKQNLEASGVRVGEALDRTTISNIEKG

NRVDLKLVFTEGVSAKIQQINIVGNHSFTTDELI  
 SRFQLRDEVPWWNVVGDRKYQKQK  
 LAGDLETLSFYLDRGYARFNIDSTQVSLTPDKK  
 GIYVTINITEGPQFKLNSVIVSGN  
 LAGHQSEAELTKIEPGELFNGSKVTRMEDDIKK  
 MLGRYGYAYPRVVTQPEINDDDKT  
 VKLHINVDAGNRFYVRHIRFEGNDTSKDSVLRRE  
 MRQMEGAWLGNDQVEAGKERLNRL  
 GYFETVDVETQVRPGAADLVDVTKVKERN TGSL  
 NFGIGYGTESGVSFQVGVQQDNWL  
 GTGNTVGVINGTKNDYQTYAEFTLMDPYFTVDGVS  
 LGGRIFYNDFKADNADLSGYTNSS  
 YGADGTLGFPIENNSLRVGVGVVHNDLSDMLPQ  
 VAMWRYLESVGERPGYDREGFTT  
 DDFTLNLGWTYNNLDRGFFPTSGVKSSVNTKITV  
 PGSDNEFYKVTFDTSAYQPLNEDR  
 SWVLLGRGRLGYGDGIGSKEMPFYENFYAGGSST  
 VRGFRSNNIGPKAAYYANGGATVT  
 NSTDAVGGNAMAVASIELITPTPFISEKYSNSVR  
 TSIFIDSGTVWDTNWENTAKTRAA  
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 PVKDYEGDKSEQQFNIGKTW"  
 /gene="YPO1052"  
 /note="Pfam match to entry PF01103  
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 antigen, score 1444.20, E-value 0"  
 /gene="YPO1052"  
 /note="1 probable transmembrane  
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 /gene="ompH"  
 /note="synonym: YPO1053"  
 /gene="ompH"  
 /note="Similar to Yersinia  
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 OmpH SW:OMPH-YEREN (P31519) (164  
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 in 165 aa, and to Escherichia coli  
 histone-like protein Hlp-1  
 precursor SW:HLPA-ECOLI (P11457)  
 (161 aa) fasta scores: E():  
 1.3e-30, 67.1% id in 167 aa"  
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 /note="synonyms: firA, omsA,  
 YPO1054"  
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 SW:LFXD-ECOLI (P21645) (340 aa)  
 fasta scores: E(): 0, 82.6% id in  
 339 aa, and to Yersinia  
 enterocolitica  
 UDP-3-o-[3-hydroxymyristoyl]  
 glucosamine N-acyltransferase  
 SW:LFXD-YEREN (P32203) (339 aa)  
 fasta scores: E(): 0, 95.3% id in  
 339 aa"  
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misc-feature 74390..74449

gene 76917..77414

CDS 76917..77414

gene 77418..78440

CDS 77418..78440

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N-acyltransferase"
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SAVISPOATLGEQSVGVANAVIESGVVLGDNVVI
GAGCFIGKNTHIGAGSRLWANVSI
YHEVVIGQNCLIQSGTVIGADGFGYANDRGNWVK
IPQLGSVHIGDRVEIGACTTIDRG
ALDNTIIGNGVIIDNQCQIAHNVVIGDNTAVAGG
VIMAGSLKVGRYCMIGGASVINGH
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                    /note="PS00101 Hexapeptide-repeat
                    containing-transferases
                    signature."
misc-feature      77742..77795
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misc-feature      77805..77891
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                    /note="PS00101 Hexapeptide-repeat
                    containing-transferases
                    signature."
misc-feature      77850..77903
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                    /note="Pfam match to entry PF00132
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misc-feature      77904..77957
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                    /note="Pfam match to entry PF00132
                    hexapep, Bacterial transferase
                    hexapeptide (four repeats), score
                    18.50, E-value 0.15"
misc-feature      78015..78068
                    /gene="lpxD"
                    /note="Pfam match to entry PF00132
                    hexapep, Bacterial transferase
                    hexapeptide (four repeats), score
                    13.90, E-value 3.8"
misc-feature      78081..78134
                    /gene="lpxD"
                    /note="Pfam match to entry PF00132
                    hexapep, Bacterial transferase
                    hexapeptide (four repeats), score
                    19.10, E-value 0.1"
misc-feature      78090..78176
                    /gene="lpxD"
                    /note="PS00101 Hexapeptide-repeat
                    containing-transferases
                    signature."
misc-feature      78135..78188
                    /gene="lpxD"
                    /note="Pfam match to entry PF00132
                    hexapep, Bacterial transferase
                    hexapeptide (four repeats), score
                    12.90, E-value 7.7"
misc-feature      78207..78260
                    /gene="lpxD"
                    /note="Pfam match to entry PF00132
                    hexapep, Bacterial transferase
                    hexapeptide (four repeats), score
                    6.50, E-value 1e+02"
gene              78598..79143
                    /gene="fabZ"
                    /note="synonyms: sefA, YP01055"
CDS               78598..79143
                    /gene="fabZ"
                    /EC-number="4.2.1.-"
                    /note="Similar to Escherichia coli
                    FabZ SW:FABZ-ECOLI (P21774) (151

```

		in 151 aa, and to Yersinia enterocolitica FabZ SW:FABZ-YEREN (P32205) (201 aa) fasta scores: E(): 0, 90.1% id in 181 aa" /codon-start=1 /transl-table=11 /product="(3R)-hydroxymyristoyl-(a cyl carrier protein) dehydratase (EC 4.2.1.-)" /protein-id="CAC89897.1" /db-xref="GI:15979122" /db-xref="SWISS-PROT:Q8ZH57" /translation="MTTDTHTLHIEEILDLLPHR FPFLLVDRVLDFFEEGKFLRAVKNV SFNEPFFQGHFPGKPIFPGVLILEAMAQATGILA FKSRGKLEPGELYFFAGIDEARFK RPPVPGDQIMIMEVEFVKERRGLTRFTGVAKVDGE IVCTATMMCARSKPAAPAESVVVK PDVVKPDVVKPDVVNPVVKES" /gene="fabZ" /note="Pfam match to entry PF01377 Thioester-dehyd, Thioester dehydrase, score 286.40, E-value 3.5e-82"
misc-feature	78619..79017	
gene	79147..79935	/gene="lpxA"
		/note="synonym: YPO1056"
CDS	79147..79935	/gene="lpxA"
		/EC-number="2.3.1.129"
		/note="Similar to Escherichia coli acyl-[acyl-carrier-protein]--UDP-N -acetylglucosamine O-acyltransferase LpxA SW:LPXA-ECOLI (P10440) (262 aa) fasta scores: E(): 0, 81.3% id in 262 aa, and to Yersinia enterocolitica acyl-[acyl-carrier-protein]--UDP-N -acetylglucosamine O-acyltransferase LpxA SW:LPXA-YEREN (P32201) (262 aa) fasta scores: E(): 0, 90.1% id in 262 aa" /codon-start=1 /transl-table=11 /product="acyl-[acyl-carrier-prote in]--UDP-N- acetylglucosam ine O-acyltransferase" /protein-id="CAC89898.1" /db-xref="GI:15979123" /db-xref="SWISS-PROT:Q8ZH56" /translation="MIDKTAFIHPSSIVEEGAIL GAGVYIGPFCIVGSQVEIGAGTEL KSHVVVNGITKIGCDNQIYQFASIGEANQDLKYA GEPTREVEVGDRNRIRESVTIHRGT TQGGGVTKVGCNLLMVNTHVAHDCVIGNRCILA NNAALGGHVEIDDYAIIGGMTAIH QFCVIGAHVMVGGCSGITQDVPPFVIAQGNHATP FGINIEGLKRRGFDKESLHAIRSA YKLLYRSGRTLDEVKPEIAELAEQYPVVKAFNDF FARSTRGIIR" /gene="lpxA" /note="Pfam match to entry PF00132 hexapep, Bacterial transferase hexapeptide (four repeats), score 21.70, E-value 0.017"
misc-feature	79195..79248	
misc-feature	79204..79290	/gene="lpxA"
		/note="PS00101 Hexapeptide-repeat containing-transferases signature."
misc-feature	79249..79302	/gene="lpxA"
		/note="Pfam match to entry PF00132 hexapep, Bacterial transferase hexapeptide (four repeats), score 11.10, E-value 24"
misc-feature	79303..79356	/gene="lpxA"

misc-feature	79393..79446	hexapep, Bacterial transférse hexapeptide (four repeats), score 8.50, E-value 54" /gene="lpxA" /note="Pfam match to entry PF00132
misc-feature	79468..79521	hexapep, Bacterial transferase hexapeptide (four repeats), score 7.90, E-value 65" /gene="lpxA" /note="Pfam match to entry PF00132
misc-feature	79522..79575	hexapep, Bacterial transferase hexapeptide (four repeats), score 0.80, E-value 5.9e+02" /gene="lpxA" /note="Pfam match to entry PF00132
misc-feature	79594..79647	hexapep, Bacterial transferase hexapeptide (four repeats), score 14.40, E-value 2.7" /gene="lpxA" /note="Pfam match to entry PF00132
misc-feature	79603..79689	hexapep, Bacterial transferase hexapeptide (four repeats), score 17.80, E-value 0.26" /gene="lpxA" /note="PS00101 Hexapeptide-repeat containing-transferases signature."
gene	79939..81123	/gene="lpxB" /note="synonyms: pgsB, YPO1057"
CDS	79939..81123	/gene="lpxB" /EC-number="2.4.1.182" /note="Similar to Escherichia coli lipid-A-disaccharide synthase LpxB SW:LPXB-ECOLI (P10441) (382 aa) fasta scores: E(): 0, 82.2% id in 377 aa" /codon-start=1 /transl-table=11 /product="lipid-A-disaccharide synthase" /protein-id="CAC89899.1" /db-xref="GI:15979124" /db-xref="SWISS-PROT:Q8ZH55" /translation="MQNSPLTADCSLNAGRPLTI GLVAGETSGDILGAGLIRALKVQV PNARFVGAVGPLMQAEGCEAWYEMEELAVMGVVE VLERLPRLKIRKDLTQRFSELSP DVFVGIDAPDFNITLEGRLKQRGIRTIHYVSPSV WAWRQKRVFKIGKATDMVLAFLPF EKAFYDRFNVPFCRFIGTMDAMPLVPDQQAARA ELGIAPNATCLALLPGSRHSEVEM LSADFLRTAVILRDKLPNLEVVPVPLVNSKRREQF ERIKAEIAPDLSVHLLDGKARVAM IASDAALLASGTAALCMLAKCPMVVGYRMKPF FWLAERLVKTPYVSLPNLLAGEEL VTELLQQECQPQKLKAGALLPLLQGGSEIAALKER FLVLHQSIKRCGADEQAQAQAVLELA DR"
gene	81120..81716	/gene="rnhB" /note="synonyms: b0183, YPO1058"
CDS	81120..81716	/gene="rnhB" /EC-number="3.1.26.4" /note="Similar to Escherichia coli ribonuclease hII SW:RNH2-ECOLI (P10442) (198 aa) fasta scores: E(): 0, 84.5% id in 193 aa" /codon-start=1 /transl-table=11 /product="ribonuclease HII" /protein-id="CAC89900.1" /db-xref="GI:15979125" /db-xref="SPTREMBL:Q8ZH54" /translation="MSETFIYPQANLIAGVDEVG RGPLVGAVVTAAVILDPNRPIVGL ADSKKLSEKRRRLSLYDEITEKALSWSLGRAEPEE IDQLNILHATMLAMQRAVSGSLHIV



		SILAKVTRDREMTELDLLFPEYGF AQHKGYPYTAFLHLEKLAALGATVHHRRSFGPVKRV LGLV"
misc-feature	81159..81692	/gene="rnhB" /note="Pfam match to entry PF01351 RNase-HII, Ribonuclease HII, score 305.80, E-value 5.1e-88"
gene	81846..85361	/gene="dnaE" /note="synonyms: polC, YPO1059"
CDS	81846..85361	/gene="dnaE" /EC-number="2.7.7.7" /note="Similar to Escherichia coli DNA polymerase III, alpha chain DnaE SW:DP3A-ECOLI (P10443) (1160 aa) fasta scores: E(): 0, 89.0% id in 1160 aa" /codon-start=1 /transl-table=11 /product="DNA polymerase III, alpha chain" /protein-id="CAC89901.1" /db-xref="GI:15979126" /db-xref="SPTREMBL:Q8ZH53" /translation="MIQSTHFWYLDMAEPRFVHL RVHSDYSMIDGLAKIGPLVKRAAA LGMPALAITDFTNLCGLVKFYGSAHGAGIKPIIG ADFYVQSEILGDELAHLTVLARNN EGYQNLTLTLLISEAYQRGYGAAGPIIDRDWLIKHK EGLILLSGGRMGDVGKFLLRGNQV QVDQCLAFYQEHFPDCYYLELIRTGRPDEENYLH AAVALATERGLPVVATNDVRFIDE SFDFAHEIRVAIHGFTLVDPKRPKNYSPOQFMR DEEQMCELFADIPEALINSVEIAK RCNVTIRLGEYFLPQFPTGEMSTEDFLVEKAKQG LEERLEFLFPDPEVRLQKRPEYDE RLDIELKVINQMGPFGYFLIVMEFIQWSKDNGVP VGPGRGSGAGSLVAYALKITDIDP LEFDLLFERFLNPERVSMPDFDVDFCMEKRDLVI EHVAEMYGRDAVSQIITFGTMAAK AVIRDVGRVLGHPYGFVDRISKLIPLDPGMTLEK AFAAEQPQLAEIYEADDEEVRALIDM ARKLEGVTRNAGKHAGGVVIAPTKITDFAPLYCD AEGNNPVTQFDKNDVEYAGLVKFD FLGLRTLTIINWALEMINARRAKTGLEPIDIASI PLEDKKSFDMLQRSETTAVFQLES RGMKDLIKRLKPDCEFMIALVALFRPGPLQSGM VDNFIIDRKHGREAISYPDIEWQHE SLKPVLEPTYGIILYQEQVMQIAQVLSGYSLGGA DMLRRAMGKKNPAEMAKQRSVPED GAKNQGIDGELAIKIFDLVEKFAGYGFNKSHSAA YALVSYQTLWLKAHYPAEFMAAVM TADMDNTDKVVGVLVDECWRMGLKILPPDINSGLY HFHVNDGGEIVYGIGAIGVGEGP IEAILEARKEGGYFKELFDLCARVDTKKLNKRIL EKLIMSGAFDRLGPHRAALMSSLG DALKAADQHAKEAIGQVDMFGVLADAPEQVEQS YANVPPWQEQVLDGERETLGLYL TGHPITQYLKEIERYAGGMRLKDMHPTDRGKMTT AVGLVIAARVMVTKRGNRIGICTL DDRSRLEVMFLFTDALEKYQHLLEKDRIILIATGQ VSFDDFSGGLKMTARELMDISEAR EKYASGLAISLTDRQIDDQLLNRLRQSLEPHRAG TIPVHLYYQREDARARLRFGATWR VTPTDRLLIDLRTLVLGNEQVELEFD"
misc-feature	81897..82094	/gene="dnaE" /note="Pfam match to entry PF02231 PHP-N, PHP domain N-terminal region, score 115.50, E-value 1e-30"
misc-feature	84873..85097	/gene="dnaE" /note="Pfam match to entry PF01336 tRNA-anti, tRNA synthetase anti-codon binding domain, score 43.00, E-value 6.7e-09"
gene	85374..86333	/gene="accA"

CDS

85374..86333

```
/gene="accA"  
/EC-number="6.4.1.2"  
/note="Similar to Escherichia coli  
acetyl-coenzyme A carboxylase  
carboxyl transferase subunit alpha  
AccA SW:ACCA-ECOLI (P30867) (318  
aa) fasta scores: E(): 0, 90.5% id  
in 317 aa"  
/codon-start=1  
/transl-table=11  
/product="acetyl-coenzyme A  
carboxylase carboxyl transferase  
subunit alpha"  
/protein-id="CAC89902.1"  
/db-xref="GI:15979127"  
/db-xref="SPTREMBL:Q8ZH52"  
/translation="MSLNFLDFEQPIAELEAKID  
SLTAVSRQDEKLDINLDEEVQRLR  
EKSVELTRKIFSDLGAWQIAQLARHPRRPYTLDY  
IANIFTDFEELAGDRAYADDKAIV  
GGIARLDGRPVMII GHQKGRETKEKIRRNFGMPA  
PEGYRKALRLMEMAERFKLPITF  
IDTPGAYPGVGAEERGQSEAIARNLREMSRLNVP  
IVCTVIGEGSGGALAIGVGDKVN  
MLQYSTYSVISPEGCASILWKSADKAPLAAEAMG  
ITAHRLKELKMIDSVIPEPLGGAH  
RDYAAIAISLKAQLLADLNDLDVLNDEELLNRRY  
ORLMNYGYC"
```

gene  
CDS

86517..86915  
86517..86915

```
/gene="YPO1061"  
/gene="YPO1061"  
/note="Similar to Escherichia coli  
hypothetical protein YaeR  
SW:YAE-ECOLI (P52096) (129 aa)  
fasta scores: E(): 0, 71.1% id in  
128 aa, and to Vibrio cholerae  
glyoxylase I family protein  
VCA0890 TR:Q9KL58 (EMBL:AE004416)  
(127 aa) fasta scores: E():  
1.1e-27, 59.2% id in 125 aa"  
/codon-start=1  
/transl-table=11  
/product="conserved hypothetical  
protein"  
/protein-id="CAC89903.1"  
/db-xref="GI:15979128"  
/db-xref="SPTREMBL:Q8ZH51"  
/translation="MLAINKIHIAIICSQDYQAS  
KRFYCEVLGFNLISEVYREERDSW  
KADLALHDQYTIELFSFPSPVPRPSRPEACGLRH  
LAFQVDDIDLALKELVVAGVVCEA  
VRIDPYTQSRFTFFNDPDGLPLELYELKAE"
```

gene  
CDS

86917..88299  
86917..88299

```
/gene="YPO1062"  
/gene="YPO1062"  
/note="Similar to Escherichia coli  
putative cell cycle protein MesJ  
SW:MESJ-ECOLI (P52097) (432 aa)  
fasta scores: E(): 0, 55.2% id in  
440 aa"  
/codon-start=1  
/transl-table=11  
/product="conserved hypothetical  
protein"  
/protein-id="CAC89904.1"  
/db-xref="GI:15979129"  
/db-xref="SPTREMBL:Q8ZH50"  
/translation="MNLVTSKPNVLLNPLFAQLG  
ENRHVLVGFSGLDSTVLLHLLVC  
LRQQLIPELNIRATHIHGHNLPQADSWVKHCMQQ  
CDQWKIELKVVRVNIDPRQNGIEA  
AARTARYQAFSANLAAKEVLLTAQHLLDDQCETFL  
LALKRGS GPAGLSAMA AKMPFAHS  
QLLRPLLA FSREILENYAQAQQLQWIEDDSNQDD  
RFDRNFLRLNVLPILNQRWPHFAQ  
ATARSAGLCAEQEQLLELLAENLQQQLQGPDRSL  
SIDGLLQASMAKRAAILRRWLASL
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gene	88536..88853	RRFRQHLYLMLPLAEITTNYPW ATVKAAPNSSIIPLLPEPLWLPADLGVLRFVSAG GQAVRPAAVGEEISVRFGLQGDIK IVGRHHSRQSKKVWQELGIPPWQRERIPLLYFGE QLIAAAGVFVTQAGQANENEP CWH LDWDKPLRLG"
CDS	88536..88853	/gene="YPO1063" /gene="YPO1063" /note="Similar to Vibrio cholerae cytochrome C554 VC2241 TR:Q9KPX1 (EMBL:AE004296) (107 aa) fasta scores: E(): 1.6e-14, 50.5% id in 105 aa, and to Shewanella violacea soluble cytochrome CB CytCB TR:Q9RHJ5 (EMBL:AB032405) (206 aa) fasta scores: E(): 9.1e-10, 37.7% id in 106 aa, and to Pseudomonas aeruginosa cytochrome C4 precursor PA5490 TR:AAG08875 (EMBL:AE004961) (201 aa) fasta scores: E(): 2.5e-09, 40.4% id in 104 aa" /codon-start=1 /transl-table=11 /product="putative cytochrome" /protein-id="CAC89905.1" /db-xref="GI:15979130" /db-xref="SPTREMBL:Q8ZH49" /translation="MMKL VVSM AVL LSLCSFQVW AKNDIEAGRAKSSSCVACHGMNGK VSVPMYPNLAGQNALYLQQSLEAYKKGSRSGQA EVMRAYVSGLSDEDFSDLAAYYAS LKP"
misc-feature	88602..88847	/gene="YPO1063" /note="Pfam match to entry PF00034 cytochrome-c, Cytochrome c, score 47.20, E-value 3.6e-10"
misc-feature	88638..88655	/gene="YPO1063" /note="PS00190 Cytochrome c family heme-binding site signature."
gene	complement(89118..89378 )	/gene="YPO1064"
CDS	complement(89118..89378 )	/gene="YPO1064"  /note="Similar to Escherichia coli ROF protein SW:ROF-ECOLI (P52098) (84 aa) fasta scores: E(): 1.4e-26, 73.8% id in 84 aa" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAC89906.1" /db-xref="GI:15979131" /db-xref="SPTREMBL:Q8ZH48" /translation="MSMSEEYQPIN CDDYDNLEL ACQHHLILTLKLRGGEIVEGKASD LLLRKKVEYLIVEQEGTMRELRLDHIASFHPEI GTVVVSAS"
gene	complement(89365..89565 )	/gene="YPO1064a"
CDS	complement(89365..89565 )	/gene="YPO1064a"  /note="Similar to Escherichia coli hypothetical protein YaeP SW:YAEF-ECOLI (P52099) (66 aa) fasta scores: E(): 1.5e-18, 74.2% id in 66 aa" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAC89907.1" /db-xref="GI:15979132" /db-xref="SPTREMBL:Q8ZH47" /translation="MQQYCELVRRFYAEIGSGDL GYVPDALRCVLKALDEVAANDALP"

gene	89807..90355	/gene="YPO1065"
CDS	89807..90355	/gene="YPO1065"
		/note="Similar to Escherichia coli hypothetical protein YaeQ SW:YAEQ-ECOLI (P52100) (181 aa) fasta scores: E(): 0, 61.8% id in 178 aa" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAC89908.1" /db-xref="GI:15979133" /db-xref="SPTREMBL:Q8ZH46" /translation="MALKATIHKAAINIADMDRN FFQDINLTIAQHPSETDQRMMLRL LAWICHADERLLFTKGLSADDEPEVWRHNDHNGI ELWIELGLPEEKRLRKACNQSKQV VLYAYSERAARKVWWPQVQEKLAGHRNLRVRFLLD EQMAKLAALSNNRMSLQATLQEGT IWLSDVQNNLEISFAEWQNYGQ"
gene	90358..90774	/gene="YPO1066"
CDS	90358..90774	/gene="YPO1066"
		/note="Similar to Escherichia coli hypothetical protein YaeJ SW:YAEJ-ECOLI (P40711) (140 aa) fasta scores: E(): 0, 65.2% id in 135 aa, and to Pseudomonas putida hypothetical protein SW:YAEJ-PSEPU (P45388) (137 aa) fasta scores: E(): 8.6e-31, 65.2% id in 135 aa, and to Streptomyces coelicolor hypothetical protein SCD95A.11 TR:Q9KXW3 (EMBL:AL357432) (145 aa) fasta scores: E(): 7.4e-13, 41.5% id in 135 aa" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAC89909.1" /db-xref="GI:15979134" /db-xref="SPTREMBL:Q8ZH45" /translation="MLIISNSVTLASGEIELTAI RAQGAGGQHVNKTSTAIHLRFDIK ASSLPEYYKERLLLLNSHLVTAEGVVIKAQEYR SQDMNREAALARLVALIRQAMVVE KARRATKPTKSGKIRRVGKVRKGATKALRGKIH QE"
gene	90814..91542	/gene="cutF"
CDS	90814..91542	/note="synonyms: nlpE, YPO1067" /gene="cutF"
		/note="Similar to Escherichia coli copper homeostasis protein CutF precursor SW:CUTF-ECOLI (P40710) (236 aa) fasta scores: E(): 0, 48.3% id in 230 aa" /codon-start=1 /transl-table=11 /product="putative copper homeostasis lipoprotein" /protein-id="CAC89910.1" /db-xref="GI:15979135" /db-xref="SPTREMBL:Q8ZH44" /translation="MTSFHIYRTQYGRITVSKLT ITLLLAVALGALSLLGCNNRSQPAEQ VLQPMQQSYQGVLPACDCSGLDTSFLDSGTFI LKEVYLGTKDGDQTFAEYGKWART ADKLVLTLNGQGEKRYFHPVDKSLVMLDQQGLPIK STLNYQLEPSDQPLSKTPMPLSGM YKYFADAAIFTDCTGKAFPVENNIELETGYLNA RRNPGEFVFLTLNGYFDSRPSMEE GRTNKTLIPEGDIQFNANKSCEKK"
misc-feature	90886..90918	/gene="cutF" /note="PS00013 Prokaryotic

gene complement(91676..93394) attachment site." /gene="proS"

CDS complement(91676..93394) /note="synonyms: drpA, YPO1068" /gene="proS"

/EC-number="6.1.1.15"  
 /note="Similar to Escherichia coli  
 prolyl-tRNA synthetase  
 SW:SYP-ECOLI (P16659) (572 aa)  
 fasta scores: E(): 0, 84.2% id in  
 571 aa"  
 /codon-start=1  
 /transl-table=11  
 /product="prolyl-tRNA synthetase"  
 /protein-id="CAC89911.1"  
 /db-xref="GI:15979136"  
 /db-xref="SPTREMBL:Q8ZH43"  
 /translation="MRTSQYLLSTQKETPADAEV  
 ISHQLMLRAGMIRKLASGLYTWLP  
 TGVRLVKKVENIVREEMNAGAIEVSMPPVQPAD  
 LWQESGRWEQYGPPELLRFVDRGER  
 PFVLGPTHEEVITDLIRGEINSYKQLPLNFFQIQ  
 TKFRDEVPRFRGVMRAREFLMKDA  
 YSFHTTQESLQETYDAMYTAYSKIFSRMDLNFA  
 VLADTGSIGGSASHEFQVLAESGE  
 DDIVFSTGSDYAANIEFAEALAPTEPRAPATEEL  
 RIVDTPNAKTIAELVEQFKLPIEK  
 TVKTLVHAHEESGHKLVALLVRGDHLNEIKAE  
 KLPQVAKPLTFASEEEIRAAIGAG  
 PGSGLGPVNLSPVIADHSVAVMSDFGAGANIDGK  
 HYFGINWERDLALPLVADLRNVVE  
 GDISPDGKGTLOIKRGIEVGHIFQLGTKYSEVMK  
 ATVQGEDGRNQVMTMGCYGIGVSR  
 VVAAAEQNHDDRGIIWPDIAIPFQVAILPMNMH  
 KSFVRKELAEELYTTLRSHGIDVI  
 LDDRKERPGVMFADMELIGVPHNIVIGDRNLDSE  
 EVEYKNRRVGEKQMIKTSEIVEFL LSQIKR"

misc-feature complement(91730..93010) /gene="proS"

/note="Pfam match to entry PF00587  
 tRNA-synt-2b, tRNA synthetase  
 class II (G, H, P, S and T), score  
 244.70, E-value 1.3e-69"

misc-feature complement(92918..92980) /gene="proS"

/note="PS00179 Aminoacyl-transfer  
 RNA synthetases class-II signature  
 1."

gene complement(93498..94205) /gene="YPO1069"

CDS complement(93498..94205) /gene="YPO1069"

/note="Similar to Escherichia coli  
 hypothetical protein YaeB  
 SW:YAEB-ECOLI (P28634) (235 aa)  
 fasta scores: E(): 0, 71.1% id in  
 235 aa, and to Vibrio cholerae  
 hypothetical protein VC0876  
 TR:Q9KTM6 (EMBL:AE004172) (231 aa)  
 fasta scores: E(): 0, 50.0% id in  
 232 aa"  
 /codon-start=1  
 /transl-table=11  
 /product="conserved hypothetical  
 protein"  
 /protein-id="CAC89912.1"  
 /db-xref="GI:15979137"  
 /db-xref="SPTREMBL:Q8ZH42"  
 /translation="MSTFSFNQIGVIRSPYKEKF  
 AVPRQPGLVEDGGGELQLLAPYNQ  
 PESVRGLSDFSHLWVIFVFHQTMEGGWRTVRPP  
 RLGGNTRMGVFATRSTFRPNPIGM  
 SLIELKGVRQNGEVILALGSLDLVDGTPVIDIK  
 PYLPFAESQPQARAGFAQSPADTE"

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misc-feature      complement(93774..94154) /gene="YPO1069"
)
/Note="Pfam match to entry PF01980
UPF0066, Uncharacterised protein
family UPF0066, score 254.10,
E-value 2e-72"

misc-feature      complement(93912..93947) /gene="YPO1069"
)
/Note="PS01318 Uncharacterized
protein family UPF0066 signature."

gene              complement(94202..94609) /gene="rcsF"
)
/Note="synonym: YPO1070"

CDS               complement(94202..94609) /gene="rcsF"
)
/Note="May be involved in
regulation of exopolysaccharide
biosynthesis. Similar to
Escherichia coli RcsF protein rcsF
SW:RCSF-ECOLI (P28633) (133 aa)
fasta scores: E(): 2.1e-27, 63.5%
id in 137 aa"
/codon-start=1
/transl-table=11
/product="putative lipoprotein"
/protein-id="CAC89913.1"
/db-xref="GI:15979138"
/db-xref="SPTREMBL:Q8ZH41"
/translation="MRALPLCLLALSLTGCTLLP
SKPSTTDNPIKQPPPVIERSPATA
PRPAPVKLYKSAEELVGKPFRLGGEVSGESCQST
VQDSPPSISTARKRMQIRASYMKA
NAVLLHECEIQSGVPGCYQQAVCQGSALNVSSK"

misc-feature      complement(94562..94594) /gene="rcsF"
)
/Note="PS00013 Prokaryotic
membrane lipoprotein lipid
attachment site."

gene              complement(94727..95542) /gene="YPO1071"
)

CDS               complement(94727..95542) /gene="YPO1071"
)
/Note="Similar to Escherichia coli
putative lipoprotein YaeC
precursor SW:YAE-ECOLI (P28635)
(271 aa) fasta scores: E(): 0,
90.4% id in 271 aa, and to Vibrio
cholerae lipoprotein VC0905
TR:Q9KTJ7 (EMBL:AE004174) (275 aa)
fasta scores: E(): 0, 68.3% id in
271 aa"
/codon-start=1
/transl-table=11
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/protein-id="CAC89914.1"
/db-xref="GI:15979139"
/db-xref="SWISS-PROT:Q8ZH40"
/translation="MSLKFKSIAAISALIGTLTL
VCGGPTEKAPNHIKVGIVVGAEQQ
VAEVAQKVAKKEYGLDVELVTFNDYVLPNEALSK
GDIDLNAFQHKPYLDQQIKDRGYK
LVS VGNSFVYPIAGYSKKIKSLDELQPGSQVALP
NDPTNLGRSLLLQLQSVGLIKLKDQ
VGLLP TVLDVVENPKNLKLELEAPQLPRSLDDQ
QIALAIINTTYASQIGLTPAKDGL
FVEDKESPYVNLIVAREDNKDAENVKKFVQAYQS
DEVYDAANKAFNGGAVKGW"

misc-feature      complement(95474..95506) /gene="YPO1071"
)
/Note="PS00013 Prokaryotic
membrane lipoprotein lipid
attachment site."

gene              complement(95606..96259) /gene="YPO1072"
)

```

CDS	complement(95606..96259	/gene="YPO1072"	/note="Similar to Escherichia coli hypothetical ABC transporter permease protein YaeE SW:YAE-ECOLI (P31547) (217 aa) fasta scores: E(): 0, 90.8% id in 217 aa, and to Vibrio cholerae ABC transporter, permease protein VC0906 TR:Q9KTJ6 (EMBL:AE004174) (225 aa) fasta scores: E(): 0, 54.3% id in 210 aa" /codon-start=1 /transl-table=11 /product="ABC transporter permease protein" /protein-id="CAC89915.1" /db-xref="GI:15979140" /db-xref="SWISS-PROT:Q8ZH39" /translation="MSEAMMWLMARGVWETLMMTFVSGFFGFVLGLPVGVLVYVTRPGQIIANNKIYRTLSGVVNIFRSIPFIILLVWMIPFTRMIVGTSIGLQAAIVPLTVGAAPFIARMVENALLEIPSGLVEAARAMGATPMQIIKKVLLPEALPGLVNAATITLITLVGYSAMGGAVGAGGLGQIGYQYGYIGYNATVMNTVLVLLVILVYLIQLSGDRIVKAVTHK"
misc-feature	complement(95651..95716	/gene="YPO1072"	
misc-feature	complement(95717..95929	/gene="YPO1072"	/note="one of 5 probable transmembrane helices predicted for YPO1072 by TMHMM2.0"
misc-feature	complement(95762..95827	/gene="YPO1072"	/note="Pfam match to entry PF00528 BPD-transp, Binding-protein-dependent transport systems inner membrane component, score 66.00, E-value 8.1e-16"
misc-feature	complement(95840..95926	/gene="YPO1072"	/note="one of 5 probable transmembrane helices predicted for YPO1072 by TMHMM2.0"
misc-feature	complement(95948..96013	/gene="YPO1072"	/note="PS00402 Binding-protein-dependent transport systems inner membrane comp. sign."
misc-feature	complement(96029..96094	/gene="YPO1072"	/note="one of 5 probable transmembrane helices predicted for YPO1072 by TMHMM2.0"
misc-feature	complement(96134..96199	/gene="YPO1072"	/note="one of 5 probable transmembrane helices predicted for YPO1072 by TMHMM2.0"
gene	complement(96252..97283	/gene="abc"	/note="one of 5 probable transmembrane helices predicted for YPO1072 by TMHMM2.0"
CDS	complement(96252..97283	/gene="abc"	/note="synonym: YPO1073"
			/note="Similar to Escherichia coli ATP-binding protein Abc SW:ABC-ECOLI (P30750) (343 aa) fasta scores: E(): 0, 80.2% id in



		/codon-start=1 /transl-table=11 /product="ABC transporter ATP-binding protein" /protein-id="CAC89916.1" /db-xref="GI:15979141" /db-xref="SWISS-PROT:Q8ZH38" /translation="MIKLTHISKVFQQGSRTITA LSDVSLHVPAGQIYGVIGASGAGK STLIRCANMLERPTSGQVLVDDQDLTTLSEGQLT RARRQIGMIFQHFNLLSSRTVYGN IALPLELDNTSRADIKKRVNELLDLVGLTDKQDA YPANLSGGQKQORVAIARALASNP VLLCDEATSALDPATTRSILELLKDINRRLGLTI LLITHEMDVVKRICDQVAVISEGK LIEKDSVSEVFSHPKTPLAQQFIQSTLHLDIPED YAKRMSPEPTVDHVPLLKLEFTGK SVDAPLISQAVRRFNIDIGILSSQMDYAGGVKFG VMLAELHGDVQDGLAAIKFLQDHH VKVEVLGYV" /gene="abc"
misc-feature	complement(96633..97193)	/Note="Pfam match to entry PF00005 ABC-tran, ABC transporter, score 258.10, E-value 1.2e-73" /gene="abc"
misc-feature	complement(96819..96863)	/Note="PS00211 ABC transporters family signature." /gene="abc"
misc-feature	complement(97149..97172)	/Note="PS00017 ATP/GTP-binding site motif A (P-loop)." /gene="YPO1074" /gene="YPO1074" /Note="Similar to Escherichia coli hypothetical protein YaeD SW:YAED-ECOLI (P31546) (191 aa) fasta scores: E(): 0, 80.3% id in 188 aa, and to Escherichia coli O157:H7 phosphatase YaeD TR:BAA93568 (EMBL:AB035926) (191 aa) fasta scores: E(): 0, 80.3% id in 188 aa" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAC89917.1" /db-xref="GI:15979142" /db-xref="SPTREMBL:Q8ZH37" /translation="MTQSVPAIFLDRDGTVNVDH GYVHEIDNFFQFIDGVIDACRELKE MGFALVLVTNQSGIARGMFTEEQFLSLTEWMDWS LADRGVDLDGIYFCPHHPDGSVAE FSETCECRKPLPGMLLQAQNELNIDMAASYMVG KIEDMQAALAANIGTKVLVVRTGKP VTAEGEAAADWVLNLSLADLPKAIKARYK"
gene CDS	97470..98036 97470..98036	
gene rRNA	98505..99993 98505..99993	/gene="16S-rRNA" /gene="16S-rRNA" /Note="match to 16S-rRNA 1..1489 (EMBL:YPE16SA)"
tRNA	100157..100232	/product="tRNA-Glu" /Note="tRNA Glu anticodon TTC, Cove score 56.95"
gene rRNA	100485..103391 100485..103391	/gene="23S-rRNA" /gene="23S-rRNA" /Note="match to 23S-rRNA 1..2906 (Y. enterocolitica 23S EMBL:U77925)"
gene rRNA	103391..103624 103391..103624	/gene="5S-rRNA" /gene="5S-rRNA" /Note="match to 5SrRNA 1..234 blast score 1131 percent identity 98 (incl. 23S-5S spacer)"

gene	104177..104980	/note="tRNA Asp anticodon GTC, Cove score 90.47"
CDS	104177..104980	/gene="YPO1075" /gene="YPO1075" /note="Similar to Escherichia coli hypothetical oxidoreductase in aspU-mltD intergenic region YafB SW:YAFB-ECOLI (P30863) (267 aa) fasta scores: E(): 0, 74.9% id in 267 aa, and to Corynebacterium sp 2,5-diketo-D-gluconic acid reductase TR:P06632 (EMBL:M12799) (278 aa) fasta scores: E(): 6.3e-31, 41.6% id in 255 aa" /codon-start=1 /transl-table=11 /product="putative aldo/keto reductase" /protein-id="CAC89918.1" /db-xref="GI:15979143" /db-xref="SWISS-PROT:Q8ZH36" /translation="MSIPVFGLGTFRLQDQIVID SVSQALTILGYRAIDTAQIYENEAP VGQAIQESGINRDELFITTKIWIANLSKDKLIPS LRESIQKLKTDYVDLTLIHWPSPN DEVSVAEFMSSELLKAKGLGLTRQIGISNFTIDLM KQAIAAVGAEEIATNQIELSPLLQ NRNVVDFAKQNGIAVTSYMTLAYGKALAEPIKT IAEQHGATPAQVILSWAMQLGYGV IPSSTKAANLASNLLAQKLCLNAADMALIALTLDR NERLVSPDGLAPKWD"
misc-feature	104177..104941	/gene="YPO1075" /note="Pfam match to entry PF00248 aldo-ket-red, Aldo/keto reductase family, score 357.70, E-value 1.3e-103"
misc-feature	104261..104314	/gene="YPO1075" /note="PS00798 Aldo/keto reductase family signature 1."
misc-feature	104516..104569	/gene="YPO1075" /note="PS00062 Aldo/keto reductase family signature 2."
gene	105015..105479	/gene="YPO1076"
CDS	105015..105479	/gene="YPO1076" /note="no significant database hits" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="CAC89919.1" /db-xref="GI:15979144" /db-xref="SPTREMBL:Q8ZH35" /translation="MRWFFILVHPDGAETGSVKS VRMDMELPPSMCAVIVGTNLMRAY QVRGEQRVDNSIVKKHGNEAMDQLSLRPDNGS QVESAGQGNCEASIGTERMDTLLP FNRGGRGDWNSWIGGDKENCVACYGGSGKGRIYE QRCLEEVFYRKGLIYQQ"
gene	105840..106622	/gene="YPO1077"
CDS	105840..106622	/gene="YPO1077" /note="Similar to Escherichia coli hypothetical protein YafD SW:YAFD-ECOLI (P30865) (259 aa) fasta scores: E(): 0, 75.2% id in 254 aa" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAC89920.1" /db-xref="GI:15979145" /db-xref="SPTREMBL:Q8ZH34" /translation="MPKRTYAMRYVAGQPVEQIF PGAQKQLDKGLPLGEPLPTAELLR VVVWNIFKQQRAGWLPVLKELGRDTQLMLLQEAQ"

		PQHPSGVMTLAAAHVPVYCCPLREREP LLRLSKSA LVTVPYPIHDGRLLMVVNIHAVNFS LGVDVYSKQLDPIGDQIASHRGPVILAGDFNAWS RQRINALQHFAQDAGLQEV EFRVD HRSRAFGRLDFIFYRGLTVIDASVLVTRASDHN PLIVEFQP"
gene	complement(106664..108091)	/gene="mldD"
CDS	complement(106664..108091)	/note="synonyms: dniR, YPO1078" /gene="mldD"  /EC-number="3.2.1.-" /note="Similar to Escherichia coli membrane-bound lytic murein transglycosylase D precursor MldD SW:MLTD-ECOLI (P23931) (452 aa) fasta scores: E(): 0, 63.4% id in 470 aa" /codon-start=1 /transl-table=11 /product="membrane-bound lytic murein transglycosylase D precursor" /protein-id="CAC89921.1" /db-xref="GI:15979146" /db-xref="SPTREMBL:Q8ZH33" /translation="MIARLLSNHIDTHMKT KAIL LASVLLVGCQTSKQDAQAP EQHAQ SLSSAGQASEAGEYTNSTREGSARWLESESSYAQ QDLWNFIKDELKMKVPENSRIREQ KQKYLKNKSYLHDVTLRAEPYMYLIVEQIKKRKM PMELVLLPIVESAFDPHATSSANA AGLWQIVPSTGRNYGLKQONQWYDGRRDVVASTKA ALDILERLNKMFNGDWLLTVAAYN SGEGRVMQAIKANKAKGKPTDFWALS LPRETSIY VPKMLALGDLLKNSKKYGITLPET DKDRALARVDVDQQIELTQAAEMAGMSLT KLKSF NSGYKRNVTAPDGHGPRYIMLPKA HAEQLKDSLADTDITAVQPTKLATNSTKSASSSQ YKVRPGDTLSTIAKRLNIKTSDLQ SWNNLRKSTLKVGTQLQLASNTTSKSITYQVRK GDSFASIAKRHGVNTDDVMRWNSV VSKANNLQPLGLKLT L FVNDKSTPEA"
misc-feature	complement(106694..106828)	/gene="mldD"
misc-feature	complement(106856..106987)	/note="Pfam match to entry PF01476 LysM, Putative peptidoglycan binding domain, score 44.10, E-value 3.2e-09" /gene="mldD"
misc-feature	complement(107372..107722)	/note="Pfam match to entry PF01476 LysM, Putative peptidoglycan binding domain, score 62.30, E-value 1e-14" /gene="mldD"
misc-feature	complement(107579..107665)	/note="Pfam match to entry PF01464 SLT, Transglycosylase SLT domain, score 122.70, E-value 6.7e-33" /gene="mldD"
misc-feature	complement(108005..108037)	/note="PS00922 Prokaryotic transglycosylases signature." /gene="mldD"
gene	complement(108124..108879)	/note="PS00013 Prokaryotic membrane lipoprotein lipid attachment site." /gene="gloB"
CDS	complement(108124..108879)	/note="synonym: YPO1079" /gene="gloB"  /EC-number="3.1.2.6"

probable hydroxyacylglutathione  
hydrolase GloB SW:GLO2-ECOLI  
(Q47677) (251 aa) fasta scores:  
E(): 0, 57.4% id in 251 aa, and to  
Arabidopsis thaliana  
hydroxyacylglutathione hydrolase,  
mitochondrial precursor Glx2-1  
SW:GL2M-ARATH (O24495) (331 aa)  
fasta scores: E(): 2.9e-32, 39.0%  
id in 236 aa"  
/codon-start=1  
/transl-table=11  
/product="putative  
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/protein-id="CAC89922.1"  
/db-xref="GI:15979147"  
/db-xref="SPTREMBL:Q8ZH32"  
/translation="MNLISIPAFQDNYIWLLANR  
QKHCVIVDPGESAPVLATLAQGQY  
VPQAILLTHHHNDHVGGVADLRHHFPDIPVYGPQ  
ETAKKGATVIVNDGDSLTIAGQNY  
TIIAVPGHTLGHIAYYSSPYLFCGDTLFSAGCGR  
LLEGTPEQMYASIQRLAQLPDETL  
ICCAHEYTLNLKFAHAILPADQDIATYQQQIEQ  
LRSKNLPSLPVKLQFERKINVFLR  
CNDIDLQRKIGTTSPDLSLVSVFCELSRKDSF"  
/gene="gloB"

misc-feature complement(108385..1088  
61)  
/note="Pfam match to entry PF00753  
lactamase-B,  
Metallo-beta-lactamase  
superfamily, score 162.10, E-value  
9.3e-45"

gene 108924..109643  
CDS 108924..109643  
/gene="YPO1080"  
/gene="YPO1080"  
/note="Similar to Escherichia coli  
hypothetical protein YafS  
SW:YAFS-ECOLI (P75672) (240 aa)  
fasta scores: E(): 0, 63.6% id in  
236 aa, and to Vibrio cholerae  
hypothetical protein VC2235  
TR:Q9KPX7 (EMBL:AE004295) (245 aa)  
fasta scores: E(): 0, 44.2% id in  
233 aa"  
/codon-start=1  
/transl-table=11  
/product="conserved hypothetical  
protein"  
/protein-id="CAC89923.1"  
/db-xref="GI:15979148"  
/db-xref="SPTREMBL:Q8ZH31"  
/translation="MKPAQIRQNIETPASWAELP  
WGEYYRAALEQQQLQPWWPKFFGFH  
LLKVGHLISAEIASDKCAIAHQVNVGEWGKNMQVL  
ASPYQLPFAEKSVDACLLSHTLAY  
AANPHRILREVDRVLIDDGWLVISGFNPFSLLGL  
GKLVPVLRQRPYISRMFTQMRL  
DWLSLLNYEVVHLSCFHVLPFNKNGGHFISTHLP  
ALGCVNLIIARKRTVPLTFNPMKF  
GVRKPWFSSRAVGATKSYRDQP"  
/gene="rnhA"

gene complement(109698..1101  
62)  
/note="synonyms: dasF, herA, rnh,  
sdrA, YPO1081"

CDS complement(109698..1101  
62)  
/gene="rnhA"  
/EC-number="3.1.26.4"  
/note="Similar to Escherichia coli  
ribonuclease HI SW:RNH-ECOLI  
(P00647) (155 aa) fasta scores:  
E(): 0, 84.8% id in 151 aa"  
/codon-start=1  
/transl-table=11  
/product="ribonuclease HI"  
/protein-id="CAC89924.1"

		/db-xref="SWISS-PROT:Q8ZH30" /translation="MTKQVEIFTDGSC LGNPGPG GYGAILRYKQHEKTFSAGYYLTTN NRMELMAAIVALEALTSPCEVTLSQYVRQGI TQWIHNWKKRGWKTADRKPVRNVD LWQRLDLAIQSHTIQWEWVKGHAGHPENERCDEL ARQGANSPTLDDTGYNPD" /gene="rnhA"
misc-feature	complement(109737..110159)	
gene	110232..110996	/note="Pfam match to entry PF00075 rnaseH, RNase H, score 227.00, E-value 2.8e-64" /gene="dnaQ"
CDS	110232..110996	/note="synonyms: mutD, YPO1082" /gene="dnaQ" /EC-number="2.7.7.7" /note="Similar to Escherichia coli DNA polymerase III, epsilon chain SW:DP3E-ECOLI (P03007) (243 aa) fasta scores: E(): 0, 75.9% id in 237 aa" /codon-start=1 /transl-table=11 /product="DNA polymerase III, epsilon chain" /protein-id="CAC89925.1" /db-xref="GI:15979150" /db-xref="SPTREMBL:Q8ZH29" /translation="MIITPTRQIVLDTETTGMNK LGVHYEGHRIIEIGAVEVINRRRLT GRNFHVYVKPDRLVDPEAYGVHGISDEFLADKPT FADITPEFLDFIRGAELVIHNAAF DIGFMDYEFRLQDDIPKTETFTCTITDSLLMARR LFPGKRNNLDALCDRYQIDNTKRT LHGALLDAEILADEVYLAMTGGQTSLTFSMEGEVS QNNASEDIQRITRPASALKIIYAT EDELANHESRLDFVMKKGGSC LWRMPLEAEETK AE" /gene="dnaQ"
misc-feature	110253..110780	/note="Pfam match to entry PF00929 Exonuclease, Exonuclease, score 171.30, E-value 1.6e-47" /product="tRNA-Asp" /note="tRNA Asp anticodon GTC, Cove score 94.51" /gene="YPO1083"
tRNA	111109..111185	
gene	complement(111242..112726)	/gene="YPO1083"
CDS	complement(111242..112726)	/gene="YPO1083" /note="Similar to Pseudomonas aeruginosa probable permease TR:AAG03865 (EMBL:AE004485) (575 aa) fasta scores: E(): 0, 39.1% id in 465 aa, and to Streptomyces coelicolor putative transmembrane transporter SC1A6.06 TR:O69811 (EMBL:AL023496) (522 aa) fasta scores: E(): 0, 32.6% id in 481 aa" /codon-start=1 /transl-table=11 /product="putative permease" /protein-id="CAC89926.1" /db-xref="GI:15979151" /db-xref="SPTREMBL:Q8ZH28" /translation="MPNNEKISASSINPHYSPLK TNEDLAPTRKQNWGWYNIFSFWMT DVHSMGGYVVAASFFALGLSSWQVLLSLLVGICI VQICANLVAKPSQIAGVPYAVICR QSFGVFGANIPAVIRGLIAVAWYGIQTYLAGNAF MLVMLKFFPSLIPLAQSQWLGLST LGWICFSIMWVLQAMVFWHGMNAIKRFIDFAGPA VYVVMLSLALWIVYQTGWSNISFT LASKILSPSEQVWQMLTATALVVS YFAGPLL NFG DFSRYGKSMQEI RRGNRWGLPFNF

		GVAIALGLLTMIATIGINIVANF VSPAFDNFNCSPQRINFRTGGMIAAVGSVLLTPW NLFQSPIIHYTLVDVLGAFMGPLF GILIADFYLIKRGQLYVDDLNFNASSSGRYWYRGG FNPKAIMALLPAVAIGLMIIFIPN LQIISFSWFIGAFLGGSIYRFIARNDPNNAALFIRPEIGKD"
misc-feature	complement (111305..111370)	/gene="YPO1083"  /note="one of 12 probable transmembrane helices predicted for YPO1083 by TMHMM2.0"
misc-feature	complement (111341..112648)	/gene="YPO1083"  /note="Pfam match to entry PF02133 Transp-cyt-pur, Permeases for cytosine/purines, uracil, thiamine, allantoin, score 272.50, E-value 1.8e-78"
misc-feature	complement (111383..111448)	/gene="YPO1083"  /note="one of 12 probable transmembrane helices predicted for YPO1083 by TMHMM2.0"
misc-feature	complement (111536..111601)	/gene="YPO1083"  /note="one of 12 probable transmembrane helices predicted for YPO1083 by TMHMM2.0"
misc-feature	complement (111614..111679)	/gene="YPO1083"  /note="one of 12 probable transmembrane helices predicted for YPO1083 by TMHMM2.0"
misc-feature	complement (111719..111784)	/gene="YPO1083"  /note="one of 12 probable transmembrane helices predicted for YPO1083 by TMHMM2.0"
misc-feature	complement (111845..111910)	/gene="YPO1083"  /note="one of 12 probable transmembrane helices predicted for YPO1083 by TMHMM2.0"
misc-feature	complement (111971..112036)	/gene="YPO1083"  /note="one of 12 probable transmembrane helices predicted for YPO1083 by TMHMM2.0"
misc-feature	complement (112091..112156)	/gene="YPO1083"  /note="one of 12 probable transmembrane helices predicted for YPO1083 by TMHMM2.0"
misc-feature	complement (112196..112261)	/gene="YPO1083"  /note="one of 12 probable transmembrane helices predicted for YPO1083 by TMHMM2.0"
misc-feature	complement (112307..112372)	/gene="YPO1083"  /note="one of 12 probable transmembrane helices predicted for YPO1083 by TMHMM2.0"
misc-feature	complement (112466..112531)	/gene="YPO1083"  /note="one of 12 probable transmembrane helices predicted for YPO1083 by TMHMM2.0"
misc-feature	complement (112547..112612)	/gene="YPO1083"  /note="one of 12 probable transmembrane helices predicted for YPO1083 by TMHMM2.0"
gene	113065..113283	/gene="YPO1084"

CDS	113065..113283	/gene="YPO1084" /note="Appears to have been interrupted by the insertion of downstream IS100. Similar to N-terminus of Pseudomonas aeruginosa hypothetical protein TR:AAG04906 (EMBL:AE004580) (308 aa) fasta scores: E(): 6.7e-13, 56.5% id in 69 aa, and to N-terminus of Schizosaccharomyces pombe hypothetical 36.2 kDa protein C19G12.03 in chromosome I SPAC19G12.03 TR:O13842 (EMBL:Z97209) (320 aa) fasta scores: E(): 3.6e-06, 44.4% id in 63 aa" /pseudo /codon-start=1 /transl-table=11 /product="conserved hypothetical protein (pseudogene)"
misc-feature	complement(113283..115236)	/note="insertion sequence, IS100"
misc-feature	113283..113310	/note="IS100 inverted repeat"
gene	complement(113349..114131)	/gene="YPO1085" /note="synonym: ypmt1.57c"
CDS	complement(113349..114131)	/gene="YPO1085"  /note="Similar to Escherichia coli insertion sequence IS21 putative ATP-binding protein, IstB SW:ISTB-ECOLI (P15026) (265 aa) fasta scores: E(): 0, 47.4% id in 249 aa. Also almost identical to Yersinia pestis and Escherichia coli putative IS100 transposase ypmt1.57c TR:Q9R3L5 (EMBL:AL117211) (260 aa) fasta scores: E(): 0, 99.6% id in 260 aa." /codon-start=1 /transl-table=11 /product="insertion sequence IS100, ATP-binding protein" /protein-id="CAC89928.1" /db-xref="GI:15979152" /db-xref="SPTREMBL:Q9R3L5" /translation="MMELQHQRMLALAGQLQLE SLISAAPALSQQAVDQEWSYMDFL EHLLEHEKRLARHQRKQAMYTRMAAFPAVKTFEEY DFTFATGAPQKQLQSLRSLSFIER NENIVLLGPSGVGKTHLAIAMGYEAVRAGIKVRF TTAADLLQLSTAQRQGRYKTTLQ RGVMAPRLLIIDEIGYLPFSQEEAKLFFQVIAKR YEKSAMILTSNLPFGQWDQTFAGD AALTSAMLDRIHHSHVQIKGESYRLRQKRKAG VIAEANPE"
misc-feature	complement(113424..113963)	/gene="YPO1085"  /note="Pfam match to entry PF01695 IstB, IstB-like ATP binding protein, score 367.20, E-value 1.7e-106"
misc-feature	complement(113781..113804)	/gene="YPO1085"  /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
gene	complement(114128..115150)	/gene="YPO1086"
CDS	complement(114128..115150)	/note="synonyms: y1093, ypmt1" /gene="YPO1086"  /note="Similar to Escherichia coli transposase for insertion sequence"



(P15025) (390 aa) fasta scores:  
E(): 3e-27, 33.1% id in 329 aa.  
Identical to the previously  
sequenced *Yersinia pestis*,  
*Yersinia pseudotuberculosis*, and  
*Escherichia coli* pesticin plasmid  
insertion sequence transposase  
Y1055 TR:P74993 (EMBL:U59875) (340  
aa) fasta scores: E(): 0, 100.0%  
id in 340 aa"  
/codon-start=1  
/transl-table=11  
/product="transposase for  
insertion sequence IS100"  
/protein-id="CAC89929.1"  
/db-xref="GI:15979153"  
/db-xref="SPTREMBL:P74993"  
/translation="MVTFETVMEIKILHKQGMSS  
RAIARELGISRNTVKRYLQAKSEP  
PKYTPRPAVASLLDEYRDYIRQRIADAHYPKIPA  
TVIAREIRDQGYRGGMTILRAFIR  
SLSVPQEQEPAVRFETEPGRQMQVDWGTMRNGRS  
PLHVFVAVLGYSRMLYIEFTDNMR  
YDTLETCHRNAFRFFGGVPREVLVDNMKTVVLQR  
DAYQTGQHRFHPSLWQFGKEMGFS  
PRLCRPFRAQTKGKVERMVQYTRNSFYIPLMTRL  
RPMGITVDVETANRHGLRWLHDVA  
NQRKHETIQARPCDRWLEEQQSMLALPPEKKEYD  
VHLDENLVNFDKHLHPLHSIYDS FCRGVA"  
/misc-feature complement(114272..1148 /gene="YPO1086"  
05)  
/note="Pfam match to entry PF00665  
rve, Integrase core domain, score  
81.90, E-value 1.6e-22"  
/misc-feature complement(115034..1150 /gene="YPO1086"  
99)  
/note="Predicted helix-turn-helix  
motif with score 2147 (+6.50 SD)  
at aa 18-39, sequence  
MSSRAIARELGISRNTVKRYLQ"  
/misc-feature complement(115043..1151 /gene="YPO1086"  
26)  
/note="Pfam match to entry PF00239  
recombinase, Site-specific  
recombinases, score 25.70, E-value  
4.7e-06"  
/misc-feature complement(115209..1152 /note="IS100 inverted repeat"  
36)  
gene complement(115239..1153 /gene="intA"  
40)  
CDS complement(115239..1153 /note="synonym: YPO1086a"  
40) /partial  
/gene="intA"  
/note="Probable gene remnant.  
Similar to N-terminal regions of  
*Escherichia coli* prophage Cp4-57  
integrase IntA SW:INTA-ECOLI  
(P32053) (413 aa) fasta scores:  
E(): 2.8e-05, 61.765% id in 34 aa,  
and *Haemophilus influenzae* Cp4-57  
integrase-like protein TR:Q9L8P3  
(EMBL:AF198256) (408 aa) fasta  
scores: E(): 0.00043, 52.941% id  
in 34 aa. CDS is truncated by the  
insertion of the downstream IS100  
element and subsequent  
recombination events"  
/codon-start=1  
/transl-table=11  
/product="phage integrase  
(partial)"  
/protein-id="CAC89930.1"  
/db-xref="GI:15979154"  
/db-xref="SPTREMBL:Q8ZH27"

gene	115752..116063	KDLTLHDGDGLFLL"
CDS	115752..116063	/gene="YPO1087"
		/note="Similar to plasmid proteins. Similar to Xylella fastidiosa hypothetical protein XFA0045 TR:Q9PHG3 (EMBL:AE003851) (106 aa) fasta scores: E(): 3e-14, 54.2% id in 72 aa, and to Pseudomonas alcaligenes hypothetical 11.2 kDa protein TR:Q9XAX7 (EMBL:U88088) (99 aa) fasta scores: E(): 4e-06, 50.0% id in 54 aa"
		/codon-start=1
		/transl-table=11
		/product="putative prophage protein"
		/protein-id="CAC89931.1"
		/db-xref="GI:15979155"
		/db-xref="SPTREMBL:Q8ZH26"
		/translation="MMKTIKHYLTPEGRDLYMEY LKSLRDSIAKAKISSRVNRIASGN FGDHKPCREGVWELRIDQPGYRVYYSLVAVKSC CCFWAVISARRMPTSIRLLCVLKI I"
gene	116071..116391	/gene="YPO1088"
CDS	116071..116391	/gene="YPO1088"
		/note="Similar to Xylella fastidiosa hypothetical protein XFA0046 TR:Q9PHG2 (EMBL:AE003851) (108 aa) fasta scores: E(): 4.3e-10, 40.0% id in 95 aa, and to Pseudomonas alcaligenes hypothetical 10.3 kDa protein TR:Q9XAX6 (EMBL:U88088) (96 aa) fasta scores: E(): 2e-05, 36.6% id in 82 aa"
		/codon-start=1
		/transl-table=11
		/product="putative DNA-binding prophage protein"
		/protein-id="CAC89932.1"
		/db-xref="GI:15979156"
		/db-xref="SPTREMBL:Q8ZH25"
		/translation="MIMAKARLHDDAMVQLLMED PEFAQVYLHQALLDIDEEGGQEAF LMAIRHVVEARGGMASVAKKAGVSRETLYRTLSP SGNPTLKTLLSVVSATGFQFSHLA SITA"
misc-feature	116236..116301	/gene="YPO1088"
		/note="Predicted helix-turn-helix motif with score 1826 (+5.41 SD) at aa 56-77, sequence GGMAVAKKAGVSRETLYRTLS"
gene	complement(116740..117828)	/gene="YPO1089"
CDS	complement(116740..117828)	/gene="YPO1089"
		/note="Weakly similar to many from plasmids and bacteriophage. Similar to unidentified replication protein A repA TR:Q03086 (EMBL:M73777) (290 aa) fasta scores: E(): 6.1e-07, 30.7% id in 238 aa, and to uncultured eubacterium plasmid putative DNA helicase repA TR:Q9L3P0 (EMBL:AJ271879) (279 aa) fasta scores: E(): 0.00012, 25.7% id in 237 aa, and to Escherichia coli regulatory protein RepA repA SW:REPJ-ECOLI (P20356) (279 aa) fasta scores: E(): 0.00022, 27.6% id in 192 aa, and to uncultured eubacterium plasmid pIE1115 putative DNA helicase repA"

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aa) fasta scores: E(): 0.00036,
26.7% id in 191 aa, and to
lactococcal bacteriophage bIL170
complete genome e5 TR:O80155
(EMBL:AF009630) (316 aa) fasta
scores: E(): 0.51, 22.2% id in 203
aa"
/codon-start=1
/transl-table=11
/product="putative regulatory
prophage protein"
/protein-id="CAC89933.1"
/db-xref="GI:15979157"
/db-xref="SPTREMBL:Q8ZH24"
/translation="MKTPLILLEREVPVSLTTNLP
LRKGSDDGYNTPQDYNIKGHLPSNT
LASIYGPSGSYKSLAVSWACHIAITGKPWASRRV
TQGSVVYIIVGEGGIGVPRRIRAWG
MEFNNGGTPIESLYRIDCPVFPASPESAIQVIKAA
QDVTEQTGSPVRLIVLDTLARCFCG
GSDENAAKDMGAFFIQGCDYIKAETGATVLVIHHS
GKDLDDKGARGSSAFRAALDVEFNV
RREGDGGALVLSCTKMKDSEPTTRAYDLSPLNL
YIDNDGEEVNSLVLCCKGREVSDE
GSPYEAELASIQRLTANHIALWQSIRSRTASGEA
CTKSLVRDDMRGMGFDVAKKFTRW
LDKLETDGLIHIDGENICPNSLSNTARN"
gene complement(117825..1187 /gene="YPO1090"
84)
CDS complement(117825..1187 /gene="YPO1090"
84)

/note="Similar to the N-terminal
regions of bacteriophage P4
putative P4-specific DNA primase
alpha SW:PRIM-BPP4 (P10277) (777
aa) fasta scores: E(): 0, 35.8% id
in 324 aa, and Escherichia coli
DNA primase TraC SW:TRC5-ECOLI
(P27190) (1448 aa) fasta scores:
E(): 1.5e-10, 27.8% id in 270 aa.
Possible truncated protein."
/codon-start=1
/transl-table=11
/product="putative prophage DNA
primase"
/protein-id="CAC89934.1"
/db-xref="GI:15979158"
/db-xref="SPTREMBL:Q8ZH23"
/translation="MSRFVSDIIRASQHHWSNIL
SSLAIPIPHLNKKGPCPVCGGKDR
FRFDDKKGRGTWFCNYCGHGDGLDLVTLVRQCDV
IQAAREISRLTDLAPTAPAKERTE
QPLHSDMTQKVTALLAACSQGTSDYLLHKGLNHP
VFLMPANSAKNIGGVHFNVGSMVL
PLVDLSGNTTGALLINRRGEKRLLPKSRIKSSFI
PITHHTLSQTIIITEGFATGLVIS
RFVTATVVA AISATNLTQVAVALRERYPDAQIII
AADNDVTNSDNNPGKQQA EYAALA
VNGLVTLPPPTCGKADWDDYRQQVGTDAARIEFFR
QLYNPREWI"
gene complement(118777..1193 /gene="YPO1091"
19)
CDS complement(118777..1193 /gene="YPO1091"
19)

/note="Similar to Shigella
flexneri insertion sequence IS2
DNA TR:Q54157 (EMBL:Z23101) (179
aa) fasta scores: E(): 0.0091,
28.8% id in 132 aa, and to
Bacteriophage P4 ASH protein cI
SW:VASH-BPP4 (P05462) (137 aa)
fasta scores: E(): 0.25, 37.5% id
in 72 aa"
/codon-start=1
/transl-table=11

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protein"
/protein-id="CAC89935.1"
/db-xref="GI:15979159"
/db-xref="SPTREMBL:Q8ZH22"
/translation="MIFYFFLAGALQYNPFAAAK
SVAGISVPKIFLIPSLVIQTWSFI
GMACAHPSMVAQAGAPKGAPVSKKSGNANSVWAT
TQGISVSGGSHYNYFLEAAQWLLP
FTVCTRNTFVPIRGCAMHNSSPLTIEEIVDHCHA
LVLAMLEITDPTAKELLLFILAER
LDLLQLMLDEVPAEEANHE"
gene      complement(119512..1204 /gene="YPO1092"
08)
CDS      complement(119512..1204 /gene="YPO1092"
08)

/note="Similar to Pseudomonas
aeruginosa integrase/recombinase
XerD TR:AAG07125 (EMBL:AE004793)
(298 aa) fasta scores: E(): 0.027,
28.0% id in 239 aa, and to
Chlamydia pneumoniae
integrase/recombinase XerC or
CP0752 TR:Q9Z9F7 (EMBL:AE001587)
(312 aa) fasta scores: E(): 0.16,
23.3% id in 232 aa"
/codon-start=1
/transl-table=11
/product="putative DNA-binding
prophage protein"
/protein-id="CAC89936.1"
/db-xref="GI:15979160"
/db-xref="SPTREMBL:Q8ZH21"
/translation="MFVMSRLSREMKMLAKQAGG
SHKTVHDIRIMDRFSRHLLALNI
QVRDVKHLKAKHIESYITDRFSQGIAIRSLHNEM
AALRTVFRFAGRDKIVLSERLTNK
ALGLGGASRAGSKFAIPEEVYQAALRTAQQQDKG
LACALQLARLLGLRSQEAVQCANS
LKTWQKELEQNRSKLTVVFGTKGGRSRETRILDP
EAVKRAVKEAQQIAETRGGKLIDK
PDLKTAMNFWRSHTTRLGLTGHYSPhSLRYAWAQ
DAINYLAAGFSRIEARALTSMDL
GHGDGRGRYVERVYTRKEANYV"
misc-feature complement(120319..1203 /gene="YPO1092"
84)

/note="Predicted helix-turn-helix
motif with score 1045 (+2.75 SD)
at aa 9-30, sequence
REMKMLAKQAGGSHKTVHDIR"
gene      complement(120421..1207 /gene="YPO1092a"
11)
CDS      complement(120421..1207 /gene="YPO1092a"
11)

/note="No significant database
matches"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="CAC89937.1"
/db-xref="GI:15979161"
/db-xref="SPTREMBL:Q8ZH20"
/translation="MTPQHKPASAFEISDFTQHV
MHLTPLOQYVRLTAFYKIFEPIPRQ
ANSLGDDLQKQEAAPSASPIRNTSTAARSGAQV
SFKADNLPFPMRQRNAAS"
gene      complement(120803..1209 /gene="YPO1094"
76)
CDS      complement(120803..1209 /gene="YPO1094"
76)

/note="No significant database
matches"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="CAC89938.1"

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gene	121207..121434	/db-xref="SPTREMBL:Q8ZH19"
CDS	121207..121434	/translation="MPIGDTVIGYQLSERLASVE QRPLKPVVYHDGAVFAHLNQDASL HQKTPYTSISGAC"
		/gene="YPO1095"
		/gene="YPO1095"
		/note="No significant database matches"
		/codon-start=1
		/transl-table=11
		/product="hypothetical protein"
		/protein-id="CAC89939.1"
		/db-xref="GI:15979163"
		/db-xref="SPTREMBL:Q8ZH18"
		/translation="MQVIRIILILETLGAVIDSE FTWGKLRQKLNSGKLLAVIRKSN ERGATSLSNLCHLRIFPLASLPKRALHAYSA"
misc-feature	121566..124482	/note="Low GC region"
gene	complement(121596..1232	/gene="YPO1096"
	66)	
CDS	complement(121596..1232	/gene="YPO1096"
	66)	
		/note="No significant database matches"
		/codon-start=1
		/transl-table=11
		/product="putative phage protein"
		/protein-id="CAC89940.1"
		/db-xref="GI:15979164"
		/db-xref="SPTREMBL:Q8ZH17"
		/translation="MKKLILKKIMILSDSGKSAR QFEFGEHLTLITADDDNSVGKSTL AKMIFWTFGCEPIFSEVWRTLDCTSIIEFEINNA PYIIHRYKNEIKIRHSNGKLHSFP KITGDYSKYFSELVNFNVLLPKKGQLTLETPPPA YYFIPFYIDQKRTWAKPWDSFENL QQYSSWAKPVISYHSGLFKAHFEVEKDIYVIKR ELEEEVEKGVTELNNAVIILRQNLI DTDNVLPSTEFIFSVIQESEKNKKNLLEERTNLR VEKIRLESQIKLAKGIISELDKDY IFSVENMEDGDIECPTCGTIHENSIAHRTSILID MELAKNQLESLESEVNGIINLLVI KDEEITEQSNKSERSYNNVIESDSNSLISFTNDK FEKRAHEINSKKNITIEIKKSEEK TAKKSQSDILSKEQKSEIKQSFADRLSKYITKLK VNVDISKIKSPLDYKKIYEVGGAA EDARAVLGYYLAIYEQVADSCEEALPPLVIDTPN QQEQASGNYTNIKSISDGINNDR QYVICAMEHKALEQIKTNAQVIKLDARKILLQDQ YEKISKLRNEVIFD"
gene	complement(123317..1244	/gene="YPO1097"
	05)	
CDS	complement(123317..1244	/gene="YPO1097"
	05)	
		/note="No significant database matches"
		/codon-start=1
		/transl-table=11
		/product="putative phage protein"
		/protein-id="CAC89941.1"
		/db-xref="GI:15979165"
		/db-xref="SPTREMBL:Q8ZH16"
		/translation="MDSEDTSNPLSEPQRESAG AQSYPDREYQYHWALCKAFSSYKE SNDFAIEMEYHEDVVYANSIDKNKVKFTFNQIKA NAKKTYTAKVLTGRENGTKPSLLG KLCSSVSDKKYFEKVEKLDFITTSGFNLTKNNKL NLASYKLSSLSSDEASEIIKCLSD ELANFGKFPPQEIIHFTTSDIPLESYYEHTISRIT DSVEEVYPQHLLRTKDIYRILMDS LRIRGKNVFDYENWNDALTKKALTYKDIHTVVTK IVSKGNSDLNFEAIKYILDDLNLK GTIKAKIIQKINSYSLTLLSPTLAIIKAQKEIQE LLKKNSKKIEIEMSYELLERLIID LSKDTIGLFEDNISISSAIYEMVEATN"

	83)	complement(124484..1256 /gene="YPO1098"	/note="Similar to Escherichia coli prophage CP4-57 integrase SW:INTA-ECOLI (P32053) (413 aa) fasta scores: E(): 0, 57.8% id in 389 aa, and to Vibrio cholerae phage integrase VC0516 TR:Q9KUK2 (EMBL:AE004138) (413 aa) fasta scores: E(): 0, 52.7% id in 393 aa" /codon-start=1 /transl-table=11 /product="putative prophage integrase" /protein-id="CAC89942.1" /db-xref="GI:15979166" /db-xref="SPTREMBL:Q8ZH15" /translation="MARTTRPLTHTEVQKAKATD KDLTLHDGDLFLLVKTTGKKIWR FRYQLPNSSKRTMISLGAYPALSLADAREIRA EKLQIA EESIFVNVARKWFELKESHVSAAHAKDIWRSIEK DILPSIENIPIQELKARTLIQVLE PIKARGALETVRRLVQRINEIMIYAVNVGLIDAN PASGIGNAFERPKKQHMPTIRPEE LPKLMRTIAMSNSLPTRCLEWQLLTLIRPAEA SATAWIEIDLLENKQWCIPAERMKA KRDHIVPLSEQALELLEIMRPISGNRQHVFP SRN DPRNHMNSQTANAALKRIGYGGKL VAHGLRSIASTAMNEAGFNADVIEAALAHSDKNE VRKAYNRSTYLIQRQELMNWWGLE IYTKRSI"
misc-feature	complement(124535..1250 62)	/gene="YPO1098"	/note="Pfam match to entry PF00589 Phage-integrase, Phage integrase family, score 116.60, E-value 4.7e-31"
misc-feature	complement(125799..1265 10)	/gene="tnp"	/note="IS200-like insertion sequence: IS1541. Contains an 'A' at nucleotide position 315."
gene	complement(125907..1263 65)	/gene="tnp"	/note="synonym: YPO1099"
CDS	complement(125907..1263 65)	/gene="tnp"	/note="Similar to Salmonella typhimurium and Salmonella typhi transposase for insertion sequence IS200, TnpA, SW:TNPA-SALTY (Q57334) (152 aa) fasta scores: E(): 0, 93.4% id in 152 aa. Almost identical to the Yersinia pseudotuberculosis IS1541 element transposase Tnp TR:Q9X9F5 (EMBL:AJ238014) (152 aa) fasta scores: E(): 0, 99.3% id in 152 aa" /codon-start=1 /transl-table=11 /product="transposase for the IS1541 insertion element" /protein-id="CAC89943.1" /db-xref="GI:15979167" /db-xref="SPTREMBL:Q56938" /translation="MRDEKSLAHTRWCKYHIVF APKYRRQVFYREKRRRAIGSILRKL CEWKNVNILEAEYCVDHIHMLLEIPPKMSVSGFM GYLKKGKSSMLYEQFGDLKFKYRN REFWCRGYVDTVGKNTARIQEIYIKHQLEEDKMG EQLSIPYPGSPFTGRK"
misc-feature	complement(126000..1263 11)	/gene="tnp"	/note="Pfam match to entry PF01797"

gene	126588..126951	like, -score 230.20, E-value 3e-65"
misc-RNA	126588..126951	/gene="ssrA"
		/gene="ssrA"
		/note="Similar to Escherichia coli small stable RNA molecule, tmRNA [10Sa RNA] (D12501), 91% identity in 333 nt overlap"
gene	complement(127000..127482)	/gene="smpB"
		/note="synonyms: b2620, smqB, YPO1101"
CDS	complement(127000..127482)	/gene="smpB"
		/note="Similar to Escherichia coli SsrA-binding protein SmpB SW:SMPB-ECOLI (P32052) (159 aa) fasta scores: E(): 0, 84.9% id in 159 aa, and to Vibrio cholerae SsrA-binding protein small protein B TR:Q9KTQ3 (EMBL:AE004170) (161 aa) fasta scores: E(): 0, 67.7% id in 161 aa"
		/codon-start=1
		/transl-table=11
		/product="SsrA-binding protein (small protein B)"
		/protein-id="CAC89944.1"
		/db-xref="GI:15979168"
		/db-xref="SWISS-PROT:Q8ZH14"
		/translation="MTKKKAYKPGSATIAQNKRA RHEYFIEEEFEAGLALQGWEVKSL RAGKANISDSYVMFKNGEAFLEFGATITPLNVAST HVVCEPMRTRKLLLNKRELDLSLFG RVNREGYTVVALSMYWKNAWVKVIGVAKGKKDN DKRDDIRDREWKLDKARIMKHANR "
misc-feature	complement(127243..127449)	/gene="smpB"
		/note="Pfam match to entry PF01668 SmpB, SmpB protein, score 161.50, E-value 1.4e-44"
misc-feature	complement(127351..127389)	/gene="smpB"
		/note="PS01317 Protein smpB signature."
gene	127643..128077	/gene="YPO1102"
CDS	127643..128077	/gene="YPO1102"
		/note="Similar to Escherichia coli hypothetical protein YfjG SW:YFJG-ECOLI (P52121) (158 aa) fasta scores: E(): 0, 79.3% id in 145 aa, and to Vibrio cholerae hypothetical protein VC0849 SW:Y849-VIBCH (P52122) (144 aa) fasta scores: E(): 0, 69.0% id in 142 aa"
		/codon-start=1
		/transl-table=11
		/product="conserved hypothetical protein"
		/protein-id="CAC89945.1"
		/db-xref="GI:15979169"
		/db-xref="SPTREMBL:Q8ZH13"
		/translation="MPQISRSALVPFSVKQMYQL VNDVRSYPEFLPGCTGSRVLDATE NEMIAAVDVAKAGISKTFTRNTLTDNQ SINMQL VDGPFPRKLMGGWHFTPLSADACKV ELHLDFFEFTNKLIELAFGKIFKELAGNMVQAFTQ RAKEVYSA"
gene	128070..128354	/gene="YPO1103"
CDS	128070..128354	/gene="YPO1103"
		/note="Similar to Escherichia coli hypothetical protein YfjF SW:YFJF-ECOLI (P52119) (96 aa) fasta scores: E(): 5.8e-24, 76.4% id in 89 aa, and to Vibrio



		SW:YFJF-VIBCH (P52120) (101 aa) fasta scores: E(): 2.4e-17, 60.9% id in 92 aa" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAC89946.1" /db-xref="GI:15979170" /db-xref="SWISS-PROT:Q8ZH12" /translation="MPDIRVEVVYALSERQYLRT VSLVVGSTVEDAIKASGLLELRPD IDLEKNKVGIYSRPVKLGDKLNDGDRVEIYRPLI ADPKELRRQRAEQAKK" /gene="YPO1104"
gene	complement(128504..1288	
	54)	
CDS	complement(128504..1288	/gene="YPO1104"
	54)	
		/note="Similar to Escherichia coli small protein A precursor SmpA SW:SMPA-ECOLI (P23089) (113 aa) fasta scores: E(): 0, 78.8% id in 113 aa, and to Vibrio cholerae small protein A homolog precursor SmpA TR:Q9KTQ0 (EMBL:AE004170) (136 aa) fasta scores: E(): 3.1e-12, 36.8% id in 114 aa" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAC89947.1" /db-xref="GI:15979171" /db-xref="SPTREMBL:Q8ZH11" /translation="MITMRCKMLTAAAVMLAMLT AGCSTLEKVVYRPDINQGNYSPI DASKIHKGMTQQQVAYTLGTPMLQDPFGTQTWFFY VFRQQPGHEKITQQTTLTLTFDSSG VLTDIKNEPALTGS" /gene="YPO1104"
misc-feature	complement(128786..1288	
	18)	
		/note="PS00013 Prokaryotic membrane lipoprotein lipid attachment site."
gene	complement(128959..1306	/gene="YPO1105"
	38)	
CDS	complement(128959..1306	/gene="YPO1105"
	38)	
		/note="Similar to Escherichia coli DNA repair protein RecN SW:REC�-ECOLI (P05824) (553 aa) fasta scores: E(): 0, 74.3% id in 553 aa, and to Vibrio cholerae DNA repair protein RecN SW:REC�-VIBCH (P52118) (554 aa) fasta scores: E(): 0, 53.7% id in 553 aa" /codon-start=1 /transl-table=11 /product="DNA repair protein RecN" /protein-id="CAC89948.1" /db-xref="GI:15979172" /db-xref="SPTREMBL:Q8ZH10" /translation="MYRGFTMLVQLTISNFAIVR ELEIDFQPGMTAITGETGAGKSIA VDALGLCLGNRSDGSMVRLGATRADICARFSLAD TPSARQWLENNHLLDDNNECLLRA IGADGRSRGFINGTPVPVSQLRELQHLIQIHGQ HAHQLLLKPDHQKQLLDAYANQSS LLAEMKAAAYQIWHQSCRDLALHQQSLERTARQE LLQYQLKELNSFSPQAGEYEQIDI EYKRLANSQGQLLSLSQQTLLQLLSDDEQNNILSQL YAAKHQLTELASMDEQFNLLNML EEASIQISEASDELRYHAEQLDMDPNRLYELEKR LSRQLNLARKHHVAPEELPQFHQQ LLDEQELLSQQENDHEQLSNAVNTHYQQALAIK"

SMPHKGFAIETIFEPEHLSAEGATRIEFCVTTNP  
 GQPLQALVKVASGGELSRIALAIQ  
 VITARKMDTPALIFDEVDVGISGPTAAIVGRLLR  
 QLGESTQVMCVTHLPQVAGCGHQH  
 FFVSKQTDGTETETETHMRLDKKARLQELARLLGG  
 SEVTKNLTLANAKELLAA"  
 /gene="YPO1105"  
 /note="PS00017 ATP/GTP-binding  
 site motif A (P-loop)."

misc-feature complement(130513..130536)  
 gene complement(130707..131588)  
 CDS complement(130707..131588)  
 /gene="YPO1106"  
 /note="Similar to Escherichia coli  
 hypothetical protein YfjB  
 SW:YFJB-ECOLI (P37768) (292 aa)  
 fasta scores: E(): 0, 82.9% id in  
 293 aa, and to Vibrio cholerae  
 hypothetical protein VC0853  
 TR:Q9KTP8 (EMBL:AE004170) (294 aa)  
 fasta scores: E(): 0, 59.3% id in  
 290 aa"  
 /codon-start=1  
 /transl-table=11  
 /product="conserved hypothetical  
 protein"  
 /protein-id="CAC89949.1"  
 /db-xref="GI:15979173"  
 /db-xref="SWISS-PROT:Q8ZH09"  
 /translation="MNNRRFDCIGIVGHPRHPAA  
 LATHEILYHWLKARGYAVMVEQQI  
 AHDNLNLDAITGSLADIGQKADLAVVVG DGNML  
 GAARVLARYDIK VIGVNRGNLGLF  
 TDLDPDNALQQLSDVLEGEYLSEQRFLLETHVRR  
 TNQQSRISTAINEVVLHPGKVAHM  
 IEFEVYIDDRFAFSQRS DGLIATPTGSTAYSLS  
 AGGPILTPTLDAIVLVPMFPHTLT  
 ARPLVISSSSSTIRLKF SHITSDLEISCDSQIALP  
 IQEGEEVLIRRSDFHLNLIHPKDY  
 SYFNTLSTKL GWSKKLF"  
 /gene="YPO1106"  
 /note="Pfam match to entry PF01513  
 DUF15, Domain of unknown function  
 DUF15, score 397.30, E-value  
 1.5e-115"

misc-feature complement(130746..131522)  
 gene 131712..132290  
 CDS 131712..132290  
 /gene="YPO1107"  
 /note="Similar to Escherichia coli  
 GrpE protein SW:GRPE-ECOLI  
 (P09372) (197 aa) fasta scores:  
 E(): 0, 59.2% id in 179 aa, and to  
 Vibrio cholerae GrpE protein  
 TR:Q9KTP7 (EMBL:AE004170) (200 aa)  
 fasta scores: E(): 2.1e-28, 53.9%  
 id in 167 aa"  
 /codon-start=1  
 /transl-table=11  
 /product="heat shock protein GrpE"  
 /protein-id="CAC89950.1"  
 /db-xref="GI:15979174"  
 /db-xref="SPTREMBL:Q8ZH08"  
 /translation="MSSKEQKTPNEQVSEEMENT  
 AEQQVEATQETGECVDP RVAELEV  
 QLSDALQRERESLLRAKAEVENIRRRTEL DVEKA  
 HKFALERFSSELLPVIDNLERALD  
 TADKTNTELISMIEGVELTLKSLLD AVGKFGIEV  
 VGETHVFPFNPEVHQAMTMLESADH  
 EPNHVMVMVMQKGYTLNGRLLRPAMVA VSKAKS"  
 /gene="YPO1107"  
 /note="Pfam match to entry PF01025  
 GrpE, GrpE, score 240.00, E-value  
 3.2e-68"

misc-feature 131778..132278  
 misc-feature 132141..132272  
 /gene="YPO1107"

gene	complement(132398..133678)	signature." /gene="gltA"  /note="synonyms: gluT, icdB, YPO1108" /gene="gltA"  /EC-number="4.1.3.7" /note="Similar to Escherichia coli citrate synthase GltA SW:CISY-ECOLI (P00891) (427 aa) fasta scores: E(): 0, 86.7% id in 427 aa, and to Vibrio cholerae citrate synthase VC2092 TR:Q9KQA8 (EMBL:AE004283) (431 aa) fasta scores: E(): 0, 78.0% id in 422 aa" /codon-start=1 /transl-table=11 /product="citrate synthase GltA" /protein-id="CAC89951.1" /db-xref="GI:15979175" /db-xref="SPTREMBL:Q8ZH07" /translation="MADKKATLNLGEAAIELGVL SPTLGTDVIDVRTLGSKGYFTFDP GFTSTASCESKITYIDGDQGILLHRGFPIAQLAK DSTYLEVCYILLYGETPTPEEYKT FKTTTVTRHTMIHEQITRLFHGFRRDSPMAVLCG VTGALAAFYHDALDVNNERHREIT AFRLLSKMPTVAAMCYKYSLGQPFVYPRNDLSYA GNFLHMMFSTPCEKYEVPVLER MDRILILHADHEQNASTSTVRTAGSSGANPFACI AAGIASLWGPAGGGANEACLKMLE EIKTVEHIPEFIRRAKDKNDSFRLMGFGHRVYKN YDPRATVMRETCEVLEELKLNS LLEVAMELENIALNDPYFIEKKLYPNVDFYSGII LKAMGIPSSMFTVIFAIARTIGWI AHWNEMHNDGIKIARPRQLYTGTERDFQSQLKK "
CDS	complement(132398..133678)	
misc-feature	complement(132455..133546)	/gene="gltA"  /note="Pfam match to entry PF00285 citrate-synt, Citrate synthase, score 783.50, E-value 4.5e-246"
misc-feature	complement(132737..132775)	/gene="gltA"  /note="PS00480 Citrate synthase signature."
gene	134388..134777	/gene="sdhC" /note="synonyms: cybA, YPO1109"
CDS	134388..134777	/gene="sdhC" /note="Similar to Escherichia coli succinate dehydrogenase cytochrome b556 subunit SdhC SW:DHSC-ECOLI (P10446) (129 aa) fasta scores: E(): 0, 77.2% id in 127 aa, and to Vibrio cholerae succinate dehydrogenase, cytochrome b556 subunit VC2091 TR:Q9KQA9 (EMBL:AE004283) (130 aa) fasta scores: E(): 0, 75.0% id in 124 aa" /codon-start=1 /transl-table=11 /product="succinate dehydrogenase cytochrome b-556 subunit" /protein-id="CAC89952.1" /db-xref="GI:15979176" /db-xref="SPTREMBL:Q8ZH06" /translation="MGKTVKKQRPVNLDLQTIRF PVTAIASILHRVSGVITFVAVGIL LWLLGLSVSSQEGFMAATIMNSFFVKFIFWGIL TALAYHICGGIRHLLMDFGYLEEN LAVGTRSAQVAMGLTLVLSVLAGVLVW"
misc-feature	134403..134756	/gene="sdhC"

		Sdh-cyt, Succinate dehydrogenase cytochrome b subunit, score 165.60, E-value 8.3e-46"
misc-feature	134412..134486	/gene="sdhC" /note="PS01000 Succinate dehydrogenase cytochrome b subunit signature 1."
misc-feature	134472..134540	/gene="sdhC" /note="one of 3 probable transmembrane helices predicted for YPO1109 by TMHMM2.0"
misc-feature	134601..134669	/gene="sdhC" /note="one of 3 probable transmembrane helices predicted for YPO1109 by TMHMM2.0"
misc-feature	134637..134678	/gene="sdhC" /note="PS01001 Succinate dehydrogenase cytochrome b subunit signature 2."
misc-feature	134712..134771	/gene="sdhC" /note="one of 3 probable transmembrane helices predicted for YPO1109 by TMHMM2.0"
gene	134771..135118	/gene="sdhD" /note="synonym: YPO1110"
CDS	134771..135118	/gene="sdhD" /note="Similar to Escherichia coli succinate dehydrogenase hydrophobic membrane anchor protein SdhD SW:DHSD-ECOLI (P10445) (115 aa) fasta scores: E(): 1.9e-32, 69.3% id in 114 aa, and to Vibrio cholerae succinate dehydrogenase, hydrophobic membrane anchor protein VC2090 TR:Q9KQB0 (EMBL:AE004283) (114 aa) fasta scores: E(): 1.1e-23, 57.4% id in 115 aa" /codon-start=1 /transl-table=11 /product="succinate dehydrogenase hydrophobic membrane anchor protein" /protein-id="CAC89953.1" /db-xref="GI:15979177" /db-xref="SPTREMBL:Q8ZH05" /translation="MVSNASALGRNGVHDWLLLR ASAIVITLYVFYILGFVVIVPDIT YEIWRGFFASHITKVFTLLTLLSILAHAWIGLWQ VLTDYIKPLAIRLVQLVTVVITLL VYLLYGTIVVWGA"
misc-feature	134819..134887	/gene="sdhD" /note="one of 3 probable transmembrane helices predicted for YPO1110 by TMHMM2.0"
misc-feature	134945..135013	/gene="sdhD" /note="one of 3 probable transmembrane helices predicted for YPO1110 by TMHMM2.0"
misc-feature	135041..135109	/gene="sdhD" /note="one of 3 probable transmembrane helices predicted for YPO1110 by TMHMM2.0"
gene	135119..136885	/gene="sdhA" /note="synonym: YPO1111"
CDS	135119..136885	/gene="sdhA" /EC-number="1.3.99.1" /note="Similar to Escherichia coli succinate dehydrogenase flavoprotein subunit SdhA SW:DHSA-ECOLI (P10444) (588 aa) fasta scores: E(): 0, 92.0% id in 588 aa, and to Vibrio cholerae succinate dehydrogenase, flavoprotein subunit VC2089"

		fasta scores: E(): 0, 82.3% id in 588 aa" /codon-start=1 /transl-table=11 /product="succinate dehydrogenase flavoprotein subunit" /protein-id="CAC89954.1" /db-xref="GI:15979178" /db-xref="SPTREMBL:Q8ZH04" /translation="MNLPIREFDAVVVGAGGAGM RAALQISQMGLSCALISKVFPTRS HTVSAQGGITVALGNTHEDNWEWHMYDTVKGS DY IGDQDAIEYMCKTGPEAVLELEHM GLPFSRLEDGSIYQRPFGGQSLNFGGGQAARTAA AADRTGHALLHTLYQQNLKNHTTI FSEWYALDLVKNQDGA FVGCTAINIETGEVVYFK ARATILATGGAGRIYQSTTNAHIN TGDGVGMALRAGVPVQDMEMWQFHPTGIAGAGVL VTEGCRGEGGYLLNKHGERFMERY APNAKDLAGR DVVARSIMIEIREGRGCDGPWGP AKLKLDHLGKDVLESRLPGILELS RTFAHVDPIKEPIPVIPPTCHYMMGGIPTKVTGQA ITVNEKGEDVVIPGLFAVGEIACV SVHGANRLGGNSLLDLVVFGRAAGMHLQESLMEQ GASRDASESDIEASLARMNRWNNT RSGEDPVEIRKALQACMQNNFSVFREGDAMAKGL EELKTIRERLQARLDDTSSEFNT QRIECLELDNLMETAFSTAVSANFRTESRGAHSR FDFPDRDDVNWLCHSLYLPGTESM TRREVMQPKLREAFPPKVR SY" /gene="sdhA" /note="PS00504 Fumarate reductase / succinate dehydrogenase FAD-binding site."
misc-feature	135245..135274	
misc-feature	135440..136438	/gene="sdhA" /note="Pfam match to entry PF00890 FAD-binding-2, FAD binding domain, score 733.90, E-value 7.1e-217"
gene	136935..137651	/gene="sdhB" /note="synonym: YPO1112"
CDS	136935..137651	/gene="sdhB" /EC-number="1.3.99.1" /note="Similar to Escherichia coli succinate dehydrogenase iron-sulfur protein SdhB SW:DHSB-ECOLI (P07014) (238 aa) fasta scores: E(): 0, 90.8% id in 238 aa, and to Vibrio cholerae succinate dehydrogenase, iron-sulfur protein VC2088 TR:Q9KQB2 (EMBL:AE004283) (236 aa) fasta scores: E(): 0, 80.2% id in 237 aa" /codon-start=1 /transl-table=11 /product="succinate dehydrogenase iron-sulfur protein" /protein-id="CAC89955.1" /db-xref="GI:15979179" /db-xref="SPTREMBL:Q8ZH03" /translation="MKLEFSIYRYNPDVDNAPHM QDYTLDAEEGRDMMLLDALIQLKE KDPTLSFRRSCREGVCGSDGLNMNGKNGLACITP ISALQKGNKKIVIRPLPGLPVVRD LVVDMGQFYTQYEKIKPYLLNDGKNPPAREHLQS PEQRAKLDGLYECILCACCSTSCP SFWWNPDKFVGPAGLLAAYRFLIDSRDTETASRL DDLDDAFSVFRCHSIMNCVSVCPK GLNPTKAIGHIKSMMLLQRSA"
misc-feature	136980..137177	/gene="sdhB" /note="Pfam match to entry PF00111 fer2, 2Fe-2S iron-sulfur cluster binding domains, score 8.70, E-value 0.96"
misc-feature	137379..137414	/gene="sdhB"

gene	138007..140814	iron-sulfur binding region signature." /gene="sucA" /note="synonym: YPO1113" /gene="sucA" /EC-number="1.2.4.2" /note="Similar to Escherichia coli 2-oxoglutarate dehydrogenase E1 component SucA SW:ODO1-ECOLI (P07015) (933 aa) fasta scores: E(): 0, 87.8% id in 935 aa, and to Vibrio cholerae 2-oxoglutarate dehydrogenase, E1 component VC2087 TR:Q9KQB3 (EMBL:AE004282) (936 aa) fasta scores: E(): 0, 73.8% id in 936 aa" /codon-start=1 /transl-table=11 /product="2-oxoglutarate dehydrogenase E1 component" /protein-id="CAC89956.1" /db-xref="GI:15979180" /db-xref="SPTREMBL:Q8ZH02" /translation="MQNGAMKAWLDSSYLAGANQ SYIEQLYEDFLTDPGSVDDSWRSI FQQLPTTGVPKPDQLHSQTREYFRRILAKDSTRYNS SINDPDIDAKQVKVLQLINAFRR GHQHANLDPGLWKQESVPDLDPSTYHNLTEADFQ NTFNVGSFAIGKETMKLADLYAAL KQTYCGSVGAEYMHITNTEEKRWIQQRIESVVGK PTFSDAEKRRFLSELTAEEGLERY LGAKFPGAKRFSLEGGDSLVTMLKEMIRHAGKNG TREVVLGMAHRGRLNVLINVLGKK PEDLFDEFAGKKHKEHLGTGDVKYHQGFSSDVETE GGLVHLALAFNPSHLEIVSPVIG SVRARRDRDLDEARSNMVLPIITIHGDAAITGQGVV QETLNMSQARGYEVGGTVRIVINN QIGFTTSNPLDARSTQYCTDIKVMQAPIFHVNA DDPEAVAFVTRLALDFRNTFKRDV MIDLVCYRRHGHNEADEPSATQPVMYQKIKKHPT PRKIYADKLI EQNIASLEDATEMV NLYRDALDHGDCVVEWRPMLNLSFTWSPYLNHE WDEAYPSKVEMKRLQELARRISSA PEAIEMQSRVAKIYSDRALMASGEKPFDWGGAET LAYATLVDEGIPIRLSGEDAGRGT FFHRHAVIHNQKNGSVYVPLSNIHSGQGDFQVWD SVLSEEAVLAFEYGYATAEPRTL IWEAQFGDFANGAQVVIDQFISSGEQKWGRMCGL VMLLPHGYEGQGPEHSSARLERYL QLCAEQNMQVCIPSTPAQVYHMIRRALRGMRRP LIVMSPKSLRLRHPLATSSSLDELAN GSFLPAIGEIDELDPKGIKRVVMCSGKVYYDLLE QRRKNGQTDVAIVRIEQLYPFPHQ AVQSVLEQYAHVHDFVWCQEEPLNQAWYCSQHN FREVIPIFGASLRYAGRPASASPAV GYLSVHQKQQQALVNDALNVE"
misc-feature	138625..139599	/gene="sucA" /note="Pfam match to entry PF00676 E1-dehydrog, Dehydrogenase E1 component, score 115.00, E-value 1.5e-30"
gene	140844..142067	/gene="sucB" /note="synonym: YPO1114"
CDS	140844..142067	/gene="sucB" /EC-number="2.3.1.61" /note="Similar to Escherichia coli dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex SucB SW:ODO2-ECOLI (P07016) (404 aa) fasta scores: E(): 0, 84.2% id in 406 aa, and to Vibrio cholerae 2-oxoglutarate dehydrogenase, E2 component, dihydrolipoamide"

TR:Q9KQB4 (EMBL:AE004282) (404 aa)  
fasta scores: E(): 0, 75.1% id in  
405 aa"  
/codon-start=1  
/transl-table=11  
/product="dihydrolipoamide  
succinyltransferase component of  
2-oxoglutarate dehydrogenase  
complex"  
/protein-id="CAC89957.1"  
/db-xref="GI:15979181"  
/db-xref="SPTREMBL:Q8ZH01"  
/translation="MSSVDINVPDLPESVADGSV  
ATWHKKPGDSVKRDEVLVEIETDK  
VILEVPASQDGIILDAILEDGATVTSRQVLGRIR  
PSDSSGKPTEEKSQSTESTPAQRQ  
TASLEEEESNETLSPAIRRLIAEHDLDATAIKGSG  
VGGRITREDVDSHLASRKASAVV  
ADAKAVAAAAPVLAGRSEKRVPMRLRKRVAERL  
LEAKNSTAMLTTFNEINMQPIMDL  
RKQYGEAFEKRHGVRLGFMSEFYIKAVVEALKRYP  
EVNASIDGEDVVYHNYFDVSIASV  
TPRGLVTPVLRDVTLSMADIEKKIKELAVKGRD  
GKLKVEELTGGNFTITNGGVFGSL  
MSTPIINPPQSAILGMHAIKDRPMAVNGQVVILP  
MMYLALSVDHRLIDGRESVGYLVT  
VKEMLEDPARLLLLDV"

misc-feature 140853..141074

/gene="sucB"  
/note="Pfam match to entry PF00364  
biotin-lipoyl, Biotin-requiring  
enzymes, score 90.40, E-value  
3.7e-23"

misc-feature 141402..142061

/gene="sucB"  
/note="Pfam match to entry PF00198  
2-oxoacid-dh, 2-oxo acid  
dehydrogenases acyltransferase  
(catalytic domain), score 364.60,  
E-value 1e-105"

gene 142180..143346

/gene="sucC"  
/note="synonyms: b0728, YPO1115"

CDS 142180..143346

/gene="sucC"  
/EC-number="6.2.1.5"  
/note="Similar to Escherichia coli  
succinyl-CoA synthetase beta chain  
SW:SUC-ECOLI (P07460) (388 aa)  
fasta scores: E(): 0, 92.8% id in  
388 aa, and to Vibrio cholerae  
succinyl-CoA synthase, beta  
subunit VC2085 TR:Q9KQB5  
(EMBL:AE004282) (388 aa) fasta  
scores: E(): 0, 77.1% id in 388  
aa"

/codon-start=1  
/transl-table=11  
/product="succinyl-CoA synthetase  
beta chain"  
/protein-id="CAC89958.1"  
/db-xref="GI:15979182"  
/db-xref="SWISS-PROT:Q8ZH00"  
/translation="MNLHEYQAKQLFARYGMPAP  
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VKCQVHAGGRGKAGGVKLVNSKEDIRAFAEQWL  
KKLVITYQTDANGQPVHQILVEAAT  
DIDKELYLGAVIDRSSRRVVFMASTEGGVEIEKV  
AEETPELIHKIALDPLTGPQPYQG  
RELAFKLGLTGKQVGQFTKIFMGLATLFLERDLA  
MVEINPLVVTKQGDILCLDGKLG  
DGNALFRQPELREMRDPSQEDAREAHAAQWELNY  
VALDGNIGCMVNGAGLAMGTMDIV  
KLHGGEPAFLDVGGGATKERVTEAFKIILSDDK  
VKAVFVNIFGGIVRCDLIADGIIG  
AVEEVGVNVPVVVRLEGNNALGAKKLADSG  
LNIAATSLTDAAQQVVAAGVAK"

misc-feature 142264..142773

/gene="sucC"  
/note="Pfam match to entry PF02222"



misc-feature	142915..143343	213.20, E-value 4e-60" /gene="sucC" /note="Pfam match to entry PF00549 ligase-CoA, CoA-ligases, score 280.20, E-value 2.6e-80"
misc-feature	142948..143022	/gene="sucC" /note="PS01217 ATP-citrate lyase / succinyl-CoA ligases family signature 3."
gene	143346..144218	/gene="sucD" /note="synonym: YPO1116"
CDS	143346..144218	/gene="sucD" /EC-number="6.2.1.5" /note="Similar to Escherichia coli succinyl-CoA synthetase alpha chain SW:SUCD-ECOLI (P07459) (288 aa) fasta scores: E(): 0, 90.9% id in 287 aa, and to Vibrio cholerae succinyl-CoA synthase, alpha subunit VC2084 TR:Q9KQB6 (EMBL:AE004282) (290 aa) fasta scores: E(): 0, 85.4% id in 287 aa" /codon-start=1 /transl-table=11 /product="succinyl-CoA synthetase alpha chain" /protein-id="CAC89959.1" /db-xref="GI:15979183" /db-xref="SPTREMBL:Q8ZGZ9" /translation="MSILIDKNTKVICQGFTGSQ GTFHSEQAIAYGTKMVGGVTPGKG GTQHLGLPVFNTVREAVETTGATASVIYVPAPFC KDSILEAIDAGIKLIICITEGIPT LDMLVVKVRLEQSDARMIGPNCPGVITPGECKIG IMPGHIHLPGKVGIVSRSGTLTYE AVKQTTDIGFGQSSCVGIGDPIPGSNFIDILKL FQEDPQTEVIVMIGEIGGNAEEEA AAYIKEHVTKPVVGYIAGVTAPKKGKRMGHAGAI AGGKGTADDKFAALEAAGVKT VRS LAEIGNAVKAVLPQ"
misc-feature	143742..144185	/gene="sucD" /note="Pfam match to entry PF00549 ligase-CoA, CoA-ligases, score 225.20, E-value 9.4e-64"
misc-feature	143799..143888	/gene="sucD" /note="PS01216 ATP-citrate lyase / succinyl-CoA ligases family signature 1."
misc-feature	144051..144092	/gene="sucD" /note="PS00399 ATP-citrate lyase / succinyl-CoA ligases family active site."
gene	144985..146553	/gene="cydA" /note="synonym: YPO1117"
CDS	144985..146553	/gene="cydA" /EC-number="1.10.3.-" /note="Similar to Escherichia coli cytochrome D ubiquinol oxidase subunit I SW:CYDA-ECOLI (P11026) (522 aa) fasta scores: E(): 0, 86.6% id in 522 aa" /codon-start=1 /transl-table=11 /product="cytochrome D ubiquinol oxidase subunit I" /protein-id="CAC89960.1" /db-xref="GI:15979184" /db-xref="SPTREMBL:Q8ZGZ8" /translation="MFDIVELSRLOFALTAMYHF LFVPLTLGLAFLLAIMESVYVLSG KQIYKDMTKFWGKLFAINFALGVATGLTMEFQFG TNWSYFSHYVGDI FGAPLAIEGLM AFFLESTFVGLFFFGWDR LTKHQHLAVTWLVALG SNFSALWILVANGWMQNPIASDFN"

GAMFILGISSYYLLKGRDIPFAKR  
 SFAIAASFGLASVLSVIVLGDESGYEMGDVQKTK  
 LAAIEAEWETQPPPAFTLFAIPN  
 QETMENRFAIQIPYALGLIATRS�DTPVIGLRDL  
 MSQHEVRIRNGIQAYSLLLEQLRGG  
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 EEQIQLAAQDSIPRVLPYFAFRI  
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 LYGIPLPWIAVEAGWFVAEYGRQP  
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 /note="Pfam match to entry PF01654  
 Bac-Ubq-Cox, Bacterial Cytochrome  
 Ubiquinol Oxidase, score 1092.40,  
 E-value 0"  
 /gene="cydA"  
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 for YPO1117 by TMHMM2.0"  
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 for YPO1117 by TMHMM2.0"  
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 transmembrane helices predicted  
 for YPO1117 by TMHMM2.0"  
 /gene="cydB"  
 /note="synonym: YPO1118"  
 /gene="cydB"  
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 /note="Similar to Escherichia coli  
 cytochrome D ubiquinol oxidase  
 subunit II SW:CYDB-ECOLI (P11027)  
 (379 aa) fasta scores: E(): 0,  
 78.4% id in 379 aa"  
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 /product="cytochrome D ubiquinol  
 oxidase subunit II"  
 /protein-id="CAC89961.1"  
 /db-xref="GI:15979185"  
 /db-xref="SPTREMBL:Q8ZGZ7"  
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 YAAAFSGFYIAMILVLAALFFRPV  
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 AFGNLLQGVPFHMNEYMRLFYTGN

misc-feature	145003..146517
misc-feature	145042..145110
misc-feature	145144..145212
misc-feature	145270..145338
misc-feature	145357..145425
misc-feature	145537..145605
misc-feature	145639..145698
misc-feature	146143..146211
misc-feature	146245..146313
misc-feature	146380..146448
gene	146568..147707
CDS	146568..147707

misc-feature 146580..147668

misc-feature 146586..146639

misc-feature 146799..146867

misc-feature 146928..146996

misc-feature 147054..147122

misc-feature 147183..147236

misc-feature 147354..147422

misc-feature 147441..147509

misc-feature 147567..147635

gene 147799..148131  
CDS 147799..148131

misc-feature 147886..147939

misc-feature 147982..148041

misc-feature 148054..148122

ELHLRSRKAQISALVMSVAFLLA  
GIWLVKGIDGFVITSVLDTAAESNPMRKEVAHQ  
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LFTILLSRFEKGAWAFLFSSLTIACVILTAGVTM  
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EFIENNKHSLY"  
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/note="Pfam match to entry PF02322  
Cyto-ox-2, , score 714.90, E-value  
3.7e-211"  
/gene="cydB"  
/note="one of 8 probable  
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for YPO1118 by TMHMM2.0"  
/gene="cydB"  
/note="one of 8 probable  
transmembrane helices predicted  
for YPO1118 by TMHMM2.0"  
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transmembrane helices predicted  
for YPO1118 by TMHMM2.0"  
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for YPO1118 by TMHMM2.0"  
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transmembrane helices predicted  
for YPO1118 by TMHMM2.0"  
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/note="one of 8 probable  
transmembrane helices predicted  
for YPO1118 by TMHMM2.0"  
/gene="YPO1119"  
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/note="Similar to Escherichia coli  
protein YbgE SW:YBGE-ECOLI  
(P37343) (97 aa) fasta scores:  
E(): 6e-22, 59.6% id in 89 aa, and  
to Vibrio cholerae hypothetical  
protein VC1841 TR:Q9KR06  
(EMBL:AE004260) (105 aa) fasta  
scores: E(): 4.3e-08, 34.5% id in  
84 aa"  
/codon-start=1  
/transl-table=11  
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protein"  
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/translation="MKPTQQLKPLTMATTMLSDK  
LYELMDKGPLRALSLVLAFAALFC  
VFWDPTRFAAATSSLEVWQEVFIVWAVCTGVIHG  
VGFRPKQVWLRAFFAPLPAIVILA TGLFYFFA"  
/gene="YPO1119"  
/note="one of 3 probable  
transmembrane helices predicted  
for YPO1119 by TMHMM2.0"  
/gene="YPO1119"  
/note="one of 3 probable  
transmembrane helices predicted  
for YPO1119 by TMHMM2.0"  
/gene="YPO1119"  
/note="one of 3 probable

gene	148263..148664	for YPO1119 by TMHMM2.0"
CDS	148263..148664	/gene="YPO1120"
		/gene="YPO1120"
		/note="Similar to Escherichia coli hypothetical protein YbgC SW:YBGC-ECOLI (P08999) (134 aa) fasta scores: E(): 0, 72.2% id in 133 aa"
		/codon-start=1
		/transl-table=11
		/product="conserved hypothetical protein"
		/protein-id="CAC89963.1"
		/db-xref="GI:15979187"
		/db-xref="SPTREMBL:Q8ZGZ5"
		/translation="MSNTLFRWPVRVYFEDTDAG GMVYHARYVAFYERARTEMLRQRN FHQQQLLSEHVAFVRSMTVEYLA PARLDDMLEV QSEVTAMRGASLTFAQRILDSHGN LLSSAEVLIACIDPHQMKPRALPKSIVAEFK"
gene	148664..149350	/gene="tolQ"
		/note="synonym: YPO1121"
CDS	148664..149350	/gene="tolQ"
		/note="Similar to Escherichia coli TolQ protein SW:TOLQ-ECOLI (P05828) (230 aa) fasta scores: E(): 0, 89.4% id in 227 aa"
		/codon-start=1
		/transl-table=11
		/product="TolQ colicin import protein"
		/protein-id="CAC89964.1"
		/db-xref="GI:15979188"
		/db-xref="SPTREMBL:Q8ZGZ4"
		/translation="MADMNILD LFLQASLFVKLI MLVLMGFSIASWAIITQTRILNA ATRDAEAFEDKFWSGIELSRLYQESQARRDTLSG SEQIFHSGFKEFARLHRANSHAPE AVIDGASRAMRISMNRELEALETHIPFLGTVGSI SPYIGLFGTVWGIMHAFISLGAVK QATLQMVAPGIAEALIATAIGLFAAIPAVMAYNR LNQHVNKLEQNYDNFMEEFIAILH RQAFATESK"
misc-feature	148706..148774	/gene="tolQ"
		/note="one of 3 probable transmembrane helices predicted for YPO1121 by TMHMM2.0"
misc-feature	148880..149296	/gene="tolQ"
		/note="Pfam match to entry PF01618 MotA-ExbB, MotA/TolQ/ExbB proton channel family, score 220.60, E-value 2.4e-62"
misc-feature	149060..149128	/gene="tolQ"
		/note="one of 3 probable transmembrane helices predicted for YPO1121 by TMHMM2.0"
misc-feature	149171..149239	/gene="tolQ"
		/note="one of 3 probable transmembrane helices predicted for YPO1121 by TMHMM2.0"
gene	149363..149791	/gene="tolR"
		/note="synonym: YPO1122"
CDS	149363..149791	/gene="tolR"
		/note="Similar to Escherichia coli TolR protein SW:TOLR-ECOLI (P05829) (142 aa) fasta scores: E(): 0, 83.1% id in 142 aa, and to Vibrio cholerae TolR membrane protein vc1838 TR:Q9KR09 (EMBL:AE004259) (146 aa) fasta scores: E(): 5.5e-15, 39.4% id in 137 aa"
		/codon-start=1
		/transl-table=11
		/product="TolR colicin import

		/protein-id="CAC89965.1"
		/db-xref="GI:15979189"
		/db-xref="SPTREMBL:Q8ZGZ3"
		/translation="MARVRGRKRRELKSEINIVP LLDVLLVLLLIIFMATAPIITQSVE VNLPDATDSKTVSSDDNPPVIVEVSGVGQYTVVV DHQRMELLPSEQVVAEAQARLKTN PKTVFLIGGAKEVPYDEI IKALNMLHQAGVTSVG LMTQPI"
misc-feature	149387..149788	/gene="tolR"
		/note="Pfam match to entry PF02472 ExbD, , score 67.50, E-value 2.8e-16"
misc-feature	149411..149479	/gene="tolR"
		/note="1 probable transmembrane helix predicted for YPO1122 by TMHMM2.0"
gene	149903..151069	/gene="tolA"
		/note="synonym: YPO1123"
CDS	149903..151069	/gene="tolA"
		/note="Similar to Escherichia coli TolA protein SW:TOLA-ECOLI (P19934) (421 aa) fasta scores: E(): 5.1e-27, 57.9% id in 423 aa, and to Pseudomonas aeruginosa TolA protein SW:TOLA-PSEAE (P50600) (347 aa) fasta scores: E(): 6.6e-09, 33.2% id in 319 aa"
		/codon-start=1
		/transl-table=11
		/product="TolA colicin import membrane protein"
		/protein-id="CAC89966.1"
		/db-xref="GI:15979190"
		/db-xref="SPTREMBL:Q8ZGZ2"
		/translation="MGKATEQNDKLNRAVIVSVV LHIILIALLIWGS LTQTTEMGGGG AGGEVIDAVMVDPGAVTEQYNRQQQQQTDAKRAE QQRQKKAEQQAAEELQKKQAAEQQR LKELEKERLQAQEDAKLAAEEQKKQVAEQKKQIA EQQKQAAEQQKIAAAAVAKAKEEQ KQAETAAQAKAEADKIVKAQAEQKKAEAEAKK EAAVAAA AKKQADADAKKAVEVAE KAAADAAEKKAAADA EKKA AA AKKVAAAAEAKKK AAAEAAASTDVDDLFGGLANAKNA PKSGSGAGAAAAGKGGGKSGASGADISGYLGQI TGAIQSKFYDADLYKGR TCDLRIK LAPDGLLIDVKAEGGDPALCQAAIAAAKQAKIPK PPSTDVYEQFKNAPLVFKPQ"
misc-feature	149939..150007	/gene="tolA"
		/note="1 probable transmembrane helix predicted for YPO1123 by TMHMM2.0"
gene	151189..152481	/gene="tolB"
		/note="synonym: YPO1124"
CDS	151189..152481	/gene="tolB"
		/note="Similar to Escherichia coli TolB protein precursor SW:TOLB-ECOLI (P19935) (430 aa) fasta scores: E(): 0, 84.9% id in 430 aa"
		/codon-start=1
		/transl-table=11
		/product="TolB colicin import protein"
		/protein-id="CAC89967.1"
		/db-xref="GI:15979191"
		/db-xref="SPTREMBL:Q8ZGZ1"
		/translation="MKQAFRVALGFLVLWASVLH AEVRIEITQGVDSARPIGVVPFKW MGPGTPPEEIGAIVGADLRNSGKFNPIDAARMPQ QPSTAAEVT PAAWTALGIDAVVVG QVQPSADGSYVVS YQLVDTSGSAGSILAQNQYKV TKQWLRYS AHTVSDEVFEKLTGIK GAFRTRIAYVVK TNGGKFPHEL RVSDYDGYNQFV"

gene 152532..153038  
CDS 152532..153038

FESGKSALVIQTLANGAIRQVASFPRHNGAPAFS  
PDGTKLAFALSKSGSLNLYVMDLA  
SGQISQVTDGRSNNTEPSWFPDSQNLAYTSDQGG  
RPQVYKVNINGGVPQRITWEGSQN  
QNADVSPDGKFLVLVSSNGGAQHIKQDLETGAV  
QVLTDTLLDETSPSIAPNGTMVIYS  
STQGLGSVLQLVSTDGRFKARLPATDGQVKFPAW  
SPYL"

/gene="pal"  
/note="synonyms: excC, YPO1125"  
/gene="pal"  
/note="Similar to Escherichia coli  
peptidoglycan-associated  
lipoprotein precursor Pal or ExcC  
SW:PAL-ECOLI (P07176) (173 aa)  
fasta scores: E(): 0, 84.4% id in  
173 aa, and to Vibrio cholerae  
peptidoglycan-associated  
lipoprotein vc1835 TR:Q9KR12  
(EMBL:AE004259) (172 aa) fasta  
scores: E(): 0, 59.9% id in 172  
aa"

/codon-start=1  
/transl-table=11  
/product="peptidoglycan-associated  
lipoprotein Pal"  
/protein-id="CAC89968.1"  
/db-xref="GI:15979192"  
/db-xref="SPTREMBL:Q8ZGZ0"  
/translation="MQLNKVLKGLMLALPVLAVA  
ACSSNKSANNDQSGMGAGTGTENG  
SNLSSEEQARLQMQELQKNNIVYFGFDKYDIGSD  
FAQMLDAHAAFLRSNPSDKVVVEG  
HADERGTPEYNIALGERRASAVKMYLQKGVSAD  
QISIVSYGKEKPAVLGHDEAAFAK NRRAVLVY"

misc-feature 152565..152597

/gene="pal"  
/note="PS00013 Prokaryotic  
membrane lipoprotein lipid  
attachment site."

misc-feature 152730..153017

/gene="pal"  
/note="Pfam match to entry PF00691  
OmpA, OmpA family, score 171.40,  
E-value 1.5e-47"

misc-feature 152829..152963

/gene="pal"  
/note="PS01068 OmpA-like domain."

gene 153048..153857

CDS 153048..153857

/gene="YPO1126"  
/gene="YPO1126"  
/note="Similar to Escherichia coli  
hypothetical 28.2 kDa protein in  
pal-lyt intergenic region  
precursor YbgF SW:YBGF-ECOLI  
(P45955) (263 aa) fasta scores:  
E(): 0, 70.0% id in 270 aa, and to  
Pseudomonas aeruginosa periplasmic  
protein TR:Q9RNV2 (EMBL:AF177774)  
(274 aa) fasta scores: E():  
6.6e-17, 34.2% id in 225 aa"

/codon-start=1  
/transl-table=11  
/product="putative exported  
protein"  
/protein-id="CAC89969.1"  
/db-xref="GI:15979193"  
/db-xref="SPTREMBL:Q8ZGY9"  
/translation="MNSNFRRLVGLSLLVGVAV  
PWAATAQAPISNVGSGSVEDRVTO  
LERISNAHSQLLTQLQQQLSDSQRDVDSLGRGQIQ  
ESQYQLNQVVERQKQIYQQMESLS  
GGQGAQNSASAASGATADNTAAGSSGNADAGAAA  
STAAPAASTGDENSDYNVAVSLAL  
EKKQYDQAITVFQSFVKQYQPKSTYQPNANYWLGO  
LYYNKGKKDDAAYYYAVVVKNYPK  
SPKSSEAMFKVGVIMQDKGQSDKAKAVYQQVIKQ  
YPNTDAKQAQKRLSAL"  
/gene="YPO1126"

misc-feature 153603..153704

misc-feature	153714..153815	TPR, TPR Domain, score 8.70, E-value 5.6" /gene="YPO1126" /note="Pfam match to entry PF00515 TPR, TPR Domain, score 11.80, E-value 2.6"
tRNA	154048..154123	/product="tRNA-Lys" /note="tRNA Lys anticodon TTT, Cove score 95.27"
tRNA	154151..154226	/product="tRNA-Lys" /note="tRNA Lys anticodon TTT, Cove score 95.27"
tRNA	154255..154324	/note="tRNA Pseudo anticodon TTT, Cove score 40.49"
gene	154693..155754	/gene="nadaA"
CDS	154693..155754	/note="synonyms: nicA, YPO1127" /gene="nadaA" /note="Similar to Escherichia coli quinolinate synthetase A NadA or Nica SW:NADA-ECOLI (P11458) (347 aa) fasta scores: E(): 0, 82.1% id in 346 aa" /codon-start=1 /transl-table=11 /product="quinolinate synthetase A" /protein-id="CAC89970.1" /db-xref="GI:15979194" /db-xref="SWISS-PROT:Q8ZGY8" /translation="MSEIFDVNAAIYPFPARPVP LDTNEKAFYREKIKTLLKQORDAVL VAHYITDPEIQALAEETGGCVADSLEMARFGNNH PASTLLVAGVRFMGETAKILNPEK KVLMPITLNAECSLDLGCVPDEFATFCDSHPDRTV VVIYANTSAAVKAKADWVVTSSIAV ELIEHLDSLGEKIIWAPDRHLGSYVQKKSGADVL CWQGACIVHDEFKTQALARMKALY PDAAVLVHPESPQAVVDMADAVGSTSQLIQAAKT LPQKTLIVATDRGIFYKMQQACPD KELFEAPTAGEGATCRSCAHCPPWMAMNGLRAIAE GLEQGGVMHEIHVDEELRQQALIP LNRMLDFANQLKLQVKGNA"
misc-feature	154777..155715	/gene="nadaA" /note="Pfam match to entry PF02445 NadA, , score 609.80, E-value 1.6e-179"
gene	155876..156601	/gene="pnuC"
CDS	155876..156601	/note="synonym: YPO1128" /gene="pnuC" /note="Similar to Escherichia coli PnuC protein SW:PNUC-ECOLI (P31215) (239 aa) fasta scores: E(): 0, 76.1% id in 238 aa" /codon-start=1 /transl-table=11 /product="integral membrane NMN transport protein PnuC" /protein-id="CAC89971.1" /db-xref="GI:15979195" /db-xref="SPTREMBL:Q8ZGY7" /translation="MDFLSTGNILVHIPLGAGGY DLWIEAIGTLFGLLCIWFASKEK IINYLFGLINVTLFAVIFQIQLYASLLLQLFFF GANIYGWYAWSKQTPDNQAEKIR WLSLPKALAWAAVCIAGIVLMTLHIDTVFAWLTR VAVTVMQSLGANVQMPPELOPDAFP FWDSTMMVLSIAAMILMTRKYVENWLIWVVIDVI SVAIFAYQGVYAMALEYAFITLIA LNGSWLWIKSAARNHSRPLSTQG"
misc-feature	155933..155992	/gene="pnuC" /note="one of 7 probable transmembrane helices predicted for YPO1128 by TMHMM2.0"
misc-feature	156011..156079	/gene="pnuC" /note="one of 7 probable



misc-feature	156089..156142	for YPO1128 by TMHMM2.0" /gene="pnuC" /note="one of 7 probable transmembrane helices predicted for YPO1128 by TMHMM2.0"
misc-feature	156203..156271	/gene="pnuC" /note="one of 7 probable transmembrane helices predicted for YPO1128 by TMHMM2.0"
misc-feature	156347..156406	/gene="pnuC" /note="one of 7 probable transmembrane helices predicted for YPO1128 by TMHMM2.0"
misc-feature	156425..156484	/gene="pnuC" /note="one of 7 probable transmembrane helices predicted for YPO1128 by TMHMM2.0"
misc-feature	156494..156553	/gene="pnuC" /note="one of 7 probable transmembrane helices predicted for YPO1128 by TMHMM2.0"
gene	complement(156716..1576 54)	/gene="YPO1129"
CDS	complement(156716..1576 54)	/gene="YPO1129"  /note="Similar to Escherichia coli hypothetical 34.7 kDa protein in pnuC-aroG intergenic region YbGR SW:YBGR-ECOLI (P75757) (313 aa) fasta scores: E(): 0, 66.1% id in 307 aa, and to Bacillus subtilis cation transport protein TR:O07084 (EMBL:U93876) (311 aa) fasta scores: E(): 0, 41.4% id in 309 aa" /codon-start=1 /transl-table=11 /product="putative cation transport protein" /protein-id="CAC89972.1" /db-xref="GI:15979196" /db-xref="SWISS-PROT:Q8ZGY6" /translation="MAVSTIFSQDSNSKRLLI AF AITTLFMVTEAIGGWLSGSLALLA DAGHMLTDSAALFIALMAVHFSQRKPDPRHTFGY LRLTTLA AFVNAAALLLIVILIVW EAVHRRFFSPHEVMGTPMLIIAIAIGLLANIFCFWI LHKGEEEEKNINVRAAALHVLSDLL GSVGAMIAAIVILTTGWTPIIDPILSVLVSVLILR SAWRLKESFHELLEGAPQEIDIN KLRKDLCTNIYEVARNIHVHLWQVGEQRLMTLHA QVIPPLDHDALLQRIQDYLLHHYR ISHATVQMEYQHCGTPDCGINQAAPADGHHRHHH HE"
misc-feature	complement(156791..1574 50)	/gene="YPO1129"  /note="Pfam match to entry PF01545 Cation-efflux, Cation efflux family, score 250.50, E-value 2.3e-71"
misc-feature	complement(157139..1572 04)	/gene="YPO1129"  /note="one of 5 probable transmembrane helices predicted for YPO1129 by TMHMM2.0"
misc-feature	complement(157244..1573 09)	/gene="YPO1129"  /note="one of 5 probable transmembrane helices predicted for YPO1129 by TMHMM2.0"
misc-feature	complement(157355..1574 20)	/gene="YPO1129"  /note="one of 5 probable transmembrane helices predicted for YPO1129 by TMHMM2.0"

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10)~
misc-feature complement(157541..157606) /note="one of 5 probable transmembrane helices predicted for YPO1129 by TMHMM2.0" /gene="YPO1129"
gene join(158103..159062, 161022..161114) /note="one of 5 probable transmembrane helices predicted for YPO1129 by TMHMM2.0" /gene="aroG"
CDS join(158103..159062, 161022..161114) /note="synonym: YPO1130" /pseudo /gene="aroG"
/EC-number="4.1.2.15"
/note="Similar to Escherichia coli phospho-2-dehydro-3-deoxyheptonate aldolase, Phe-sensitive AroG SW:AROG-ECOLI (P00886) (350 aa) fasta scores: E(): 0, 86.6% id in 320 aa. The IS insertion occurred near the C-terminal end (following codon 320). This CDS is disrupted by the insertion of IS100. The insertion occurred near the C-terminus. It is not clear whether this insertion affects the function of the protein." /pseudo /codon-start=1 /transl-table=11 /product="phospho-2-dehydro-3-deoxyheptonate aldolase, phe-sensitive, AroG (pseudogene)" /db-xref="PSEUDO:CAC89973.1" /db-xref="REMTREMBL:CAC89973" /gene="aroG"
misc-feature 158112..159092 /note="Pfam match to entry PF00793 DAHP-synth-1, DAHP synthetase family, score 755.60, E-value 2e-223" /pseudo
misc-feature complement(159063..161016) /note="insertion sequence, IS100"
misc-feature 159063..159090 /gene="aroG" /note="IS100 inverted repeat" /pseudo
gene complement(159129..159911) /gene="YPO1131"
CDS complement(159129..159911) /note="synonym: ypmt1.57c" /gene="YPO1131"
/note="Similar to Escherichia coli insertion sequence IS21 putative ATP-binding protein, IstB SW:ISTB-ECOLI (P15026) (265 aa) fasta scores: E(): 0, 47.4% id in 249 aa. Also almost identical to Yersinia pestis and Escherichia coli putative IS100 transposase ypmt1.57c TR:Q9R3L5 (EMBL:AL117211) (260 aa) fasta scores: E(): 0, 99.6% id in 260 aa." /codon-start=1 /transl-table=11 /product="insertion sequence IS100, ATP-binding protein" /protein-id="CAC89974.1" /db-xref="GI:15979197" /db-xref="SPTREMBL:Q9R3L5" /translation="MMELQHQRMLMALAGQLQLE SLISAAPALSQQAVDQEWSYMDFL EHLLEEKLARHQKQAMYTRMAAFPAVKTFEEY

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NENIVLLGPSGVGKTHLAIAMGYEAVRAGIKVRF  
 TTAADLLLQLSTAQRQGRYKTTLQ  
 RGVMAPRLLIIDEIGYLPFSQEEAKLFFQVIAKR  
 YEKSAMILTSNLPFGQWDQTFAGD  
 AALTSAMLDRIHHSHVQVQIKGESYRLRQKRKAG  
 VIAEANPE"

misc-feature	complement (159204..159743)	/gene="YPO1131"  /note="Pfam match to entry PF01695 IstB, IstB-like ATP binding protein, score 367.20, E-value 1.7e-106"
misc-feature	complement (159561..159584)	/gene="YPO1131"  /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
gene	complement (159908..160930)	/gene="YPO1132"  /note="synonyms: y1093, ypmt1"
CDS	complement (159908..160930)	/gene="YPO1132"  /note="Similar to Escherichia coli transposase for insertion sequence element IS21 IstA SW:ISTA-ECOLI (P15025) (390 aa) fasta scores: E(): 3e-27, 33.1% id in 329 aa. Identical to the previously sequenced Yersinia pestis, Yersinia pseudotuberculosis, and Escherichia coli pesticin plasmid insertion sequence transposase Y1055 TR:P74993 (EMBL:U59875) (340 aa) fasta scores: E(): 0, 100.0% id in 340 aa" /codon-start=1 /transl-table=11 /product="transposase for insertion sequence IS100" /protein-id="CAC89975.1" /db-xref="GI:15979198" /db-xref="SPTREMBL:P74993" /translation="MVTFFETVMEIKILHKQGMSSRAIARELGISRNTVKRYLQAKSEP PKYTPRPAVASLLDEYRDYIRQRIADAHYPKIPA TVIAREIRDQGYRGGMTILRAFIR SLSVPQEQEPAVRFETEPGRQMQVDWGTMRNGRS PLHVFVAVLGYSRMLYIEFTDNMR YDTLETCHRNAFRFFGGVPREVLVDNMKTVVLQR DAYQTGQHRFHPSLWQFGKEMGFS PRLCRPFRAQTKGKVERMVQYTRNSFYIPLMTRL RPMGITVDVETANRHGLRWLHDVA NQRKHETIQARPCDRWLEEQQSMALPPEKKEYD VHLDENLVNFDKHPLHPLSIYDS FCRGVA"
misc-feature	complement (160052..160585)	/gene="YPO1132"  /note="Pfam match to entry PF00665 rve, Integrase core domain, score 81.90, E-value 1.6e-22"
misc-feature	complement (160814..160879)	/gene="YPO1132"  /note="Predicted helix-turn-helix motif with score 2147 (+6.50 SD) at aa 18-39, sequence MSSRAIARELGISRNTVKRYLQ"
misc-feature	complement (160823..160906)	/gene="YPO1132"  /note="Pfam match to entry PF00239 recombinase, Site-specific recombinases, score 25.70, E-value 4.7e-06"
misc-feature	complement (160989..161016)	/note="IS100 inverted repeat"
gene	complement (161296..162048)	/gene="gpmA"  /note="synonyms: gpm, YPO1133"

48)

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/EC-number="5.4.2.1"
/note="Similar to Escherichia coli
phosphoglycerate mutase 1
SW:PMG1-ECOLI (P31217) (249 aa)
fasta scores: E(): 0, 88.0% id in
249 aa"
/codon-start=1
/transl-table=11
/product="phosphoglycerate mutase
1"
/protein-id="CAC89976.1"
/db-xref="GI:15979199"
/db-xref="SWISS-PROT:Q8ZGY5"
/translation="MAVTKLVLRHGESQWNNEN
RFTGWYDVLSEKGRSEAKAAGKL
LKDEGFTFDFAITSVLKRAIHTLWNILDELQAW
LPTEKTKLNERHYGALQGLNKSE
TAEKYGDEQVKQWRRGFATPPALEKSDEFPGH
DPYAKLTDAELPTTESLALTIER
VIPYWNVDVIKPRIASGERVIAAHGNSLRALVKY
LDDLGEDEILELNIPTGVPLVYEF
DENFKPIKHYLGNADIEIAAKAAVANQGKAK"
misc-feature complement(161386..1620 /gene="gpmA"
30)
/note="Pfam match to entry PF00300
PGAM, Phosphoglycerate mutase
family, score 447.60, E-value
1.1e-130"
misc-feature complement(161998..1620 /gene="gpmA"
27)
/note="PS00175 Phosphoglycerate
mutase family phosphohistidine
signature."
gene complement(162395..1627 /gene="psiF"
30)
/note="synonym: YPO1134"
CDS complement(162395..1627 /gene="psiF"
30)
/note="Similar to Escherichia coli
phosphate starvation-inducible
protein PsiF precursor psiF
SW:PSIF-ECOLI (P27295) (106 aa)
fasta scores: E(): 1.2e-15, 54.5%
id in 112 aa"
/codon-start=1
/transl-table=11
/product="putative
starvation-inducible protein"
/protein-id="CAC89977.1"
/db-xref="GI:15979200"
/db-xref="SPTREMBL:Q8ZGY4"
/translation="MRLFPLWLLSAGLLLSANVM
AADPPKTPSPAQAQQQQMTDCNQ
QASTQSLKGDERKNFMSQCLKAQTAPDGKALTPQ
QQKMKSCNAEAAQKMLKGDERKTF
MSTCLKKAA"
gene complement(163023..1640 /gene="galM"
92)
/note="synonym: YPO1135"
/pseudo
CDS complement(163023..1640 /gene="galM"
92)
/EC-number="5.1.3.3"
/note="Similar to Escherichia coli
aldose 1-epimerase galM
SW:GALM-ECOLI (P40681) (346 aa)
fasta scores: E(): 0, 60.2% id in
344 aa. There is a frameshift
following codon 39. The frameshift
occurs within a homopolymeric
tract of 6G. The sequence has been
checked and is believed to be
correct"
/pseudo

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		/transl-table=11 /product="aldose 1-epimerase (pseudogene)" /gene="galM"
misc-feature	complement(163038..1639 19)	/note="Pfam match to entry PF01263 Aldose-epim, Aldose 1-epimerase, score 377.60, E-value 1.3e-109" /pseudo
misc-feature	complement(163533..1635 62)	/gene="galM"  /note="PS00545 Aldose 1-epimerase putative active site." /pseudo
gene	complement(164086..1652 37)	/gene="galK"
CDS	complement(164086..1652 37)	/note="synonyms: galA, YPO1137" /gene="galK"  /EC-number="2.7.1.6" /note="Similar to Escherichia coli galactokinase SW:GAL1-ECOLI (P06976) (381 aa) fasta scores: E(): 0, 72.5% id in 382 aa" /codon-start=1 /transl-table=11 /product="galactokinase" /protein-id="CAC89979.1" /db-xref="GI:15979201" /db-xref="SWISS-PROT:Q8ZGY3" /translation="MSLKQHTQTIFRQQFDRES DITIKAPGRVNLIGEHTDYNDGFVL PCAINYETVISCGKRDDRQIRVIAADYENQQDIF SLDAPIVPHPEYRWADYVRGVVKH LQMRNADFGGADLVICGNVPOGAGLSSSASLEVA VGQALQSLYQLPLSGVELALNGQE AENQFVGCNCGIMDQLISALGKKDHALLIDCRTL ETRAVPMPENMAVVIINSNIQRGL VDSEYNTRRQQCEAAARFFGVKALRDVEPSLFFS IQDELDPVVAKRARHVISENARTL AAADALAAGNLKLMGQLMQESHISMRRDDFEITVP PIDRLVEIVKSVIGDQGGVRMTGG GFGGCIIALMPLELVEQVVRTTVAQEYPAHSGGKK ETFYVCQASQGAGLC"
misc-feature	complement(164737..1649 64)	/gene="galK"  /note="Pfam match to entry PF00288 GHMP-kinases, GHMP kinases putative ATP-binding proteins, score 83.90, E-value 2.5e-22"
misc-feature	complement(164842..1648 77)	/gene="galK"
misc-feature	complement(165124..1651 59)	/note="PS00627 GHMP kinases putative ATP-binding domain." /gene="galK"
gene	complement(165234..1662 86)	/note="PS00106 Galactokinase signature." /gene="galT"
CDS	complement(165234..1662 86)	/note="synonyms: galB, YPO1138" /gene="galT"  /EC-number="2.7.7.10" /note="Similar to Escherichia coli galactose-1-phosphate uridylyltransferase GalT or GalB SW:GAL7-ECOLI (P09148) (348 aa) fasta scores: E(): 0, 82.4% id in 347 aa" /codon-start=1 /transl-table=11 /product="galactose-1-phosphate uridylyltransferase" /protein-id="CAC89980.1"

		/db-xref="SPTREMBL:Q8ZGY2" /translation="MTHFNPVDHPHRRYNPLKDQ WVLVSPHRAKRPWQGOQOEAPATEN LPAHDPDCFLCPGNTRVTGDVNPDYSSSTVFTND FAALMPDTPDAPPSHDLPLMRSQSA RGTSRVICFSPDHSKTLPLQLTLPALQVQVQVQWQ QSAELGKIYPWVQVFENKGAAMGC SNPHPHGQIWANSFLPNEAEQEDRLQQQYFQQHQ SPMLLDYVERERRDQRTVVETE WLAVVPYWAAWPFETLLLPKAAVLRLEDLSAEQR SDLALALKKLTSRYDNLFSCSFPY SMGWHGAPYNANDNTHWQLHAHFYPPLLRASVR KFMVGYELLAETQORDLTAEQAAAL LRVSDVHYKEAGAKS" /gene="galT"
misc-feature	complement(165252..166283)	/note="Pfam match to entry PF01087 GalP-UDP-transf, Galactose-1-phosphate uridyl transferase, score 702.60, E-value 1.8e-207" /gene="galT"
misc-feature	complement(165783..165836)	/note="PS00117 Galactose-1-phosphate uridyl transferase family 1 active site signature." /gene="galE"
gene	complement(166296..167312)	/note="synonyms: galD, YPO1139" /gene="galE"
CDS	complement(166296..167312)	/EC-number="5.1.3.2" /note="Similar to Escherichia coli UDP-glucose 4-epimerase Gale or GalD SW:GALE-ECOLI (P09147) (338 aa) fasta scores: E(): 0, 76.0% id in 338 aa. Previously sequenced in Yersinia pestis as TR:AAG22000 (EMBL:AF282311) (338 aa) fasta scores: E(): 0, 100.0% id in 338 aa" /codon-start=1 /transl-table=11 /product="UDP-glucose 4-epimerase" /protein-id="CAC89981.1" /db-xref="GI:15979203" /db-xref="SWISS-PROT:Q9F7D4" /translation="MYVLVTGGSGYIGSHTCVQL IEAGYKPVILDNLCSKSSVLARI HSLTGYTPELYAGDIRDRTLDSIFAAHPIHAVI HFAGLKAVGESVNRPLEYNNNVF GTLVLLEAMRAAQVKNLIFSSSATVYGDQPQIPY VESFPTGSPSSPYGRSKLMVEQIL QDVQLADPQWNMTILRYFNPVGAHPSGLMGEDPQ GIPNNLMPFIAQVAVGRRESLAIF NGGYPTPDGTGVRDYIHVVLDLADGHVAAMKTLHG KPGVHIFNLGAGVGHSLQVVAAF SKACGKPLAYHFAPRREGDLPAYWADATKAAEQ L GWRVSRSLDEMAADTWHWQSKNPQ GYPD" /gene="gale"
misc-feature	complement(166314..167306)	/note="Pfam match to entry PF01370 Epimerase, NAD dependent epimerase/dehydratase family, score 559.10, E-value 2.9e-164" /gene="YPO1140"
gene	complement(167672..168490)	/gene="YPO1140"
CDS	complement(167672..168490)	/note="Similar to Vibrio cholerae hypothetical protein VC1074 TR:Q9KT31 (EMBL:AE004189) (276 aa) fasta scores: E(): 0, 45.5% id in 275 aa"

```

/transl-table=11
/product="putative membrane
protein"
/protein-id="CAC89982.1"
/db-xref="GI:15979204"
/db-xref="SPTREMBL:Q8ZGY1"
/translation="MWGVLATSLFLPLSQVLSL
LFLVSSLAMACYSGVLTFPATAFL
LAIILVLLLQKYRQRNGVAAGLELLLVLGVIAL
FLHLVPGFHNKVLDKVRTGPLSA
PFTMYYNLDKALVPFILLACLPTLFKVKKHPSVG
RMGWVVLILSVPALLLLAVALGGL
KIELHTPVWIGSFIIANLFFVCLAEEALFRGYLQ
QRLGQWLGSYPALVITALLFGSAH
FAGGPILLMLFAALAGVIYGLAWLWSGRLWVAVAF
HFALNLMHLLFFTYPLYLPH"
misc-feature complement(167681..1677 /gene="YPO1140"
46)
misc-feature complement(167768..1678 /gene="YPO1140"
33)
misc-feature complement(167849..1678 /gene="YPO1140"
99)
misc-feature complement(167939..1679 /gene="YPO1140"
95)
misc-feature complement(168011..1680 /gene="YPO1140"
76)
misc-feature complement(168113..1681 /gene="YPO1140"
78)
misc-feature complement(168239..1683 /gene="YPO1140"
04)
misc-feature complement(168326..1683 /gene="YPO1140"
91)
misc-feature complement(168404..1684 /gene="YPO1140"
69)
gene complement(168707..1701 /gene="modF"
97)
CDS complement(168707..1701 /gene="modF"
97)
/note="one of 9 probable
transmembrane helices predicted
for YPO1140 by TMHMM2.0"
/note="one of 9 probable
transmembrane helices predicted
for YPO1140 by TMHMM2.0"
/note="one of 9 probable
transmembrane helices predicted
for YPO1140 by TMHMM2.0"
/note="one of 9 probable
transmembrane helices predicted
for YPO1140 by TMHMM2.0"
/note="one of 9 probable
transmembrane helices predicted
for YPO1140 by TMHMM2.0"
/note="one of 9 probable
transmembrane helices predicted
for YPO1140 by TMHMM2.0"
/note="one of 9 probable
transmembrane helices predicted
for YPO1140 by TMHMM2.0"
/note="one of 9 probable
transmembrane helices predicted
for YPO1140 by TMHMM2.0"
/note="one of 9 probable
transmembrane helices predicted
for YPO1140 by TMHMM2.0"
/note="synonyms: phrA, YPO1142"
/note="Similar to Escherichia coli
putative molybdenum transport
ATP-binding protein ModF or PhrA
SW:MODF-ECOLI (P31060) (490 aa)
fasta scores: E(): 0, 75.0% id in
484 aa"
/codon-start=1
/transl-table=11
/product="putative molybdenum

```



```

modF"-
/protein-id="CAC89983.1"
/db-xref="GI:15979205"
/db-xref="SPTREMBL:Q8ZGY0"
/translation="MSELQISQGCFLSQTQTLI
LPALHIQAGDCWAFVGGANGSGKSA
LAKALSGELALLEGSRSQSHFRHGVRLSFEQLQQL
VNEEWQRNNTDLLSADEDDTGRTT
AEIIQEAARDPQRCQQLAALFGISHLLSRRFKYL
STGETRKTLLCQALMPQPDLLILD
EPFDGLDVAARAQLAEMLSLTAQGVTLVLVLNR
FDDIPDFVQYVGVADCHLTHMGP
RQQILSEALIAQLAHSENLDGLSLPETEDPQHHL
RIPKNEPLIILNDGVVEYNDRPIL
HNLSWQVNPGEHWQIIGQNGAGKSTLLSLITGDH
PQGYSDNLTFLGRRRGSGETIWDI
KRHIGYVSGSLHLDYRVSTRVTVILSGFFDSIG
LYQAASDRQQQLADQWLSLLGFST
SVANQPFHSLSWGQQLVLIARALVKHPALLILD
EPLQGLDPLNRLLVRRFIDVMIGE
GETQLLFVSHHAEDAPQCITHRLTFVPFGDIYHY
QQEKSPSQPVK"

```

misc-feature complement(168761..1693 42) /gene="modF"

```

/note="Pfam match to entry PF00005
ABC-tran, ABC transporter, score
155.20, E-value 1.1e-42"

```

misc-feature complement(169298..1693 21) /gene="modF"

```

/note="PS00017 ATP/GTP-binding
site motif A (P-loop)."

```

misc-feature complement(169565..1701 13) /gene="modF"

```

/note="Pfam match to entry PF00005
ABC-tran, ABC transporter, score
87.10, E-value 3.7e-22"

```

misc-feature complement(170069..1700 92) /gene="modF"

```

/note="PS00017 ATP/GTP-binding
site motif A (P-loop)."

```

gene complement(170307..1710 98) /gene="modE"

```

/note="synonyms: modR, YPO1143"

```

CDS complement(170307..1710 98) /gene="modE"

```

/note="Similar to Escherichia coli
molybdenum transport protein
SW:MODE-ECOLI (P46930) (262 aa)
fasta scores: E(): 0, 70.5% id in
264 aa"

```

```

/codon-start=1
/transl-table=11
/product="molybdenum transport
protein Mode"

```

```

/protein-id="CAC89984.1"
/db-xref="GI:15979206"
/db-xref="SWISS-PROT:P58497"
/translation="MQAEILLTLKLQQLFADPR
RIALLKQIQHTGSISQGAKLAGIS
YKSAWDAINDMNTLSEEILVERATGGKGGGAHL
TRYGERLIQLYDLLATIQQKAFDT
LKDDSLPLDSLAAISRFSLQTSARNQFFGTIE
RDHQVQVQHVNILLSGKTRLTAA
ITQQSADRLQLSAGKEVLALIKAPWVKLVTDPAL
AGAADNALPGTVASIEPGNDHSEV
IVTLTGGANLCSSTQNNSELHALNLRVGSAVIAQF
NADRVIIATLC"

```

gene 171415..171567 /gene="YPO1144"

CDS 171415..171567 /gene="YPO1144"

```

/note="Similar to Escherichia coli
hypothetical 5.3 kDa protein in
modE-modA intergenic region
precursor YbhT SW:YBHT-ECOLI
(P75759) (49 aa) fasta scores:
E(): 8.4e-11, 82.5% id in 40 aa.

```

many eukaryotic ATPase subunits  
 eg. Mesembryanthemum crystallinum  
 vacuolar H<sup>+</sup> ATPase subunit C  
 TR:Q9S953 (EMBL:UNKNOWN ACCESSION)  
 (76 aa) fasta scores: E(): 3.9,  
 54.5% id in 33 aa"  
 /codon-start=1  
 /transl-table=11  
 /product="putative membrane  
 protein"  
 /protein-id="CAC89985.1"  
 /db-xref="GI:15979207"  
 /db-xref="SPTREMBL:Q8ZGX9"  
 /translation="MFELLKSLVFAVVMVPVMA  
 VILGLIYGLGEVFNVISKTGHPKE RNTLRS"

misc-feature 171433..171501

gene 171802..172581

CDS 171802..172581

/gene="YPO1144"  
 /note="1 probable transmembrane  
 helix predicted for YPO1144 by  
 TMHMM2.0"  
 /gene="modA"  
 /note="synonym: YPO1145"  
 /gene="modA"  
 /note="Similar to Escherichia coli  
 molybdate-binding periplasmic  
 protein precursor ModA  
 SW:MODA-ECOLI (P37329) (257 aa)  
 fasta scores: E(): 0, 71.1% id in  
 246 aa"  
 /codon-start=1  
 /transl-table=11  
 /product="molybdate-binding  
 periplasmic protein precursor"  
 /protein-id="CAC89986.1"  
 /db-xref="GI:15979208"  
 /db-xref="SPTREMBL:Q8ZGX8"  
 /translation="MKNQYGVSYWVAGAVLLTA  
 FSGPAFAADKITVFAAASLTNALQ  
 DIAVQYKQEKQVDVVASYASSSTLARQIEQGAPA  
 DLFISADQQWMDYAIKQQIVANT  
 RYTLLGNELVLIAPQDSQIDKVEIDKKTDWKKLL  
 EGGRLAVGDPDHVPAGIYAKESLE  
 NLGAWSTLAPEMARANNVRSAMALVERAEAPLGI  
 VYGSDAVASKKVKVVGIFPEASHK  
 PVEYPMATVKGHDNPTVTAFYDYLKSPAAAVIFK  
 NYGFTPR"

misc-feature 171826..171885

gene 172581..173276

CDS 172581..173276

/gene="modA"  
 /note="1 probable transmembrane  
 helix predicted for YPO1145 by  
 TMHMM2.0"  
 /gene="modB"  
 /note="synonyms: chlJ, YPO1146"  
 /gene="modB"  
 /note="Similar to Escherichia coli  
 molybdenum transport system  
 permease protein Modb or ChlJ  
 SW:MODB-ECOLI (P09834) (229 aa)  
 fasta scores: E(): 0, 76.3% id in  
 228 aa"  
 /codon-start=1  
 /transl-table=11  
 /product="molybdenum transport  
 system permease protein ModB"  
 /protein-id="CAC89987.1"  
 /db-xref="GI:15979209"  
 /db-xref="SPTREMBL:Q8ZGX7"  
 /translation="MILSEYEWQAIILSLKVSGV  
 AVACSLPLGILMAWVLVRCRFPKG  
 SLLDSVIHLPLVLPVVIYLLLLISMGRRGFIGE  
 WLYSWFGINFSSFSWRGAALASAVV  
 AFPLMVRAIRLALEAVDTRLELAARTLGATPWRV  
 FFTITLPLSLPGVIAGTVLSFARS  
 LGEFGATITFVSNIPGETRTIPLAMYTLIETPGA  
 EAAAARLCVIAIILSLVSLLLSEW  
 LANWGGKKRMGAPC"  
 /gene="modB"

misc-feature 172623..172691

misc-feature	172725..172793	transmembrane helices predicted for YPO1146 by TMHMM2.0" /gene="modB" /note="one of 5 probable transmembrane helices predicted for YPO1146 by TMHMM2.0"
misc-feature	172851..172919	/gene="modB" /note="one of 5 probable transmembrane helices predicted for YPO1146 by TMHMM2.0"
misc-feature	172920..173150	/gene="modB" /note="Pfam match to entry PF00528 BPD-transp, Binding-protein-dependent transport systems inner membrane component, score 78.90, E-value 1e-19"
misc-feature	172980..173048	/gene="modB" /note="one of 5 probable transmembrane helices predicted for YPO1146 by TMHMM2.0"
misc-feature	173169..173237	/gene="modB" /note="one of 5 probable transmembrane helices predicted for YPO1146 by TMHMM2.0"
gene	173270..174349	/gene="modC" /note="synonyms: chlD, narD, YPO1147"
CDS	173270..174349	/gene="modC" /note="Similar to Escherichia coli molybdenum transport ATP-binding protein ModC or ChlD or NarD SW:MODC-ECOLI (P09833) (352 aa) fasta scores: E(): 0, 69.1% id in 349 aa" /codon-start=1 /transl-table=11 /product="molybdenum transport ATP-binding protein ModC" /protein-id="CAC89988.1" /db-xref="GI:15979210" /db-xref="SPTREMBL:Q8ZGX6" /translation="MLELNFSQQLGDLHLQVATD LPAQGITAIFGLSGAGKTSLINVI GGLTRPQQGRVILNGRVLVDAEKNIYLPPEKRRV GYVFQDARLFPHYRVRGNLQYGMA ASMRGQFDAIVGLLGIEPLLNRFPTLSGGEKQR VAIGRALLTAPELLLMDEPLASLD LPRKRELLPYLERLAQDVNTPILYVSHSMDEILR LADQVVVMDAGKVRAVGGLLEEVWA SSALRPWLQREEPSSILRVSVIGHH DRYAMTALA LGDQRLWVGKLDAAEGNSMRIRIN AADVSLALQPPHSSSIRNIPVKVAECLDVDGQV DVKLAIGEQLWARITPWARDELG LKPGQWVYAQIKSVSFNRQNGPVPD"
misc-feature	173339..173884	/gene="modC" /note="Pfam match to entry PF00005 ABC-tran, ABC transporter, score 203.30, E-value 3.7e-57"
misc-feature	173360..173383	/gene="modC" /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
misc-feature	173654..173698	/gene="modC" /note="PS00211 ABC transporters family signature."
gene	complement(174405..175226)	/gene="YPO1148"
CDS	complement(174405..175226)	/gene="YPO1148"  /note="Similar to Escherichia coli hypothetical protein YbhA SW:YBHA-ECOLI (P21829) (272 aa) fasta scores: E(): 0, 64.0% id in 272 aa, and to Vibrio cholerae hypothetical protein VCA0243"

fasta scores: E(): 0, 39.2% id in  
 273 aa"  
 /codon-start=1  
 /transl-table=11  
 /product="conserved hypothetical  
 protein"  
 /protein-id="CAC89989.1"  
 /db-xref="GI:15979211"  
 /db-xref="SPTREMBL:Q8ZGX5"  
 /translation="MTYRIIALDLDTLLDHKKR  
 ILPESLSALAQARAEGVKVIVVTG  
 RHHVAIHPFYQALQLDTPAICNGTYIYDYQNKK  
 VLDSNPLTPQQAVQVLQLEKTQI  
 HGLMYVDDAMLYQQITGHVTRTLSPAESLPPAQR  
 PTFLLQVNSLLDAHSATAIWKFAT  
 SHPDTAQLKAFAARVEAEMGLACEWSWHDQVDIA  
 QAGNSKGKRLQQWVESQGLSMQEV  
 IAFGDNFNLDLSMLEAAGLGVMGNSDDAIKQRAD  
 LVITDNEQPGIAAVIRQHVLA"  
 /gene="YPO1148"  
 /note="Pfam match to entry PF00592  
 DUF3, Cof family DUF3, score  
 280.90, E-value 1.6e-80"  
 /gene="YPO1148"  
 /note="PS01229 Hypothetical cof  
 family signature 2."  
 /gene="YPO1149"  
 /gene="YPO1149"  
 /note="Similar to Escherichia coli  
 hypothetical protein YbhE  
 SW:YBHE-ECOLI (P52697) (331 aa)  
 fasta scores: E(): 0, 56.8% id in  
 329 aa, and to Buchnera aphidicola  
 (subsp. Acyrthosiphon pisum)  
 hypothetical protein BU293  
 SW:Y293-BCUAI (P57380) (334 aa)  
 fasta scores: E(): 0, 35.8% id in  
 330 aa"  
 /codon-start=1  
 /transl-table=11  
 /product="conserved hypothetical  
 protein"  
 /protein-id="CAC89990.1"  
 /db-xref="GI:15979212"  
 /db-xref="SPTREMBL:Q8ZGX4"  
 /translation="MKQAVYVASPDSQQIHVWQL  
 DSAGELTLLQTVDPVPGVQVPMAS  
 PNQRHLYVGVPRDFGIVSYHIADDGTLTAAGMAP  
 LPGSPTHIDTDROGRFLFSASYSF  
 NCVSISPIDTHGVVQAPIQQLDDLPAHPSANIDP  
 TNQILLVPCLKEDKVRLFDLSAEG  
 QLTPHAQADITVAAGAGPRHMAFHPNHQVAYCVN  
 ELNSSVDVYQISNNGQEYHLVQSL  
 DAMPADFTGTRWAADIHITPNGRYLYISDRTANL  
 LGIFTVSEDGRVISLVGHHLTEAQ  
 PRGFNIDHSGNFLIASGQKSDHIEVYRIDQNTGE  
 LTTTLKRYPVGKGPMWVSIRGAQNS "  
 /gene="bioA"  
 /note="synonym: YPO1150"  
 /gene="bioA"  
 /EC-number="2.6.1.62"  
 /note="Similar to many eg.  
 Escherichia coli  
 adenosylmethionine-8-amino-7-oxono  
 nanoate aminotransferase BioA  
 SW:BIOA-ECOLI (P12995) (429 aa)  
 fasta scores: E(): 0, 74.6% id in  
 417 aa"  
 /codon-start=1  
 /transl-table=11  
 /product="adenosylmethionine-8-ami

misc-feature complement(174447..1752  
 14)  
 misc-feature complement(174498..1745  
 66)  
 gene 175517..176521  
 CDS 175517..176521  
 gene complement(176706..1779  
 74)  
 CDS complement(176706..1779  
 74)

		<pre> aminotransferase" /protein-id="CAC89991.1" /db-xref="GI:15979213" /db-xref="SPTREMBL:Q8ZGX3" /translation="MTPSDLVFDQQHIWHPYTSMT TEPLPCYPVVGAEGLVQLADGRR LIDGMSSWWAAIHGYNHPVLNFAAHQQLDKMSHV MFGGITHPPAVKLCRQLVAMTPPP LECVFLADSGSVSVEVALKLMALQYWQAKGERRQR ILTLRHGYHGDFTFGAMSVCDPQNS MHSLYQGYLAENLFANAPQCGFDDPWDPQDIANF VALITQHANEIAAVILEPVVQAG GMRIYHPSYLREVRALCDKHQILLIADDEIATGFG RTGKLFACEHAQIVPDILCLGKAL TGGYLTLSATLTTRAVAETISKGDAGCFMHGPTF MANPLACAVASANLSLLAENSWQQ QVSKIEDQLKRELLPLAQEDTVADVRVLGAIGVV EMKKPVNVARLQRSFVEQGVWIRP FGKLIYLMPPYIISQHALTRLTAAVDRGS" /gene="bioA" </pre>
misc-feature	complement(176766..177875)	<pre> /note="Pfam match to entry PF00202 aminotran-3, Aminotransferases class-III pyridoxal-phosphate, score 527.10, E-value 8.3e-183" /gene="bioA" </pre>
misc-feature	complement(177138..177251)	<pre> /note="PS00600 Aminotransferases class-III pyridoxal-phosphate attachment site." /gene="bioB" </pre>
gene	178073..179110	<pre> /note="synonym: YPO1151" /gene="bioB" </pre>
CDS	178073..179110	<pre> /EC-number="2.8.1.6" /note="Similar to many eg. Escherichia coli biotin synthase BioB SW:BIOB-ECOLI (P12996) (346 aa) fasta scores: E(): 0, 84.6% id in 344 aa" /codon-start=1 /transl-table=11 /product="biotin synthase" /protein-id="CAC89992.1" /db-xref="GI:15979214" /db-xref="SPTREMBL:Q8ZGX2" /translation="MATYHHWTVGQALALFDKPL LELLFEAQQVHRQHFDPRQVQVST LLSIKTGACPEDCKYCPQSSRYKTGLESERLMQV EQVLESAKKAKAAGSTRFCMGAAW KNPHERDMPYLAKMVEGVKALGMETCMTLGSLSK QQAHLADAGLDYYNHNLDTSPEF YGSIIITRSYQERLDTLNEVRDAGIKVCSGGIVG LGETVRDRAGLLVQLANLPKPES VPINMLVKVKGTPLENNAEVDAFEFIRTIAVARI MMPSSYVRLSAGREQMNEQTQAMC FMAGANSIFYGCKLLTTPNPDEDKDLQLFRKLGL NPQQTATSHGDREQQQALTEQLLH GDTAQFYNAAV" /gene="bioB" </pre>
misc-feature	178085..179005	<pre> /note="Pfam match to entry PF01792 Biotin-synth, Biotin synthase, score 689.90, E-value 1.2e-203" </pre>
gene	179110..180261	<pre> /gene="bioF" </pre>
CDS	179110..180261	<pre> /note="synonym: YPO1152" /gene="bioF" /EC-number="2.3.1.47" /note="Similar to many eg. Escherichia coli 8-amino-7-oxononanoate synthase BioF SW:BIOF-ECOLI (P12998) (384 aa) fasta scores: E(): 0, 65.8% id in 383 aa" /codon-start=1 /transl-table=11 /product="8-amino-7-oxononanoate </pre>

		/protein-id="CAC89993.1"
		/db-xref="GI:15979215"
		/db-xref="SPTREMBL:Q8ZGX1"
		/translation="MSWQDKIAQGLQRRRDAAAY RTRQVNEGANGRWLQSGERQYLNF SSNDYLGLSQNDEVIAAWQQGARRYGVGSGGSGH VTGYSQPHARLEQQALADWLGYPRA LLFISGYAANQAVLTALTADDDRILADKLSHASL LEAAAHSPAQLRRFQHNQPEALQN LLIKPCQGGQTLVVTEGVFSMDGDSAPLAALQQQT SAAGGWLLVDDAHGIGVHGEGRG SCWLQGVQPELLVVTFGKAFGLSGAAVLCQEPVA EYLLQYARHLIYSTAMPPAQACAL QAALRQVQQGDALRQQQLQQRIRQFRATAAHLPLQ LGASKTAIQPLLVGDNQQSLIWAE QLRAAGLWVTAIRPPTVPPGSARLRITLSAAHQ EDIDRLLEVLYGLCH"
misc-feature	179350..180186	/gene="bioF" /note="Pfam match to entry PF00222 aminotran-2, Aminotransferases class-II, score 337.40, E-value 1.6e-97"
misc-feature	179806..179835	/gene="bioF" /note="PS00599 Aminotransferases class-II pyridoxal-phosphate attachment site."
gene	180245..181048	/gene="bioC"
CDS	180245..181048	/note="synonym: YPO1153" /gene="bioC" /note="Similar to many eg. Escherichia coli biotin synthesis protein BioC SW:BIOC-ECOLI (P12999) (251 aa) fasta scores: E(): 0, 49.6% id in 250 aa" /codon-start=1 /transl-table=11 /product="biotin synthesis protein BioC" /protein-id="CAC89994.1" /db-xref="GI:15979216" /db-xref="SPTREMBL:Q8ZGX0" /translation="MASVTEHAQWGVGCLPPLNV DKQAIAAAFSRAAESYDSAANLQR ETGHRLVQLGQQHTGFVVLDAGCGTGHFSQHWRL LGKRVIALDLAAGMLDYARQQQVA DDYLLGDIEHIPLPDQSDICFSNLAVQWCSDLG AALSEFYRVTRPGGIIILFSTLAEG SLDELGQAWQQVDGQRHVNDLPLQHIQTACQYY RHHLTTALYQPRFPNVIALMRSLO GIGATHLHHGRQAGLQGRQRLAALQRAYVMQSGG YPLSYHVMVYGVYRD"
gene	181041..181763	/gene="bioD"
CDS	181041..181763	/note="synonym: YPO1154" /gene="bioD" /EC-number="6.3.3.3" /note="Similar to many eg. Escherichia coli dethiobiotin synthetase BioD SW:BIOD-ECOLI (P13000) (224 aa) fasta scores: E(): 0, 71.2% id in 229 aa" /codon-start=1 /transl-table=11 /product="dethiobiotin synthetase" /protein-id="CAC89995.1" /db-xref="GI:15979217" /db-xref="SWISS-PROT:Q8ZGW9" /translation="MTKRWFITGTDTDVGKTVAS CALLQAATAQGYRTAGYKPVASGS QMTADGLRNSDALALQANSSQRLGYSQVNPFTFL EATSPHIASESEGRAIPLTALSQ LRQLEPSADWILIEGAGGWFTPLSPQATFADWVQ QEQLPVIMVVGKLGKINHALTA QAIQHAGLTLAGWVANEVTPAGRRQAQAYQATLTR MITAPLLGIIPYLSDIEENPVTR RDLGHYLDLTVLRAAEREAVNM"

-	25)	-	
CDS	complement(181915..1826	/gene="YPO1155"	
	25)		/note="Similar to Synechocystis sp high-affinity branched-chain amino acid transport ATP-binding protein TR:Q55753 (EMBL:D64002) (249 aa) fasta scores: E(): 5.8e-31, 43.3% id in 238 aa, and to Escherichia coli high-affinity branched-chain amino acid transport ATP-binding protein LivF SW:LIVF-ECOLI (P22731) (237 aa) fasta scores: E(): 5.1e-22, 36.3% id in 237 aa" /codon-start=1 /transl-table=11 /product="putative amino acid transporter" /protein-id="CAC89996.1" /db-xref="GI:15979218" /db-xref="SPTREMBL:Q8ZGW8" /translation="MLSLTAVNQYYGNHILWDI NLELPRGQCTCLIGRNGVGKTTLI NCIMGHLPIKSGTMIWQPHHEPPQNQQPVERR NALGIGYVPQGGQIFSQLSVEDNL LVAVLAGRHKSHPIPGWVFELFPLLHDKRSQRG ELTRNQQQQLAIARALVAEPELLI LDEPGSGTSPALSEDISTVLHQLSRNLGMTLLLV EHRLPFIQHIADRFCLMAGGRNVA QGTLDDLNEGLISEHLAR"
misc-feature	complement(181984..1825	/gene="YPO1155"	
	47)		/note="Pfam match to entry PF00005 ABC-tran, ABC transporter, score 135.40, E-value 1.1e-36"
misc-feature	complement(182503..1825	/gene="YPO1155"	
	26)		/note="PS00017 ATP/GTP-binding site motif A (P-loop)."
gene	183715..185730	/gene="uvrB"	
		/note="synonym: YPO1156"	
CDS	183715..185730	/gene="uvrB"	
		/note="Similar to many eg. Escherichia coli excinuclease ABC subunit B UvrB SW:UVRB-ECOLI (P07025) (673 aa) fasta scores: E(): 0, 85.9% id in 673 aa" /codon-start=1 /transl-table=11 /product="excinuclease ABC subunit B" /protein-id="CAC89997.1" /db-xref="GI:15979219" /db-xref="SWISS-PROT:Q8ZGW7" /translation="MSKSFKLHSVFKPAGDQPEA IRKLEEGLENGLAHQTLTGVTGSG KTFTVANVIADLNRPTMILAPNKTLLAAQLYGEMK EFPDNAVVEYFVSYYDYQPEAYV PSSDTFIEKDASVNEHIEQMRLSATKALLERRDV VVVASVSATYGLGDPDLYLKMLH LTRGMIIDQRSILRRLSELQYSRNDQVFQRGTR VRGEVIDIFPAESDEWALRVELED EEVERLSIFDPLTGQLQHEVPRFTVYPKTHYVTP RERILQAMEEIKVELAERRQVLLA NNKLLEEQRLSQRTQFDLEMMNELGYCSGIENYS RYLSGRGPGEAPPTLFDYLPADGL LIVDESHVTIPQIGGMYKGDRSRKETLVEYGFRL PSALDNRPMPRFEEFEALAPQTIYV SATPGKYELEKSGGDIIEQVVRPTGLLDPLIEVR PVATQVDDLLSEIRIRAAINERVL VTTLTKRMAEDLTDYLSEHGAKVRYLHSDIDTVE RVEIIRDLRLGEFDVLVGINLLRE GLDMPEVSLVAILDADKEGFLRSERSLIQTIGRA ARNLNGKAILYGDRITASMEKAIG ETERRRAKQQAYNEERRIIPQGLNKKIGDILQLG	



		LSPKALDQKIRELEAKMYTYAQNLEFEQAAELRD QVHQLRQQFIAIS" /gene="uvrB" /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
misc-feature	183829..183852	
misc-feature	185092..185352	/gene="uvrB" /note="Pfam match to entry PF00271 helicase-C, Helicases conserved C-terminal domain, score 78.20, E-value 1.7e-19"
misc-feature	185605..185712	/gene="uvrB" /note="Pfam match to entry PF02151 UVR, UvrB/uvrC motif, score 58.00, E-value 2e-13"
gene	186022..186267	/gene="YPO1157"
CDS	186022..186267	/gene="YPO1157" /note="Similar to Vibrio cholerae hypothetical protein VC1816 TR:Q9KR31 (EMBL:AE004257) (71 aa) fasta scores: E(): 6.9e-17, 64.7% id in 68 aa, and to Vibrio marinus genes, complete cds, similar to eicosapentaenoic acid synthesis gene cluster TR:Q9RA23 (EMBL:AB025342) (72 aa) fasta scores: E(): 1.2e-16, 68.3% id in 63 aa" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAC89998.1" /db-xref="GI:15979220" /db-xref="SPTREMBL:Q8ZGW6" /translation="MSEHLSKDPLHGITLEQLLT KLVENYGWDGLADRIQINCFISDP SIKSSLKFLR RTPWARQKVEALYIEMSDKAEWLK GQS"
gene	complement(186398..1873 21)	/gene="YPO1158"
CDS	complement(186398..1873 21)	/gene="YPO1158"  /note="Similar to Escherichia coli hypothetical protein YbhK SW:YBHK-ECOLI (P75767) (302 aa) fasta scores: E(): 0, 77.7% id in 301 aa, and to Vibrio cholerae hypothetical protein VC1023 TR:Q9KT82 (EMBL:AE004184) (296 aa) fasta scores: E(): 0, 53.9% id in 297 aa" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAC89999.1" /db-xref="GI:15979221" /db-xref="SWISS-PROT:P58589" /translation="MRNRTLADLERVVALGGGHG LGRVMSSLSSLSRLTGIVTTTDN GGSTGRIRRSEGGIAWGDTRNCLNQLITEPSVAS AMFEYRFTGNGELAGHNLGNLMLK ALDHL SIRPIEAINLVRSLKVDALLIPMSEQPV DLMAIDHEGHPIYGEVNIDQLAQM PQEMLLSPPVHATREAVEAINQADVILIGPGSFL TSLMPLLLLDLTQALRRSSASMI YIGNL GRELSPAAAALSLQDKLTIMESKIGRKII DAVIVSPTIDISGVKDRIIVQQPL EAKDIPHRHDRELLRQALENTLQQLNGADSV"
misc-feature	complement(186416..1872 88)	/gene="YPO1158"  /note="Pfam match to entry PF01933 UPF0052, Uncharacterised protein family UPF0052, score 345.20, E-value 7.4e-100"

CDS	187853..188833	/note="synonyms: bisA, chlA, chlA1, narA, YPO1159" /gene="moaA" /note="Similar to Escherichia coli molybdenum cofactor biosynthesis protein A MoaA SW:MOAA-ECOLI (P30745) (329 aa) fasta scores: E(): 0, 78.2% id in 326 aa, and to Vibrio cholerae molybdenum cofactor biosynthesis protein A VC1024 TR:Q9KT81 (EMBL:AE004184) (334 aa) fasta scores: E(): 0, 65.0% id in 329 aa" /codon-start=1 /transl-table=11 /product="molybdenum cofactor biosynthesis protein A" /protein-id="CAC90000.1" /db-xref="GI:15979222" /db-xref="SWISS-PROT:Q8ZGW5" /translation="MVQLTDAFARKFYYLRLSITDVCNFRCTYCLPEGYRPDGVKSFLSLDEINRVSRFAALLGTEKIRLTGGEPSMRRDFTDIIATIRQNPAIRTLAVTTNGYRLVRDVAQWRDAGLTAINVSVDSLDPRQFHAITGQDKFYQVMQGIDAAFDAGFDKVKVNAVLMRDVNDRLSAFLDWIKPRPIQLRFIELMETGEGGNLFRKHHVSGGVIRQQLLEQG WQQQDRARSDGPAQVFHHSYQGEIGLIMPYEKDFCASCNRLRVSA LGNLHLCLFGEQGITLRDLLGSDDQQDELIARIQSALQTKKQTHFLHQN SGITQNL SFIGG" /gene="moaA" /note="PS01305 moaA / nifB / pqqE family signature."
misc-feature	187907..187942	/gene="moaA" /note="PS01305 moaA / nifB / pqqE family signature."
misc-feature	188012..188656	/gene="moaA" /note="Pfam match to entry PF01444 MoaA-NifB-PqqE, moaA / nifB / pqqE family, score 258.80, E-value 7.5e-74"
gene	188934..189413	/gene="moaC" /note="synonyms: chlA3, YPO1160"
CDS	188934..189413	/gene="moaC" /note="Similar to Escherichia coli molybdenum cofactor biosynthesis protein C MoaC SW:MOAC-ECOLI (P30747) (160 aa) fasta scores: E(): 0, 87.9% id in 157 aa, and to Vibrio cholerae molybdenum cofactor biosynthesis protein C VC1026 TR:Q9KT79 (EMBL:AE004184) (160 aa) fasta scores: E(): 0, 78.5% id in 158 aa" /codon-start=1 /transl-table=11 /product="molybdenum cofactor biosynthesis protein C" /protein-id="CAC90001.1" /db-xref="GI:15979223" /db-xref="SWISS-PROT:Q8ZGW4" /translation="MTQLTHINTAGEAHMVDVSAKNETVREARAEAFVDMQAATLAMIIDGSHHKGDVFATARIAGIQA AKKTWELIPLCHPLLTKVEVKLEAQPEHNRVRIETCRLTGKTGVEMEALTAASVAALTIYDMCKAVQKDMIIGPVRLLTKSGGKSGDFKVDI" /gene="moaC" /note="Pfam match to entry PF01967 MoaC, MoaC family, score 306.40, E-value 3.3e-88"
misc-feature	188976..189383	/gene="moaC" /note="Pfam match to entry PF01967 MoaC, MoaC family, score 306.40, E-value 3.3e-88"
gene	189410..189655	/gene="moaD" /note="synonyms: chlA4, chlM, YPO1161"
CDS	189410..189655	/gene="moaD" /note="Similar to Escherichia coli

		factor, subunit 1 MoaD SW:MOAD-ECOLI (P30748) (81 aa) fasta scores: E(): 2.9e-23, 71.6% id in 81 aa, and to Vibrio cholerae molybdenum cofactor biosynthesis protein D vc1027 TR:Q9KT78 (EMBL:AE004184) (81 aa) fasta scores: E(): 2.4e-17, 63.0% id in 81 aa" /codon-start=1 /transl-table=11 /product="molybdopterin [mpt] converting factor, subunit 1" /protein-id="CAC90002.1" /db-xref="GI:15979224" /db-xref="SPTREMBL:Q8ZGW3" /translation="MIQILFFAQVRELVGVDKLO LAAEFPTVEALRQSLCQRGERWQL ALEEGKLLTAVNQSLVSAQHPLAAGDEVAFFPPV TGG" /gene="moaE" /note="synonyms: chlA5, YPO1162" /gene="moaE" /note="Similar to Escherichia coli molybdopterin [mpt] converting factor, subunit 2 MoaE SW:MOAE-ECOLI (P30749) (149 aa) fasta scores: E(): 0, 81.7% id in 120 aa, and to Vibrio cholerae molybdenum cofactor biosynthesis protein E VC1028 TR:Q9KT77 (EMBL:AE004184) (150 aa) fasta scores: E(): 0, 68.3% id in 120 aa" /codon-start=1 /transl-table=11 /product="molybdopterin [mpt] converting factor, subunit 2" /protein-id="CAC90003.1" /db-xref="GI:15979225" /db-xref="SWISS-PROT:Q8ZGW2" /translation="MMENTRIRVGAEAFSVGDEY TWLSQCDEGDGAVVTFTGKVRNHNL GASVSALTLEHYPGMTEKALTEIADARSRWSLQ RVSVIHRVGPLFPGDEIVFVGVT AHRSMAFEAAEFIMDYLLKTRAPFWKREATVEGER WVESRSDSHIAAKRW" /gene="moaE" /note="Pfam match to entry PF02391 MoeA, , score 123.70, E-value 3.4e-33" /gene="YPO1163" /gene="YPO1163" /note="Similar to Escherichia coli hypothetical 25.9 kDa protein in moaE-rhlE intergenic region SW:YBHL-ECOLI (P75768) (234 aa) fasta scores: E(): 0, 73.3% id in 236 aa, and to Borrelia burgdorferi conserved hypothetical integral membrane protein BB0539 TR:O51489 (EMBL:AE001155) (232 aa) fasta scores: E(): 0, 49.3% id in 215 aa" /codon-start=1 /transl-table=11 /product="putative membrane protein" /protein-id="CAC90004.1" /db-xref="GI:15979226" /db-xref="SPTREMBL:Q8ZGW1" /translation="MDRYPRSNNGSIVERAGSGIQ AYMAQVYGWMTCLLLTAVVAWYA ANTPSIIIFALQSNQILFFGLIIAQLGLVFVISGM VNRLSGTAATSLFMYLSALTGLTL
gene	189655..190110	
CDS	189655..190110	
misc-feature	189748..190023	
gene	190253..190963	
CDS	190253..190963	

		RDLSGMSGMLFMGLIGIILASLVN IWLKSPALMWVVTYIGVLVGVGLTAYDTQKLKNL GAQLDVNDKDSFRKYSIVGALTLY LDFINLFLMLLRIFGNRR"
misc-feature	190313..190381	/gene="YPO1163" /note="one of 7 probable transmembrane helices predicted for YPO1163 by TMHMM2.0"
misc-feature	190373..190960	/gene="YPO1163" /note="Pfam match to entry PF01027 UPF0005, Uncharacterized protein family UPF0005, score 190.90, E-value 2e-53"
misc-feature	190424..190492	/gene="YPO1163" /note="one of 7 probable transmembrane helices predicted for YPO1163 by TMHMM2.0"
misc-feature	190511..190579	/gene="YPO1163" /note="one of 7 probable transmembrane helices predicted for YPO1163 by TMHMM2.0"
misc-feature	190592..190651	/gene="YPO1163" /note="one of 7 probable transmembrane helices predicted for YPO1163 by TMHMM2.0"
misc-feature	190670..190738	/gene="YPO1163" /note="one of 7 probable transmembrane helices predicted for YPO1163 by TMHMM2.0"
misc-feature	190751..190810	/gene="YPO1163" /note="one of 7 probable transmembrane helices predicted for YPO1163 by TMHMM2.0"
misc-feature	190883..190951	/gene="YPO1163" /note="one of 7 probable transmembrane helices predicted for YPO1163 by TMHMM2.0"
misc-feature	191053..191764	/note="IS200-like insertion sequence: IS1541. Contains a 'G' at nucleotide position 315"
gene	191198..191656	/gene="tnp"
CDS	191198..191656	/note="synonym: YPO1164" /gene="tnp" /note="Similar to Salmonella typhimurium, and Salmonella typhi transposase for insertion sequence IS200 TnpA SW:T200-SALTY (Q57334) (152 aa) fasta scores: E(): 0, 94.1% id in 152 aa. Identical to the Yersinia pseudotuberculosis IS1541 element transposase Tnp TR:Q9X9F5 (EMBL:AJ238014) (152 aa) fasta scores: E(): 0, 100.0% id in 152 aa" /codon-start=1 /transl-table=11 /product="transposase for the IS1541 insertion element" /protein-id="CAC90005.1" /db-xref="GI:15979227" /db-xref="SPTREMBL:Q9X9F5" /translation="MRDEKSLAHTRWNCKYHIVF APKYRRQVFYREKRRAIGSILRKL CEWKNVNILEAECCVDHIHMLLEIPPKMSVSGFM GYLKKGKSSLMLEYEQFGDLKFKYRN REFWCRGYVDTVGKNTARIQEYIKHQLEEDKMG EQLSIPYPGSPFTGRK"
misc-feature	191252..191563	/gene="tnp" /note="Pfam match to entry PF01797 Transposase-17, Transposase IS200 like, score 236.10, E-value 5.1e-67"
gene	complement(191885..193588)	/gene="betaA" /note="synonym: YPO1165"

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/EC-number="1.1.99.1"
/note="Similar to many eg.
Escherichia coli choline
dehydrogenase BetA SW:BETA-ECOLI
(P17444) (556 aa) fasta scores:
E(): 0, 79.4% id in 553 aa, and to
Homo sapiens choline dehydrogenase
ChdH TR:Q9NY17 (EMBL:AJ272267)
(482 aa) fasta scores: E(): 0,
50.1% id in 467 aa"
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DFDHWASLSGLEDWSYLDCLPYFRKAETRDIGPN
DFHGGE GPVSVTTPKIGNNPLFHA
MVAAGVQAGYPRTDDLNGYQQEGFGPMDRTVTPK
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PVS LYPALLWFNQP KIGIEWLFNG
TGV GASNQFEAGGFIRSRDAFTWPNIQYHFLPVA
INYN GSNVKEHGFQAHVGS MRSP
SRGRIQV KSKDPRQHPSILFNYSSEQDWHEFRD
AIRITREIIAQPALDPYRGREISP
GANVQNDDELDAFIREHAETAYHPSCSCKMGDDK
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/misc-feature complement(192008..1935 /gene="betA"
82)
/note="Pfam match to entry PF00732
GMC-oxred, GMC oxidoreductases,
score 963.20, E-value 6.6e-286"
/misc-feature complement(192770..1928 /gene="betA"
14)
/note="PS00624 GMC oxidoreductases
signature 2."
/misc-feature complement(193274..1933 /gene="betA"
45)
/note="PS00623 GMC oxidoreductases
signature 1."
/gene complement(193611..1950 /gene="betB"
83)
/note="synonym: YPO1166"
CDS complement(193611..1950 /gene="betB"
83)
/EC-number="1.2.1.8"
/note="Similar to Escherichia coli
betaine aldehyde dehydrogenase
BetB SW:DHAB-ECOLI (P17445) (489
aa) fasta scores: E(): 0, 76.7% id
in 489 aa, and to Homo sapiens
aldehyde dehydrogenase, E3 isozyme
AldH9 or AldH7 or AldH9A1
SW:DHAG-HUMAN (P49189) (493 aa)
fasta scores: E(): 0, 51.3% id in
483 aa"
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dehydrogenase"
/protein-id="CAC90007.1"
/db-xref="GI:15979229"
/db-xref="SPTREMBL:Q8ZGV9"
/translation="MSRYGLQKLYINGAYTDSTS
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 AGLPAGVFNVLGTGSGDQVGQMLTE  
 HPGIAKVSFTGGIASGKKVMAAAGSTLKDVTME  
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 KRIHIGDPSDERTNFGPLVSFQHR  
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 MPVGGYKHSGVGRENGISTLEHYTQIKSIQVELG  
 SFNSVF"

misc-feature	complement (193635..195044)	/gene="betB"  /note="Pfam match to entry PF00171 aldedh, Aldehyde dehydrogenase family, score 804.40, E-value 4.1e-238"
misc-feature	complement (194214..194249)	/gene="betB"  /note="PS00070 Aldehyde dehydrogenases cysteine active site."
misc-feature	complement (194310..194333)	/gene="betB"  /note="PS00687 Aldehyde dehydrogenases glutamic acid active site."
gene	complement (195141..195737)	/gene="betI"  /note="synonym: YPO1167"
CDS	complement (195141..195737)	/gene="betI"  /note="Similar to Escherichia coli regulatory protein of the osmoregulatory choline-glycine betaine pathway BetI SW:BETI-ECOLI (P17446) (195 aa) fasta scores: E(): 0, 64.1% id in 192 aa" /codon-start=1 /transl-table=11 /product="TetR-family regulatory protein" /protein-id="CAC90008.1" /db-xref="GI:15979230" /db-xref="SPTREMBL:Q8ZGV8" /translation="MPKVGMQPIRRQQLIEATMA AVNEVGMHEASIAQIAKRAGVSNG IISHYFRDKNGLLEATMRYLIRHLGEAVKQHLAA LSVNDPRARLRAIAEGNFDDSQIN SAAMKTWLAFWASSMHSPQLYRLQQVNNRRLYSN LCAEFKRCLPREQAQLAAKGMAGL IDGLWLRSAISGEHFNREALLIIHNYIEQQLNI KYKC"
misc-feature	complement (195537..195584)	/gene="betI"  /note="PS00038 Myc-type, 'helix-loop-helix' dimerization domain signature."
misc-feature	complement (195558..195698)	/gene="betI"  /note="Pfam match to entry PF00440 tetR, Bacterial regulatory proteins, tetR family, score 53.90, E-value 2.3e-12"
misc-feature	complement (195570..195662)	/gene="betI"  /note="PS01081 Bacterial regulatory proteins, tetR family signature."
misc-feature	complement (195585..195650)	/gene="betI"

		motif with score 1758 (+5.17 SD) at aa 30-51, sequence ASIAQIAKRAGVSNGLIISHYFR"
gene	196102..198123	/gene="betT" /note="synonym: YPO1168"
CDS	196102..198123	/gene="betT" /note="Similar to Escherichia coli high-affinity choline transport protein BetT SW:BETT-ECOLI (P17447) (677 aa) fasta scores: E(): 0, 77.6% id in 678 aa, and to Erwinia amylovora high-affinity choline transport protein BetT TR:AAG31040 (EMBL:AF264948) (676 aa) fasta scores: E(): 0, 80.0% id in 681 aa" /codon-start=1 /transl-table=11 /product="high-affinity choline transport protein" /protein-id="CAC90009.1" /db-xref="GI:15979231" /db-xref="SPTREMBL:Q8ZGV7" /translation="MVTSDIDTKPQKDTLNPVVF FTSAGLILAFCLMTIFYTDLSNRW IGITLNVWSATFGWYYLLAATLYIVFVIYIATSR YGSIKLGPEQSKPEFSLVSWAAML FAAGIGIDLMFFSVAEPVTQYMPPEQGQQTLEA ARQAMVWTLFHYGLTGWSMYALMG IALGYFSYRYNPLPLTIRSAFYPIFGKRIDGPIGH SVDIAAVIGTIFGIATTLGIGVVQ LNYGLNVLFHIPESLAVQAGLILLSVMAAVSVT SGVNBKIRILSEVNVLLALGLILF LLNALVLNVGDYINRFLGMTLNSFAFDRPTQWMN SWTLFFWAWVWVWSPFVGLFLARI SRGRTIRQFVVGTLIIPFVFTLLWLSIFGNSALY QILHGNIAFANEVMEFPERGFYSL LAQYPGFTLSASVATITGLLFYVTSADSGSLVLG NETSRLADINNDSPNWLRTFWSIT IGLTLGLMLMTDGVAALQONATVIMGLPFSFVIFV VMVGLYKSLKIEDYRKASSQQTPT PTLISGNEVLNWKQRLSRVMNYPGTTYTAKILDT ICRPAMEEVAQELAVRGVKVEFNE LPPKEDEQLNRLNHLELLVHLGDEQNFFVYQIWPQ RYSVPAFTYRARGSKSHYYRLEY LLEGTQGNLMDYSKEQIINNILDQYERHNMNLFH IQSEAPGNIMTFPDQ"
misc-feature	196144..196212	/gene="betT" /note="one of 12 probable transmembrane helices predicted for YPO1168 by TMHMM2.0"
misc-feature	196156..197589	/gene="betT" /note="Pfam match to entry PF02028 BCCT, BCCT family transporter, score 909.00, E-value 1.3e-269"
misc-feature	196255..196323	/gene="betT" /note="one of 12 probable transmembrane helices predicted for YPO1168 by TMHMM2.0"
misc-feature	196384..196452	/gene="betT" /note="one of 12 probable transmembrane helices predicted for YPO1168 by TMHMM2.0"
misc-feature	196534..196602	/gene="betT" /note="one of 12 probable transmembrane helices predicted for YPO1168 by TMHMM2.0"
misc-feature	196687..196755	/gene="betT" /note="one of 12 probable transmembrane helices predicted for YPO1168 by TMHMM2.0"
misc-feature	196798..196866	/gene="betT" /note="one of 12 probable transmembrane helices predicted for YPO1168 by TMHMM2.0"



misc-feature	197026..197094	/note="one of 12 probable transmembrane helices predicted for YPO1168 by TMHMM2.0"
misc-feature	197032..197061	/gene="betT" /note="one of 12 probable transmembrane helices predicted for YPO1168 by TMHMM2.0"
misc-feature	197128..197187	/gene="betT" /note="PS01303 BCCT family of transporters signature."
misc-feature	197278..197346	/gene="betT" /note="one of 12 probable transmembrane helices predicted for YPO1168 by TMHMM2.0"
misc-feature	197434..197502	/gene="betT" /note="one of 12 probable transmembrane helices predicted for YPO1168 by TMHMM2.0"
misc-feature	197512..197571	/gene="betT" /note="one of 12 probable transmembrane helices predicted for YPO1168 by TMHMM2.0"
gene CDS	198355..199248 198355..199248	/gene="YPO1169" /gene="YPO1169" /note="Similar to many eg. Escherichia coli xanthosine operon regulatory protein WapR SW:XAPR-ECOLI (P23841) (294 aa) fasta scores: E(): 0, 38.3% id in 287 aa" /codon-start=1 /transl-table=11 /product="putative LysR-family regulatory protein" /protein-id="CAC90010.1" /db-xref="GI:15979232" /db-xref="SPTREMBL:Q8ZGV6" /translation="MQKLLFSGRINLKMIRYFLA VSDELHFGKAAERLHISQPPLSLQ IKELEDALGFPLFIRDSRNVVLTLAGEMMKAE MVDVDNIENSLSRVSYIARHEQTHL NIGIIGSALWHQLLEKFKHYKTVNPKTTWSL HELPPSKQYEALLNKKLDIGFWRCADL EQNPALIYRRVEKQRVAVAVSNESLLVNKKIL TKDLSGQTLIFLTFNHSGYSKNLYN SCLNAGCTPQAIYQFDEPQTQLAFVNSNLGIA LVPESMQEIIPWPNIKFIPLKEDLSAD LFAVYHPDSVTPALNKKLLALF"
misc-feature	198388..198816	/gene="YPO1169" /note="Pfam match to entry PF00126 HTH-1, Bacterial regulatory helix-turn-helix protein, lysR family, score 123.40, E-value 4.3e-33"
misc-feature	198427..198492	/gene="YPO1169" /note="Predicted helix-turn-helix motif with score 1460 (+4.16 SD) at aa 25-46, sequence LHFHGKAAERLHISQPPLSLQIK"
misc-feature	198430..198522	/gene="YPO1169" /note="PS00044 Bacterial regulatory proteins, lysR family signature."
gene	complement(199286..200167)	/gene="YPO1170"
CDS	complement(199286..200167)	/gene="YPO1170"  /note="Weakly similar to Bacillus subtilis hypothetical 35.8 kDa protein in lplD-pel intergenic region SW:YETK-BACSU (O31540) (330

22.5% id in 298 aa, and to Erwinia  
 chrysanthemi PecM protein pecM  
 SW:PECM-ERWCH (P42194) (297 aa)  
 fasta scores: E(): 0.00048, 20.9%  
 id in 277 aa"  
 /codon-start=1  
 /transl-table=11  
 /product="putative membrane  
 protein"  
 /protein-id="CAC90011.1"  
 /db-xref="GI:15979233"  
 /db-xref="SPTREMBL:Q8ZGV5"  
 /translation="MTTRVLKAHLQMLGFTALLG  
 GSFIASATISNALPPMVITWLRYS  
 IASLFFVVLVSQGLLTLPHYRDLGRYTLISLPP  
 LLYFACMIFSLQTTSAINSSALYT  
 TVPLMSVMVSVVFLNAKSTWPVVAALLLGILGAL  
 LIIFKGDLSQVLRSLMPSDYLF  
 FGCLGMALNPVVKKLHRGEHALVLTGWSLICAT  
 LLLTVIIAYQLPEIEWRNISVITW  
 SGVLYLATFATALSFLLFQKACIVLSPTKVSGYV  
 YLIPLSVIVTNMMLGQTINWQEIA  
 SGAILVIIAMAILVKAK"

misc-feature	complement(199292..199342)	/gene="YPO1170"  /note="one of 10 probable transmembrane helices predicted for YPO1170 by TMHMM2.0"
misc-feature	complement(199298..199678)	/gene="YPO1170"  /note="Pfam match to entry PF00892 DUF6, Integral membrane protein DUF6, score 41.70, E-value 1.6e-08"
misc-feature	complement(199358..199423)	/gene="YPO1170"  /note="one of 10 probable transmembrane helices predicted for YPO1170 by TMHMM2.0"
misc-feature	complement(199463..199528)	/gene="YPO1170"  /note="one of 10 probable transmembrane helices predicted for YPO1170 by TMHMM2.0"
misc-feature	complement(199559..199624)	/gene="YPO1170"  /note="one of 10 probable transmembrane helices predicted for YPO1170 by TMHMM2.0"
misc-feature	complement(199652..199717)	/gene="YPO1170"  /note="one of 10 probable transmembrane helices predicted for YPO1170 by TMHMM2.0"
misc-feature	complement(199748..200119)	/gene="YPO1170"  /note="Pfam match to entry PF00892 DUF6, Integral membrane protein DUF6, score 54.80, E-value 1.9e-12"
misc-feature	complement(199748..199804)	/gene="YPO1170"  /note="one of 10 probable transmembrane helices predicted for YPO1170 by TMHMM2.0"
misc-feature	complement(199820..199870)	/gene="YPO1170"  /note="one of 10 probable transmembrane helices predicted for YPO1170 by TMHMM2.0"
misc-feature	complement(199883..199948)	/gene="YPO1170"  /note="one of 10 probable transmembrane helices predicted for YPO1170 by TMHMM2.0"

	53)		/note="one of 10 probable transmembrane helices predicted for YPO1170 by TMHMM2.0"
misc-feature	complement(200066..200131)		/gene="YPO1170"
gene	200480..201343		/note="one of 10 probable transmembrane helices predicted for YPO1170 by TMHMM2.0"
CDS	200480..201343		/gene="xapA" /note="synonyms: pndA, YPO1171" /gene="xapA" /EC-number="2.4.2.-" /note="Similar to Escherichia coli xanthosine phosphorylase XapA or PndA SW:XAPA-ECOLI (P45563) (277 aa) fasta scores: E(): 0, 70.2% id in 272 aa, and to Mus musculus purine nucleoside phosphorylase SW:PNPH-MOUSE (P23492) (289 aa) fasta scores: E(): 0, 42.6% id in 265 aa" /codon-start=1 /transl-table=11 /product="xanthosine phosphorylase" /protein-id="CAC90012.1" /db-xref="GI:15979234" /db-xref="SPTREMBL:Q8ZGV4" /translation="MTTVNSNINVDADFNELPFQ AVKYIQKIKPGFKPQIAFILGSGL GDLVDQITNDTTISYADIPGFVSSVHGHAGELV LGDLCGVPVMCMKGRGHFYEGKGM SIMTNPVVRTFKLMGCEFLFCTNAAGSLRPEVLPG SVVMLKDHINTMPGTPLVGPNDNR FGPRFFSLANAYDKDLRADMAKIAQQLDIPLTEG VFVSYLGPCFETPAEIRMMQIIGG DVVGMSVVPEVLSAAHCGLKVIALTAITNLAEGL SDVVLSEQTLKFAKVASVNFTKL IEAFLKSKALR" /gene="xapA" /note="Pfam match to entry PF00896 Mtap-PNP, phosphorylases family 2, score 362.50, E-value 4.6e-105"
misc-feature	200585..201220		/gene="xapB" /note="synonym: YPO1172"
gene	201482..202126		/pseudo /gene="xapB" /note="Gene interrupted by IS1541. Similar to Escherichia coli xanthosine permease XapB SW:XAPB-ECOLI (P45562) (418 aa) fasta scores: E(): 0, 62.5% id in 216 aa, and to Escherichia coli nucleoside permease NupG nupG SW:NUPG-ECOLI (P09452) (418 aa) fasta scores: E(): 0, 49.6% id in 248 aa" /pseudo /codon-start=1 /transl-table=11 /product="xanthosine permease (pseudogene)"
CDS	201482..202126		/gene="xapB" /note="one of 6 probable transmembrane helices predicted for YPO1172 by TMHMM2.0"
misc-feature	201500..201568		/pseudo /gene="xapB" /note="one of 6 probable transmembrane helices predicted for YPO1172 by TMHMM2.0"
misc-feature	201596..201664		/pseudo /gene="xapB" /note="one of 6 probable transmembrane helices predicted for YPO1172 by TMHMM2.0"
misc-feature	201683..201742		/pseudo /gene="xapB" /note="one of 6 probable

		for YPO1172 by TMHMM2.0"
misc-feature	201770..201838	/pseudo /gene="xapB" /note="one of 6 probable transmembrane helices predicted for YPO1172 by TMHMM2.0"
misc-feature	201875..201931	/pseudo /gene="xapB" /note="one of 6 probable transmembrane helices predicted for YPO1172 by TMHMM2.0"
misc-feature	201959..202027	/pseudo /gene="xapB" /note="one of 6 probable transmembrane helices predicted for YPO1172 by TMHMM2.0"
misc-feature	202127..202838	/pseudo /note="IS200-like insertion sequence: IS1541. Contains a 'G' at nucleotide position 315"
gene	202272..202730	/gene="tnp" /note="synonym: YPO1173"
CDS	202272..202730	/gene="tnp" /note="Similar to Salmonella typhimurium, and Salmonella typhi transposase for insertion sequence IS200 TnpA SW:T200-SALTY (Q57334) (152 aa) fasta scores: E(): 0, 94.1% id in 152 aa. Also identical to the Yersinia pseudotuberculosis IS1541-like elements transposase Tnp TR:Q9X9F5 (EMBL:AJ238014) (152 aa) fasta scores: E(): 0, 100.0% id in 152 aa" /codon-start=1 /transl-table=11 /product="transposase for the IS1541 insertion element" /protein-id="CAC90014.1" /db-xref="GI:15979235" /db-xref="SPTREMBL:Q9X9F5" /translation="MRDEKSLAHTRWNCKYHIVF APKYRRQVFYREKRRRAIGSILRKL CEWKVNILEAECCVDHIHMLLEIPPKMSVSGFM GYLKGKSSLMLYEQFGDLKFKYRN REFWCRGYVVDTVGKNTARIQEYIKHQLEEDKMG EQLSIPYPGSPFTGRK"
misc-feature	202326..202637	/gene="tnp" /note="Pfam match to entry PF01797 Transposase-17, Transposase IS200 like, score 236.10, E-value 5.1e-67"
gene	203145..204074	/gene="YPO1174"
CDS	203145..204074	/gene="YPO1174" /note="no significant database hits" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="CAC90015.1" /db-xref="GI:15979236" /db-xref="SPTREMBL:Q8ZGV3" /translation="MPQVNNISTNNIHSAGFNNS NSIQKYTGAVSSISDDLRLINNEKC KSDIGTISGDIKINRHSAVYGNVNSVSGDITVKN SIVDKDITTVSGDVNAVNSTIGKN IKTVSGSIEVEQSTVSGNLETTSGGIDIDTTKIN GNVHTTSGSISMNDSTIDGSVTCK AGSVTIVNSTIKESLNVLTSEKIIVGTASCIGKIN ISPPESVNFNIMNFGNDSIVMGMR NFCISGEVNFITITNGKVFVNEQRVGHTASQSTSK KVEEVTINIAKNASVNDIVFYTKK CHIILEGNAKYNGEKKDGMQFTHVNAPKSHAYA"
gene	204368..205312	/gene="YPO1175"
CDS	204368..205312	/gene="YPO1175"

		Escherichia coli hypothetical protein YohI SW:YOH1-ECOLI (P33371) (315 aa) fasta scores: E(): 0, 83.3% id in 311 aa, and to Vibrio cholerae hypothetical protein VC1105 TR:Q9KT00 (EMBL:AE004191) (323 aa) fasta scores: E(): 0, 58.9% id in 309 aa"
		/codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAC90016.1" /db-xref="GI:15979237" /db-xref="SPTREMBL:Q8ZGV2" /translation="MSMRVILAPMEGVLDLVLRE LLSEVNDYDLCTEFLRVVDQLLP AKSFYRLCPPELHNQSRQSGTLVRIQLLGQYPEW LAENAAARAVAGSYGVLDLNCGCPS KLVNGSGGGATLLKDPPELIYQGAKAMRAAVPAHL PVTVKIRLGWDSGDRQFEIADAVQ QAGATELAVHGRTEKEDGYQAERINWQAIGEIRQR LTIPVIANGEIWDYQSAQECMKVT GCDVAVMLGRGALNVPNLSRVVKYNEPRMPWLEVV KLLQKYVQLEKQGDGTGLYHVARIK QWLGYLRKEYTEATDLFGEIRALKNSKDIALAIQ RINR"
misc-feature	204383..205297	/gene="YPO1175" /note="Pfam match to entry PF01207 UPF0034, Uncharacterized protein family UPF0034, score 428.70, E-value 5.2e-125"
misc-feature	204647..204703	/gene="YPO1175" /note="PS01136 Uncharacterized protein family UPF0034 signature."
gene	205904..206839	/gene="pbpG" /note="synonym: YPO1176"
CDS	205904..206839	/gene="pbpG" /EC-number="3.4.99.-" /note="Similar to Escherichia coli penicillin-binding protein 7 precursor PBP7 SW:PBP7-ECOLI (P33364) (313 aa) fasta scores: E(): 0, 73.5% id in 309 aa, and to Vibrio cholerae D-alanyl-D-alanine endopeptidase vca0870 TR:Q9KL77 (EMBL:AE004414) (316 aa) fasta scores: E(): 0, 61.1% id in 314 aa" /codon-start=1 /transl-table=11 /product="penicillin-binding protein 7 precursor" /protein-id="CAC90017.1" /db-xref="GI:15979238" /db-xref="SPTREMBL:Q8ZGV1" /translation="MYVKIRFALLSFLLLSTGIS VAPLAIARGSAVEVKGTAPELAS GSAMVVDLQTNKVIYANNADKVVPPIASITKLMTA MVVLDKLPDEILSVDIDQTKEL KGVFSRVVNSEISRKDMLLTLMSSENRAAASL AHHYPGGYNAFIKAMNAKAKSLGM NSTHYVEPTGLSINNVTARDLAKLLMATKQYPL IGQLSTTTEKMATEFREPNYTLFPR NTNHLVYNDKWNILQTKTGFTNQAGHCLVMRTVI GKRPVALVLDVAFGKYTHFADANR LRSWIETGKAAPIPGAAKSYRQKDSQGRLAQVS E"
misc-feature	205994..206764	/gene="pbpG" /note="Pfam match to entry PF00768 Peptidase-S11, D-alanyl-D-alanine carboxypeptidase, score 380.50, E-value 1.7e-110"
gene	complement(206960..2086	/gene="dld"

CDS	complement(206960..208675)	/note="synonym: YPO1177" /gene="dld" /EC-number="1.1.1.28" /note="Similar to Escherichia coli D-lactate dehydrogenase Dld SW:DLD-ECOLI (P06149) (570 aa) fasta scores: E(): 0, 66.1% id in 558 aa, and to Neisseria meningitidis D-lactate dehydrogenase NMB0997 TR:Q9JZL7 (EMBL:AE002450) (563 aa) fasta scores: E(): 0, 60.9% id in 558 aa" /codon-start=1 /transl-table=11 /product="D-lactate dehydrogenase" /protein-id="CAC90018.1" /db-xref="GI:15979239" /db-xref="SPTREMBL:Q8ZGV0" /translation="MMSQFNNEKIQLLLTQLQHI VGTRYLLTGERQTERYRTGFRSGK GVALAVVFPSTLLQQWQLLQACVAADTIIIMQAA NTGLTEGSTPSGDDYDRPIVILNT LRLNNIQLLDDGKQVIGFPGSTLNQLEKRLKPYG REPHSVIGSSCIGASVVGICNNS GGSLVQRGPAYTEMALYAQIDAQGELQLINHLGI SLGNTPEEILQRLQEQGYGAEDIE QTGQQASDSEYATRVRDIDATTPSRFNADPRRLF EASGCAGKLAIFAVRDLTFPSEKQ QQVFYIGTNQTQVLTELRIILRDFKHLPIAGEY LHRDIFDIAETYGKDTFVMINS MG TNNMPRFFFTLKGKIDARLNKIPHLVDHLTDRVMQ GFSQILPNHLPKRLKTYRNQYEH LLLKMSGDGITEAQOHLRAFFATAEGNFI ACTAD EGKKAFLHRFAAAGAAVRYHAVHA DQVEDILALDIALRRNEKQWFETLPPEIEKCLIA KLYYGHFLCHVFHQDYIVKKGVDV KALKEKMLSLLNDKGAEYPAEHNVGHLYLAKPAL KDFYQQIDPTNSFNPGIGKTSKRK RWQQD"
misc-feature	complement(208031..208633)	/note="Pfam match to entry PF01565 FAD-binding-4, FAD binding domain, score 104.80, E-value 1.7e-27" /gene="cyaB"
gene	208882..209421	/note="synonym: YPO1178" /gene="cyaB"
CDS	208882..209421	/EC-number="4.6.1.1" /note="Belongs to a family of thermophilic adenylate cyclases. Similar to Aeromonas hydrophila adenylate cyclase 2 CyaB TR:O69199 (EMBL:AJ223730) (190 aa) fasta scores: E(): 8.9e-33, 50.9% id in 175 aa" /codon-start=1 /transl-table=11 /product="adenylate cyclase 2" /protein-id="CAC90019.1" /db-xref="GI:15979240" /db-xref="SPTREMBL:Q8ZGU9" /translation="MSEHFVGKYEVELKFRVMDL TTLHEQLVAQKATAFTLNNHEKDI YLDANGQDLADQQISMVLRMNPISGIRLWIVKGP GAERCEASNIEDVSKVQSMLATLG YHPAFTTIEKQRSIYFVGKFHITVDHLTGLGDFAE IAIMTDDATELDKLKAECRDFANT FGLQVDQQEPRSYRQLLGF"
misc-feature	208912..209418	/gene="cyaB" /note="Pfam match to entry PF01928 Adenylate-cyc-2, Adenylate cyclase, score 136.60, E-value 4.6e-37"
gene	complement(209447..2097	/gene="YPO1179"

/note="Similar to Escherichia coli  
hypothetical protein YajD  
SW:YAJD-ECOLI (P19678) (109 aa)  
fasta scores: E(): 0, 84.7% id in  
98 aa"  
/codon-start=1  
/transl-table=11  
/product="conserved hypothetical  
protein"  
/protein-id="CAC90020.1"  
/db-xref="GI:15979241"  
/db-xref="SPTREMBL:Q8ZGU8"  
/translation="MAYIPKNYSRLESYREKAL  
KIFPWVCGKCSREFVYSNLRELTV  
HHIDHDHGNPNPEDGSNWEMLCFLCHDHEHSKYTE  
VDLYGSTVVGDDAQKDQGVATHN  
PFANLKSLMKK"

SEQUENCE (SEQ):

1	actaatcagg	ccaataaccc	atgagatcga	taacccatga	gatcgatagc	ccatgagatc
61	gataacctat	gagatcgata	gcgaatcagg	tcaaaaatag	ccagcaccag	agtgtaggtc
121	ttcacaacaa	gtggtgagtg	tgatcgcatg	tctcatcggg	tggataacaa	ataaaaataa
181	cagtaactac	attactgaat	catcttggtg	tttttgatga	atttaataaa	ttattgtggg
241	gtctactttt	ctttttataa	gcaagatgct	tcaattttca	ttgaattctg	catgattaca
301	gccaatccca	cactccatat	aaataagata	tttgcacatt	atctgtagtc	tatttcttgt
361	atTTTTgtgg	gatttttcct	tttttatatt	atacgtctta	atatttaaaa	ttgcatattc
421	agtgaattat	gatttttaaa	ccttatattt	tattttattg	ggttttttat	atcgaatgcg
481	gtgctattca	tggtctttat	acgccggtct	gattagatgt	tgatctacat	tgttttgttg
541	catcggttct	tgatgaaat	ttaaaagaac	gtataagttg	gtatggtaag	ttaaattgtg
601	cagtttttcc	tattttgcca	tttttttaggc	gcataacaat	ttctttaaca	gcatacatct
661	aagtaatggg	ctatttttca	gggccttact	gcatatgaat	cacttttttt	aaaatcttaa
721	tcgcttattc	attactgagt	tggtccaatga	cacatgtctg	tcatctgact	tatgtgatgc
781	gatcattatc	aacttaattg	acaaattaaa	aatttggtta	ggctatatat	gaatacaata
841	tttaaagtga	tttggaatgc	atctttgaat	gtctgggttg	tggtagatga	gctggcaaaa
901	ggcccgataa	aaaccaagag	cagtcgtaac	ttgatatcag	agggtgtatt	acccaaattt
961	gaacaaagta	tggtatcgaa	actgttcaga	aaaaaccttt	tggccctatc	tctgggcagt
1021	attgtttttc	taagcaccgg	ccctgtattt	gctgctgata	ttactgtcag	cacgcaggca
1081	gagctttctg	ccgcgttatc	caatggtact	tatgacaaaa	ttatttttagg	tgctgacatt
1141	acgctcattg	ggagcctgac	cgtcaaatatg	acgagtaatc	aggttgtgat	tgatggccaa
1201	ggaaagtgtg	gtctaaccgt	taacaatacgt	acaaattatg	gtctgggtgg	gtcatcgggt
1261	tcaggggacct	taacgctaca	aaatatgtcc	aaaattgact	cggccaacta	ctacagcatg
1321	gtcgtgttga	acgggtgcaa	tactgccgtc	aatgtgattt	ataacaatat	tgatttcctg
1381	ggttcctctc	aacttattta	tatggggggcc	tatggggcgg	ccaccaatag	tataatgacc
1441	tttggcgata	tcttgaacga	tgtgggtggc	aatgaccgtg	ctcaggaat	tggatgaagtc
1501	aataaaactgg	cgtttaccgg	tagatttcat	gttacgcata	cggggctcct	tgatgacatct
1561	tttgtcagca	ctggcggggg	aaataataca	tcaaccatgg	attttgccag	tgggtgctgat
1621	gtcaagatag	accggacggg	gtcgactgga	gacctgacca	gtaccggtgt	taatgccttt
1681	gcctatactt	ttgctgatgg	tgctagcttt	gagttaattg	ctaatacaga	tgttttcagc
1741	ggaaccacta	ccaatagagg	cttggaat	ggtagtata	atagtatcga	tggctttggg
1801	tccgggggtga	aaatagttct	gcaatctcgc	tccgatgggt	caattatttc	aggtaatggg
1861	attgataaac	ccaccactaa	tgccgctggt	atcaataata	atgccagtgg	tgatgctaatt
1921	gttattttaca	atctgggtga	tggctctatt	ttaaaggcca	cgaatactgg	gatttttagcg
1981	acaaaaaatg	cgaataatgc	cagtgatatt	tatatctcgt	ctgcgggtga	tatcactgct
2041	gcaacgggta	tttctgcaac	acataacgga	accggcaccg	ttaaaatcaa	gaatgatggc
2101	accatcacca	gtaccaccgc	cgggatcgcc	atcttctccg	catcaataaa	agagatcagc
2161	gttgataata	ctgacgggtac	catcacggcg	actgccggta	caggcggtta	cgtactggcc
2221	agtgccatat	taaatctggt	cgggtgcacc	attaatacct	cggcgacggc	caacggtatt
2281	acgttttcgg	gcacggaggg	tggccataacc	ctgactgatt	tgacgattaa	tctgtttggg
2341	acgggtattg	ctttgtcaaa	cgtggctggc	gtcaatttga	cgttaagtaa	cgtaacttta
2401	aacacactta	atgggacggc	gctaaatagc	ctgacagggt	taacgttagt	cgatagcctt
2461	aatgggcgta	acaccattaa	tattgaagg	gccggcatcg	gaattgcggc	gacaaatacc
2521	gaattgaata	ccttcgatgc	agaggcatta	gatattaatg	ttaatgggtg	cgggatcggc
2581	attcaagcca	ctggcggtgg	tgtcaatctc	agcgcttcta	acttgatcat	taattgtggc
2641	aatacaattg	gtactgcgt	gcaaatcacg	gatgggatag	ataataccac	caccattggc
2701	aacgaaatcc	aacttaatgc	cgagaatgcg	acggcaatta	acttcctcgg	ctcctccagt
2761	aaaacgttaa	acaacaatgg	caccattaaa	ggcagtgtga	tattcgcggg	tggtgctgac
2821	catatcatta	ataacaatgg	aacactggat	ggcacattaa	ccaccgggtg	cggtaatgac
2881	acgttagtg	tagacagtag	ctcgcaaagt	aacgatgtga	ttaacctggg	ggatggcaat
2941	aatagcgtga	ccattcagaa	tggggcgaca	gtgtcctcca	ttatcactgg	gaatggtaat
3001	gatactttca	cgatcaatgg	gaatgacgtg	gggagtacct	acctcggttc	gctggatgcg
3061	ggcacggggc	tcaataccct	aatattcaat	gcctcaaccg	acgaactagc	ggcagccacg
3121	tcacttcagg	gcttcaccaa	tattaatctt	gtcgacagcc	atatcactct	ggtgtctgac
3181	gataatatcg	gcagcgggtat	ggtcaatatc	gatagcagta	gtgagctgct	atgttgtagc



3301	aaāagcḡccā	ācḡgtgṯcḡtt	āgāḡcagggcc	āḡtātḡtṯttḡ	cṯḡḡcacḡtḡ	gcaāḡttaat
3361	cagggcgggg	cgctaaccgc	cagtaacagt	aaccaattag	gtṯcgḡccaa	gattḡggṯtḡ
3421	gacḡḡtacḡt	tgaacctgga	caacattgca	ctattcaatc	atḡtḡctḡac	cgḡḡaacḡḡc
3481	acactgaatḡ	tḡḡcgaagaa	cctṯḡccacc	accḡcḡttṯḡ	actṯṯḡḡttc	gacḡḡḡḡḡc
3541	ggḡḡcḡttṯṯ	ḡtḡḡḡatcḡt	caatctgaca	aagactactṯ	ttḡctṯṯaaḡ	tḡcḡḡataac
3601	ḡcḡḡcgḡcac	tḡḡccagṯḡc	cacctṯaaag	ctḡtḡḡatḡ	acagṯḡḡag	caccḡḡḡḡc
3661	accactḡacc	ḡcaccctḡca	cḡḡḡctḡḡat	ttḡagṯḡḡḡ	ḡtacḡctḡat	ctṯṯḡatḡḡt
3721	ḡcḡḡḡḡcḡḡc	agṯctcagac	cagcḡḡḡḡṯṯ	ḡtcacḡḡṯca	ctḡacctḡḡc	actḡaacagc
3781	ggḡacḡḡṯca	atatcaccḡḡ	ctctḡḡṯagc	tḡḡḡataaca	ccḡatccḡct	ḡḡcaacaaat
3841	ḡtḡtḡḡatcc	ttḡaacagḡa	tḡḡṯḡctḡḡc	tḡḡacḡctḡḡ	aactḡattaa	tḡccactaat
3901	ḡtḡacḡḡḡag	atattḡatḡc	ctṯḡḡattṯṯ	ctḡḡṯcaatḡ	ḡcacḡḡccat	tactṯṯṯḡḡt
3961	acḡcaagḡḡḡ	tḡcagṯctḡḡc	catccagcag	ḡḡcḡḡcagṯa	cḡḡṯagccaa	tḡccatccac
4021	aattatḡḡcc	tḡḡccagcag	taacagcaat	ḡḡṯḡacagcḡ	ḡcctḡtatḡt	gaattacacc
4081	ctḡagṯḡḡcḡc	tḡḡagṯṯḡṯṯ	agccḡatḡḡc	ḡctḡatḡcḡt	tḡṯṯḡctḡḡc	ḡaccḡaaagc
4141	ḡḡṯṯṯḡacḡḡ	ccaacagagṯ	actḡaatḡcc	ḡagctattcḡ	ḡtḡtḡḡḡḡḡ	ṯṯḡḡḡḡḡḡ
4201	ḡatḡcccaaaa	atḡḡcḡcctṯ	aacctṯḡḡct	aacḡḡcagṯa	accḡṯṯacḡa	ḡḡḡaacḡacc
4261	accḡṯcacḡḡ	cḡḡḡṯḡagṯṯ	ḡatcctcḡḡḡ	ḡcḡaatḡḡḡḡ	cctṯṯcḡḡca	ḡacḡṯcattṯ
4321	ctḡḡatattcḡ	ccagṯḡḡḡḡc	cagṯḡccaat	atṯaatḡḡct	atagccagac	ḡḡṯḡḡḡḡḡḡ
4381	ḡḡaccaaḡcḡ	tḡḡḡḡacḡḡt	ḡacactḡḡḡc	agcḡḡcḡḡḡḡ	tḡṯṯaaccaḡ	cḡḡcctḡctḡ
4441	accaatḡḡḡḡ	ḡḡatcctṯḡa	ṯṯṯaacḡḡḡḡ	ḡḡcḡcactḡa	acctḡactḡc	ḡḡḡcḡḡḡḡcc
4501	tctactḡṯḡḡ	cagḡcḡḡctṯ	ḡaccḡḡṯḡcc	ḡḡaacctḡa	atattaatḡḡ	cḡḡṯaatṯṯḡ
4561	tḡḡṯcagṯḡ	ccḡccaacag	tḡḡctṯḡagc	ḡḡccagacc	atattḡccḡa	tḡṯḡḡcctcḡ
4621	ḡḡacactḡa	ccḡataccḡḡ	cacḡṯṯagṯṯ	accagcḡccḡ	tḡḡagḡṯḡct	ḡḡḡṯacḡctḡ
4681	aaactḡaacḡ	ḡḡccaatḡc	agccatḡacc	aacḡṯactca	ḡḡḡṯḡacḡḡ	ḡacḡattaat
4741	accaacḡcḡḡ	cagṯcacḡct	ḡagcḡḡḡaat	aacagṯṯṯṯṯṯ	ḡcḡḡcḡcaca	tḡagatcḡḡṯ
4801	accḡatḡḡḡḡ	aactḡaccḡṯ	ḡḡḡacagḡcc	agṯaatctḡḡ	ḡḡḡccagcag	cḡccacḡḡṯṯ
4861	aatctḡḡḡḡca	ccctcactṯc	tcatctḡatc	ṯṯḡaatḡḡṯḡ	tḡagcḡagag	tattḡccaac
4921	ḡṯctḡḡagcḡ	ḡtḡṯḡḡcḡḡḡ	ṯṯcaacagṯc	ḡatattatcḡ	ḡcḡḡḡḡcaga	tactḡcactḡ
4981	acḡḡccaata	acagcḡḡctṯ	cctcḡḡccaa	tatḡcctṯḡḡ	cḡḡḡṯaacag	caaactḡacḡ
5041	ḡṯṯcḡṯcaā	cḡaacaaṯct	ḡḡḡḡcḡṯca	tccagṯḡṯḡḡ	cḡctḡḡcagḡ	cḡḡḡḡḡḡḡḡ
5101	actctḡṯcḡc	tḡagcḡḡctṯ	taacḡḡcacc	ṯṯṯḡḡtaaca	ḡcḡṯcacḡḡḡ	cagcḡḡṯḡṯṯ
5161	ctḡcaagṯḡa	ccḡatḡatḡc	cḡagḡṯcacc	ctḡaccagca	ḡcaacḡḡḡḡṯ	aagcaacḡcḡ
5221	ḡṯaaccaṯṯḡ	atatcḡctḡa	tḡcḡacḡṯṯṯ	aaṯctḡḡacḡ	atattḡctct	ḡṯṯṯaatcat
5281	ḡṯḡṯḡacḡḡ	ḡṯaacḡḡctṯ	ḡctḡaatḡṯḡ	ḡcḡaaaaacḡ	atḡccagcac	cḡcḡṯṯṯḡac
5341	ṯṯṯḡṯṯcḡa	cḡḡṯḡḡḡḡḡ	ḡḡcḡṯṯṯṯṯṯ	ḡḡḡatcḡṯca	atctḡaccaā	taccactṯṯṯ
5401	ḡctṯṯaaḡḡḡ	cḡḡataacḡc	ḡḡcḡḡcactḡ	ḡcḡcḡṯḡcca	cctṯṯaaaact	ḡṯcḡḡatḡac
5461	agṯḡṯḡacḡca	ccḡṯcḡḡḡcḡc	cactḡaccḡc	accctḡcacḡ	ḡḡctḡḡattṯ	aaatḡḡcḡḡṯ
5521	acḡctḡatct	ṯṯḡacḡḡṯṯc	accḡccḡcaa	tctcagḡcca	atḡḡḡḡṯcḡṯ	cacḡḡṯṯact
5581	ḡatctḡḡcac	tḡaacagcḡḡ	ḡacḡatcagṯ	attaccḡḡḡḡ	cḡḡḡṯaacṯḡ	ḡḡagaatḡaa
5641	catccḡḡṯḡa	cḡccaccḡaa	cḡṯḡṯcḡctc	ctṯḡagcagḡ	atcḡḡḡḡṯḡa	cattṯṯactḡ
5701	ḡagctḡatṯṯ	atḡccḡcaa	tḡṯcaccḡḡc	aatḡccaaca	attṯḡḡattṯ	ḡctḡḡṯṯṯṯṯṯ
5761	ḡḡcacagcca	ṯṯacctctḡḡ	tacḡcaagḡḡ	ḡṯḡagṯctḡḡ	ccatccagca	ḡḡḡḡḡḡḡḡḡ
5821	acḡḡtagcca	atḡccatcca	caactatḡḡc	ctḡaccagca	ḡṯaatḡḡcaa	tḡḡṯḡḡcagc
5881	ḡḡcctḡtatḡ	tḡaattacac	cctḡagṯḡcḡ	ctḡḡagṯṯḡṯ	tacccaatḡḡ	cḡcḡaatḡcḡ
5941	ṯṯḡṯṯḡctḡḡ	cḡaccḡaaag	cḡḡṯṯṯḡacḡ	ḡccaacagag	tactḡaatḡc	cḡagṯṯattc
6001	ḡḡṯḡṯṯḡḡḡ	ḡṯṯḡḡḡḡḡṯ	ḡḡatḡcccaa	aatḡḡcḡcct	ṯaacctṯḡḡc	ṯaacḡḡcaat
6061	aaccḡṯṯacḡ	agḡḡaacḡac	caccḡṯacacḡ	ḡcḡḡḡḡḡaat	tḡatcctcḡḡ	ḡḡcḡaatḡḡḡ
6121	ḡcatctḡḡcc	agacḡṯcatt	actḡaatatc	cḡcagṯḡḡḡḡ	ccagṯḡccaa	tattṯaatḡḡc
6181	taccḡccaga	cḡḡṯḡḡḡḡḡc	ḡḡṯḡaccaat	agcḡḡṯḡcḡḡ	ṯaacḡṯṯḡḡḡ	caacḡḡṯḡḡḡ
6241	ḡṯḡṯṯaacca	ḡṯḡḡctṯḡct	ḡaccaatḡḡc	ḡḡḡatcctṯḡ	attṯṯaacḡḡ	ḡḡḡcḡcactḡ
6301	aacctḡḡḡctḡ	cḡḡḡcḡḡatc	ḡṯctaccḡṯḡ	ḡcagḡcḡḡct	tḡaccḡḡṯḡc	cḡḡcaccctḡ
6361	aatattṯaacḡ	ḡcḡḡṯḡattṯ	ḡḡcḡḡṯcagṯ	ḡccaccaaca	ḡṯḡḡctṯḡag	cḡḡccagacc
6421	catattḡccḡ	atḡṯḡḡcctc	ḡḡṯḡaccctḡ	accḡḡḡacḡḡ	ḡṯacḡṯṯḡḡḡ	taccagcḡcc
6481	tḡcḡagḡṯḡc	tḡḡḡṯacḡct	ḡaacctḡaac	ḡḡṯḡccaatḡ	cagccatḡac	caacḡṯactc
6541	agṯḡḡḡḡḡḡc	ḡḡḡṯḡattṯṯ	ṯaccaacḡcḡ	ḡcḡḡṯcacḡc	tḡagcḡḡḡḡaa	ṯaacagctṯṯ
6601	agcḡḡcḡcac	atcagatcḡḡ	taccḡatḡḡc	ḡaactḡaccḡ	tḡḡḡacagḡc	cagṯaatctḡ
6661	ḡḡḡḡccagca	ḡcḡctacḡḡṯ	ṯaatctḡḡḡc	accctcactṯ	ctcatctḡat	ctṯḡaatḡḡṯ
6721	ḡtcagcḡaga	ḡtattḡccaa	cḡṯṯctḡagc	ḡḡṯṯḡḡḡḡḡ	ḡṯṯcaacagṯ	cḡatattatc
6781	ḡḡcḡḡḡḡcag	atactḡcact	ḡacḡḡccaat	aacagcḡḡct	tctcḡḡḡcca	atātḡcctṯḡ
6841	ḡcḡḡḡṯaacā	ḡcaaactḡac	ḡḡṯṯḡcḡṯca	acḡaacaaṯc	tḡḡḡḡḡcḡṯc	atccagcḡṯḡ
6901	ḡcḡctḡḡccḡ	ḡḡḡcḡḡḡcḡa	tactctḡṯcḡ	ctḡagcḡḡṯṯ	ṯṯaacḡḡcac	ctṯṯḡḡṯaac
6961	agcḡṯcaccḡ	ḡcagcḡḡṯḡṯ	actḡcaagṯḡ	accḡatḡatḡ	ccḡaagṯcac	cctḡaccagc
7021	agcaacḡḡḡḡ	tḡḡḡcaatac	ḡḡṯḡaagṯṯc	ḡatātḡctḡḡ	atḡcḡacḡct	ḡaacctḡaac
7081	ḡatattḡcac	tḡṯṯcḡacca	tḡṯḡctḡacc	ḡḡḡaatḡḡca	cattḡaatḡṯ	ḡḡcḡaagaac
7141	ctṯṯccacca	cḡcḡḡṯṯṯṯḡa	ctṯṯḡṯṯṯṯṯṯ	accḡṯḡḡḡḡḡ	ḡḡḡcctṯṯḡḡ	tḡḡḡatcḡṯc
7201	aatctḡacca	ataccactṯṯ	tḡṯṯṯṯṯṯṯṯ	ḡcḡḡṯṯaacḡ	cḡḡcḡḡcact	ḡḡcḡcḡḡḡcc
7261	acctṯṯṯṯṯṯ	tḡṯcḡḡatḡa	cagṯṯṯḡacc	accḡṯcḡḡca	ccactḡaccḡ	cactcctḡcac
7321	ḡḡḡctḡḡatt	ṯaaatḡḡcḡḡ	tacḡctḡatc	ṯṯṯḡacḡḡct	cḡccḡccḡca	atctcagḡcc
7381	aatḡḡḡḡṯcḡ	tḡacḡḡṯṯac	tḡatctḡḡca	ctḡaacagcḡ	ḡḡacḡatcag	cattaccḡḡḡ
7441	ḡcḡḡḡṯṯṯṯ	ḡḡḡagaatḡa	acatccḡḡṯḡ	acḡccaccḡa	acḡṯṯṯcḡct	cctṯḡḡḡcag
7501	ḡatcḡḡḡḡṯḡ	acattctḡct	ḡcaactḡatt	ḡatḡccḡata	atḡṯḡaccḡḡ	caatḡccaat
7561	ḡatctḡḡḡḡc	tḡatḡatcaa	tḡḡṯaccact	atṯṯccḡcag	ḡacaagḡḡṯṯ	ḡcagṯctact
7621	ḡṯccagcagc	ḡcḡḡḡṯatac	ḡḡṯḡḡcḡaat	ḡctacḡcata	actatḡḡcat	ḡaccagcaat
7681	ḡḡcḡḡcagṯḡ	ḡcctḡṯatḡṯ	ḡaattacacc	ctḡagṯḡcḡc	tḡḡagṯṯṯṯṯ	agccḡatḡḡc
7741	ḡctaātḡcḡṯ	tḡṯṯḡctḡḡc	ḡaccḡaaagc	ḡḡṯṯṯḡacḡḡ	ccaacagaga	ḡctḡaatḡcc

7861	āacggcaatā	ācōgttācāgā	gggāācācāc	āccgtcacgg	cgggggaatt	gatcctōggg
7921	gcgaatgggg	ctttcggcca	gacgtcatta	ctgaatatcg	ccagtggggc	cagtgcgaat
7981	attaatggct	atcgccagac	ggtggggcg	gtgaccaata	ccggtacggt	aacgltgggc
8041	aacggtgggg	agttaaccag	tactgacacc	ttgatcaata	ccggaatgat	taatgtgacc
8101	gatggcatcc	tgaatctgga	gaatggggg	gcttctagca	ttagcggcgg	cttaacgggc
8161	aacgggtatcc	tgaatatcaa	gggtggcgat	ttcaccatca	gcacgcgataa	caatggtctg
8221	gcggggcaaaa	ccaatatctc	cgatggtgca	tcagtcactc	ttggtaatgg	ggggaccatt
8281	atcggaaccg	gtaatttggg	cagcagcggt	attgatgtgc	tgggggatct	aaacctgggtc
8341	gcggataaatt	cactggctaa	cgtgatcagt	ggtgacggga	cgattaatac	cacagcaaca
8401	gtgacgctga	gcgggaatag	cagctttagt	ggtgcacatc	agattggtac	caatggcgaa
8461	ctgaccgtgg	gtcaggccag	taatctgggg	gccagcagcg	ccacgggttaa	cttgggcacc
8521	cttacttctc	atctgatctt	gaatggcggt	agcgagagta	ttgccaaagt	tctgagcggg
8581	gtggcggggt	caacagtcga	tattatcggc	ggagcagata	ccgcactgac	ggccaataac
8641	agcggtctcc	tcggccaata	tgccttggcg	ggtaacagca	aactgacggt	tgcgtcaacg
8701	aacaatctgg	gggcgtcatc	cagcgtggcg	ctggcagggg	cgggcgatac	cctgtcgctg
8761	agcggtctta	acggcacctt	tggtaacagc	gtcaccggca	gcggtgtact	gcaagtgacc
8821	gatgatgccg	aagtcaccct	gaccagcagc	aacggggtaa	gcaacgcggt	aactattgat
8881	atcgctgatg	cgacgctaaa	tctggacgat	attgctctgt	ttaatcatgc	tttgaccggg
8941	aacggcttgc	gtaatgtggc	gaaaaacgat	gccagcaccg	cgtttgactt	tgggtgctacc
9001	gtgggcgggg	ccttcaccgg	cacagtcaac	ctgaacaatt	ctacttttga	tttaagcggc
9061	aataacacca	cagtattggc	ccaggctacg	ttgaaattat	ccagcggtaa	cctgacctcg
9121	gtgggtaacg	gtgtgcagaa	tattggcaca	ttggcgatga	atggcggcac	gttgctgttt
9181	gataatattg	ttgataacgc	aggcattatc	acttcagatg	ggacgattgc	ggctaatagc
9241	atcaatacca	ccggggggcg	tgaagttcgg	gttaattttac	cgagcaatct	ggcaccgaagt
9301	ctggatgggc	tctcggtgat	ggaactggat	gaaggcgaaa	tcattgtcac	tctggcaact
9361	ggggcggcga	cagggacagg	ccatgagttg	acgttgacgg	atgagaatgg	tgatccgatc
9421	agcgcggtca	cttatcaggg	ggtccataac	gctggcagta	cctcagccgc	cgccaccggg
9481	tcgttttaatt	acggcatgac	cactggcgag	gattatgatg	gctgtatgtg	caattacggt
9541	ctgaccgcgt	tagaactatt	gagcaggggc	agcgaggcgt	tggatttgac	cgccatcttg
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9661	gcctttgcgt	cggtaatga	tggcagcacg	gcatecttat	ctaatagcac	caacagctat
9721	actggtacca	cttgggtctc	ttcaggtaat	ttgcgtctgg	atgctgattc	agcactgggg
9781	caaacctcct	tgcctggcgat	gagtaccgcc	actcatgttg	atatcaacgg	taccagcag
9841	gtggtgggtg	agttagccac	cgaagggggc	agtacactgg	atctcaacga	cggtaaagta
9901	accgtaacgg	ggggcgccca	aattgatggt	gcattgactg	gcggtgggta	actggtactg
9961	agtgggtggt	tgtgaatgt	ttctttgat	aacgctggct	ttactggcag	tactgatatt
10021	gccaatggcg	cggtggcaca	cctgtctcag	gcgcaggggc	tagggaaacgg	caccattaat
10081	aacaacggca	cacttcatct	ggataaatac	atcgggacac	tgtttaacgc	tttgaccggg
10141	agtgatggcg	aggtattgct	aagtaacaat	gccagtgctc	aattggccgg	tgataacagc
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22201	tgatgcttat	aaaggtcaag	taaatgcagt	ttataccttt	gatgataattg	attttacctc
22261	ggttagtgtc	tatgtagacg	aaagaaaagt	tgataatcaa	gacctcgatt	ttacgcgatt
22321	atcaattagt	gaactattga	tgaatcgaaa	aacaaaacaa	ttttcacaag	agtttcggtt
22381	gaactctaaa	tacagcgggc	catttaattg	gttgataggg	agctattatt	tttatcaaga
22441	tgatgaaaat	gaaattgatt	tccgctatct	gccctataac	ttagcacaac	tccggaaatc
22501	cgatatcaag	accaataact	acgcagtgtt	tggcaatgtt	aattattacc	tgctgaatga
22561	tgttgagctt	gtggcgggtg	caaggtatga	ctatgagaaa	aagaaactta	actttttgat
22621	ggataaatggg	tttaacccat	atcagccgta	ttctcatgat	aataatagta	attcatttgg
22681	ggctttttttg	cctaaggtag	ggttgaatta	ttatattact	ggcgacgcca	tgctatatac
22741	cagcatagca	cggggggtata	aaagtggcgg	gtttaacacg	ttagggcctc	aatctagtcg
22801	cgctttataat	gcagaatata	tgacgactta	tgaggccggg	gttaaaaccg	aatggtttga
22861	tagaacgggt	cgtttgaata	cgtctctatt	ctggaatgat	atgaaagatc	agcaagtcca
22921	tagggcggtat	tatcctattt	cttattcggg	taacagcggg	aagtcattaa	gcggtgggtt
22981	ggagtctgaa	cttgctgggc	gtattacggc	tggcctgact	gtatctgcaa	atgtaggcta
23041	tactgatgcg	tatttttaaaa	atttcccaac	agaaataaaa	gtagataata	actatattcc
23101	tgtaactat	aaaggtaatc	gaccggctaa	ttcgccaggg	tacacttata	gtattggtgc
23161	cgattataaac	ttccttaacg	gttattttgt	taatgctact	tataatgtta	aaggaagtac
23221	ttatcttgat	aatgcgaata	gtaaaaaaca	accagcttat	gggctattag	atcttactgc
23281	cggttatgag	aataagatt	atggtgtcaa	tgtttggata	aagaatatct	ttgatgaac
23341	ttatgtgact	cgtgctttca	aaatggatga	tgggatatgg	tatgggcgcg	cggtggaacc
23401	tattaatttt	gggggttaatt	tcaatgttaa	attttaataa	atattaataa	tacatatggc
23461	tgtgactatt	agatacagcc	acataattaat	tttggtgtaa	aagagctatg	tctgtgggc
23521	acttttatgtt	tatgcataga	gtcgttgatt	tatcaaaagt	gatctatatg	caactacagg
23581	taatgggtatg	aatttattaa	ataatgaaac	tcgttgggtg	agggaggcgt	tatttgaaca
23641	ggcaacaaag	tccaaatatg	atgtcgcatt	gcgttattgt	gataaagatg	atgtagattc
23701	ttactcttat	agccaactga	tatcactggg	ctattcgtta	gctacacaga	ttgaaataga
23761	aaacaatccg	cctgggcctg	ctattctgct	catgccagga	ggctcgcttt	ttgtcataag
23821	ctttatcgct	tgtattatta	gggggggtgcc	ggctgtccct	gtgcatctaa	ccaatcattt
23881	taaattgggt	cgcagtattg	ataccctgtc	ccataattttg	gctgatagcc	atgggtgaata
23941	tatatctacc	ttaagttcgt	tatccgacga	aattaaaaaa	caaggttggc	atcgtaaca
24001	tcagattgtt	tttgttgatc	aacaactcac	cggtagtcgt	cgctattttc	ccacgaaaaa
24061	aaattatgat	gcacttttatt	atcccagtc	tttacctgtg	tatctgcaat	attcttctgg
24121	ttccacagca	aagccaaaag	cggtatgtaa	ttacgatcat	aatatgcggg	tgcaacatca
24181	tatcttgctt	gaattacatc	tgcattgtca	gccaaaaatc	atcaccgcga	actggctgcc
24241	tttttatcat	gatttaggca	tgttcagcgg	tttggtattg	ccattgttat	ccgggtggtg
24301	ctgtaatttc	atgcttctgt	tgcactttat	tacagagcca	tttcgttggc	tgaaaatgat
24361	taatgattat	caggctaaact	ccggggctgc	ccccgatttt	gcgtgggatt	tgtgtaccac
24421	aatgggtgacg	gacgaacaca	tttgccagtt	ggatctctcc	tccatcaaga	tggcaatgaa
24481	tggggctgaa	cccattcgcc	cagagacaat	ggcaaatttt	gcggcccgtt	ttgcatccac
24541	agggttttgat	gcccacagtt	tcacgcccgg	ttatgggatg	gccgaagcaa	ctctgaccgt
24601	aagccataag	cctatcgata	ctgattactg	ctgtttggca	tttaacccaa	tggcattagc
24661	ggcaggtaaa	gccatttttag	atccgcgaag	gtgtcgggtg	gtaagctcag	ggcattgtgt
24721	tagagcatgg	caattgcaga	ttgttgatcc	ccagacatgt	cagcccttgc	ctgaggcgaa
24781	cattgggggaa	gtctgggttc	gaggcgggtc	tgtggcgggg	gggtattggc	agcagcccga
24841	actcacaanaa	gccacttttc	acaatacact	ggcaggtaac	tctcaccatg	attatttacg
24901	tacgggggat	cttgcccttg	tgtatcaagg	ggaactcttt	atttgtgggc	gattaaaaga
24961	tctcattatt	gtggctgggc	aaaatttat	gcccaggat	attgaaacag	caattgagta
25021	cgctgcatg	gatatccaca	cggggggagt	gtgtgtgtgt	cagcattttg	acagcggcga
25081	atttattgtg	atggccgagg	tctatcggtc	tttaacatca	acggcacttc	agcgtattgc
25141	tcagcagatt	gtggcgactg	tagcccgcga	ttttcaactg	aaatctgaca	aggctatctt
25201	actcgcccg	ggaaagctct	taaaaacatc	gagtggcaag	atccgcgcga	gtcatatgct
25261	ttctctctat	ttcacgcaac	aattgagcgc	gctttatgta	caggagtcac	agagaaagac
25321	tcaagatgaa	atgttatttg	atcaagaaag	cgtgttattt	gagcaagagg	ccatactgtt
25381	tgattggctc	cataaaaacg	ggtgtgaatt	actcggttgc	gaggcgatca	atcctgatag
25441	tgggctacat	caggcagggt	taaccagttt	gttagcgata	caattttgtc	agagtattaa
25501	tcattttctg	ggctgtcatc	tcaatgtcgc	agatctcttc	gcctatccta	cattacggca
25561	actgacctta	tttttatctc	agcaccaaga	agatatcgcc	tcttcaagtt	caacggaagc
25621	aggagatgat	cgggatgtcg	cgattgtggc	tatcagttgt	cgcttaccgg	ggcagggtggg
25681	ggtgagctgg	gcggactatt	gcacagaatt	atccgcaggt	aacagcgcgg	tacgtcatga
25741	aaaaaactcga	ctcgcacact	gtgttttacc	gataggcgca	ttagaagata	ttgatcagtt
25801	cgacgtctg	ttcttttaata	tcagcgaacg	agaagccatc	ttactcgatc	cacaacagcg
25861	tcataatttta	gagctgagtt	ggcacctgtt	tgagcaggcg	ggttggcaac	ctgaacaatt
25921	gaaacaaggc	gatattgggt	tttacattgg	tcaaagtggc	agcgaatatg	ggcaaattgtt
25981	gttacagaaa	aatgaccccg	attatgccaa	aagttatctg	gcgacgggga	tttgtagcag

26101	tācċgcttgt	ċōtċtċtċgċ	tġgtcgcact	gġātagcgċg	ātġttġċac	tacagcaaāa
26161	acagtgcagc	gċgċgtgtcġ	tġgggggċgt	gaatttactc	ctatcġgċac	aaatagaaca
26221	aactċttatc	aatgċgggta	tġttatcacc	caaggggċac	tġtgctacgt	tcagtġatġa
26281	tġctġatgġc	tatgċċċġag	gagaaġggġc	gġtattattc	ċtġttaaaac	ċttatċġtca
26341	gġċċġtgata	ġatgġċġatc	ċtġċtċtġag	ġatcattġag	gġċagġtċġ	tġġċġagġa
26401	tġġtgagagc	agcagċċtġa	cġġcaccġaa	tċcaccagċt	caagċġġċta	tġatġtċġca
26461	gċttttacag	cġagċatċat	tġġtċċċġa	tġatātċtċġ	ttattġġaaa	ċċcatġġaac
26521	gġġtacttċġ	ttagggġatc	ċġġttġagċt	aagċġċċatt	ġatċġtġtċt	atġġtċaacġ
26581	aaaaacġċca	ttacġtċtġag	ggġġġagġaa	aagġcagġtt	ggġcacttġġ	aggċġġtġċ
26641	ggggggattt	ġcattagċċa	ggġċtġtċġc	ġcagataċaa	caacagaaġġ	ċċtttġġtca
26701	ċċċċċġċta	aatagċtata	acċcactġat	agcagaaaaa	ttatcagġtt	attatttċġa
26761	taaagatācċ	tġċċċtġġġ	taatċaaacġ	tġtċġċċatc	aatġċttċtċa	ġtċttaccġġ
26821	aacġatġġċt	gġġġċġtġt	tġagaaagċċ	tacġġcagġtt	ġċtagatċaa	taaagġċaat
26881	tacatċaata	aagġcagċċa	ċatċaataaa	atċagttācā	tċaataaatġ	taacġaacġġ
26941	tġċaatagġġ	atċċacācċċ	aacġċċtġaa	atċagatċċa	ggġġġtaatc	tġċtċtċċtġ
27001	attcagġġagā	ġtttātġġtċ	acttttġgagā	ċagttātġġā	aattāaaatc	ċtġcācāagċ
27061	aggġaatġag	tagċċġġġġc	attġċċagag	aactġġġġat	ċtċċċġċaat	acċġttāaac
27121	ġttātġtġġcā	ġġċāaaatċt	ġagċċġċāā	aatātācġċċ	ġġacċġtġċt	ġttġċttċac
27181	tċċtġġatġā	atācċġġġat	tātattċġtċ	aacġċatċġc	ċġatġċtċat	ċċttācāaaa
27241	tċċċġġcāac	ġġtaātċġċt	ċġġagatċā	ġagaccagġġ	atātċġtġġċ	ġġaatġācċā
27301	ttċtċagġġċ	attċattċġt	tċtċtċtċġġ	ttċċtċagġā	ġċagġagċċt	ġċċġttċġġt
27361	tċġaaactġā	acċċġġācġā	ċagatġċagġ	ttġactġġġġ	ċactātġċġt	aatġġtċġċt
27421	ċacċġċttċā	ċġtġttċġtt	ġċtġttċtċġ	ġatacagċċġ	aatġċtġtāc	atċġaattċā
27481	ċtġācāaatāt	ġċġttātġāc	acġtġġgāġā	ċċtġċċatċġ	taatġċġttċ	ċġċttċttġġ
27541	ġtġġtġtġċċ	ġġġġāagġġ	ttġtātġācā	atātġāaaac	tġtġġttċtġ	ċaacġtġācġ
27601	ċatātċagāc	ġġtċagċāc	ċġġttċċatċ	ċttċġċtġtġ	ġċagttċġġċ	aagġagātġġ
27661	ġċttċtċtċċ	ċġactġtġt	ċġċċċttċā	ggġċācagāc	tāaagġtāag	ġtġġāacġġā
27721	tġġtġċagġtā	ċacċċġtāac	agtttttācā	tċċcactāat	ġactċġċċtġ	ċġċċġatġġ
27781	ġġatċactġt	ċġatġttġāā	acagċċāacċ	ġċċcġġtċt	ġġġtġġġtġ	ċġġatġtġġ
27841	ċtāacċāacġ	āaagċatġāā	acāatċcagġ	ċċġtċċċtġ	ċġatċġtġġġ	ċtġāagāġċ
27901	agċagġċċat	ġġtġġcactġ	ċċtċċġġāġā	āāāāagāġtā	tġāġtġġċat	ċttġatġāāā
27961	atċtġġtġāā	ċttċġācāāā	ċacċċċċtġċ	atċatċċact	ċtċċatċtāc	ġactċattċt
28021	ġċagāġġagġt	ġġġtġatġā	tġġāactġġā	acatċāacġā	ċtġatġġġġċ	tċġċġġġġā
28081	ġttġġāactġ	ġāāagċċttā	tāagċġġācġ	ġċċtġġġtġ	tċācāacāġġ	ċagġagācċā
28141	ġġaatġġagġt	tātātġġact	tċċtġġāġā	tċtġġttċat	ġāāāāāāāc	ġġġcāġtċā
28201	tċāacġtāāā	ċagġġatġt	atācċġāat	ġġġġġċtċ	ċġġġġġtġā	āāacġttċġā
28261	agāġtātġāc	ttċācattċġ	ċcācġġāġġ	acġġcāġāāġ	ċāactċcāġt	ċġttācġġtċ
28321	actċagġttċ	atāġāacġtā	atġāāāatāt	ċġtattactġ	ggġċċatċāġ	ġtġtġġġġāā
28381	aacċċatċtġ	ġċāatāġġā	tġġġġtātġā	agċagġċġt	ġċagġtātċā	aagġttċġċt
28441	ċācāacāġġā	ġċagātċtġt	tāttċcāġtt	atċtācġġā	ċāacġtċagġ	ġċċġttātāā
28501	aacġācġċtt	ċāġġtġġāġ	taatġġċċċ	ċġċċtġġtċ	atċattġatġ	āaatāġġċtā
28561	tċtġġċġttċ	agġcāġāāġ	āagġāāāġġt	ġttċttċcāġ	ġtċatċġġtā	āacġttācġā
28621	āaagāġġġā	atġatċċtġā	ċatċcāatċt	ġċġttċġġġ	ċagġġġātċ	āāacġttċġċ
28681	ċġġtġatġġā	ġċactġācċt	ċāġġatġġt	ġġācġġtātċ	ttācācċact	ċāatġtċġt
28741	tċāaatċāāā	ġġāġāāāġt	atċġactċāġ	acāġāāacġā	āagġċġġġġ	ttātāġġāġā
28801	agġtāatċċt	ġāġtāāāacġ	ġtġġātċāat	attġġġċġt	tġġtġġāġat	ātāagġġāġ
28861	ċacttttċat	ċġġtċġttā	ċāāātāacġċ	tċċġġtācā	āāāāġāġatġ	ġġtttttācġ
28921	ġtġttġāāā	tācāġċċāā	ġġġġtāacā	tċatāctċāġ	tagċċċġġā	ġācġtātċtċ
28981	ġtċtġġttāt	ċtċāāġċġt	ggġġġtātāā	ġġttātġtāġ	tġāācāācāā	tċċatġġġāġ
29041	ġċatċċattt	atġċċtttāġ	tġġtċāatġt	ċttġtċtācċ	ċcactċāacġ	ġġcāġċāac
29101	acġāacġġġ	ġġttttācċt	tġċċtġāāat	ġatġġtġġġ	ċtāagtttċġ	ġtāġċċtġat
29161	agġġtġāġġ	acāġġācāġġ	tċttācċċāā	ātātāāġċāġ	ċāaatttċġġ	tġttġġācāā
29221	ġċattātċġċ	ċttġāatġāġ	taatġāatċā	ġġġatġġġġ	ġġatġġāġā	āāatċtġġġ
29281	ċagāġġġġġ	ttttġġċācġ	ġġāaatġtċā	ggġġġāġġċ	ātāacġtāġā	āacattātċt
29341	ċġġtġāāacġ	ġġtċactċtt	ġċċtġattġt	tġġttātġat	ċttāattġġā	atġġġāġatġ
29401	ġġāāġġġġġ	āāacātċāāġ	agġġcāāātā	ttttġġġtāt	ċġġtācġġā	ātāāāġġtt
29461	āġāġātċāġ	ċġtġġġāac	tġāactġċċā	tġġċġtġġt	tġġġāāāāac	tġtttġatċċ
29521	acġāġatġtt	actġtġactċ	actttttċġt	āacċċċtċtġ	tċtġġġāac	ttttċāaat
29581	ġġġġtġtġġ	ggġġātāāāā	ċġġġtāatċċ	agġtātċċāc	ċatċagġtġā	ċttācċttāt
29641	ċġtġġāāt	āacġtātġāc	ġċagġtāttt	ċāacġāġġā	ġcagġācċċt	ġġġġġġtt
29701	atġācacttt	tttċtttġġġ	attāttttġġ	ċtatċāġġā	tācātċġġā	attāġācāat
29761	atċċāġāāā	ttācċġġāġā	ġġāācāacġċ	tātttācġġġ	ċttācāātċā	ġġtġāātċā
29821	tċactċāact	ggġġtġtċāġ	ċcāġġġtġġ	ġġġtċāġāā	tācċttġġġġ	ġġtāġġttċā
29881	ġċatġġċatt	ġċatġġġācā	tċāġġāġtċ	ġġġtāāāāāġ	ċttġġġtāā	ġġġtċatċā
29941	ċtġġġġtt	tttttātċtċ	āāāāġāġāā	agġtċttċġċ	ttġġġtġġt	ċċċċġġtġ
30001	atġġtttācċ	āacġtġttāā	āātġāāġġā	ġttācāġġāā	ġttċġġġāā	ttātċāġttġ
30061	attġācācġċ	ċtċatġġttġ	ġttġġātttt	tġċċċtġātā	āġġātġġāā	ġttttġċċtċ
30121	ġātātāātāc	ċāāacācġġt	tātġġācāāā	ċtātttċāġt	ġġāġācāġġċ	ġġtttċāacċ
30181	tācġtċācċt	ġġtġġātċ	āġġtāctġġ	āagttttġāt	tġċġġātāā	tttttċtċāā
30241	tċtċactact	ggġġtāctġ	ċāatācċātċ	āġġċactttt	acāġġġġtt	ġċċtċċtċat
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30361	ācċċġāāāġā	ācġġtġġġā	ċċtġāāġtġā	āacāġġġtġ	ġcactātċġċ	ċāātttātċġ
30421	atġġġātġā	ggġġġātġġ	ċġġāātttā	ġġtāāāġtt	ġātāācċġġċ	ċāāġactċġċ
30481	ċāġtāġāāt	āāġġġātġġ	ttttġttċāā	ċtġāġātġāt	ttāġġġātġ	tātācġġāt
30541	ācċtġttġġġ	ċāġactċatt	ātċāāġttāġ	āġtātċāac	ġtċāġġāact	ātċċatċāġċ

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41461	gccagcḡct	gcḡttaccac	cḡtḡḡtaatc	cattaaatct	tgatḡtactḡ	gctḡttgat
41521	aagcatcaat	ggttgattta	cctatḡatḡḡ	cḡcḡcttaat	tgccḡcatta	cctḡccaagg
41581	ccaaggtgat	attccttḡgt	gaccḡtgacc	aactḡḡcctc	ggttgaggcg	ggggcḡgttc
41641	tgggggatat	ctḡccḡttt	gcccgaattag	gttacagcga	gcaacgggca	cagcaattaa
41701	ctcagttaac	ggḡctattta	ttactaata	atḡcattaac	cagcaatḡta	ctaaccaata
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42241	atagcḡcact	tgḡcttattc	aacḡḡḡgata	ttḡḡtattḡc	cttacatḡat	aatḡaagcḡḡ
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42361	ttcccagcca	tḡaaaccḡct	tatḡctatḡa	cḡḡttcataa	atcḡcagḡḡt	tcagagtḡtḡ
42421	aacacacagc	attḡḡtatta	cctaacacḡt	tcatḡcccḡt	gttaactcḡt	gaattḡḡtct
42481	ataccḡccat	taccḡcḡḡcc	cḡtcagcātḡ	tgacḡcttta	ttḡcagcḡat	gcccḡḡctaa
42541	gtcatḡccat	acḡtacaccḡ	actctcḡḡc	tgagtḡḡḡct	agttḡatcḡc	ttḡaatatc
42601	taaatcgcca	ataatctcag	ggcataagcḡ	ccctḡagtta	tctḡtttcaa	ataagtattt
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42721	cḡccctḡacc	cccaatttca	tttacḡcatḡ	tataaagggḡ	atagggḡḡct	atagatcḡḡc
42781	cagtaagatc	ttcḡaacḡḡc	ḡctḡatagtt	atacagttcc	tgtttttgaa	tagḡtaaaac
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63841	aaaggggctt	tcagatgacg	acgggcatgg	cgcaaacgcc	ggacggtagt	ggagtaaata
63901	cctttaatat	cctgattgcg	caccatcaga	tagaacatcc	gcatgatcgc	ttcaggctga
63961	cgaacaaata	ggttctcatc	accgagatca	ataaatctc	cccgtagttg	aaactcttcg
64021	tcaagtggac	cgggtttttc	attcgcctct	aatgccagta	tggcttcac	aaacaattgc
64081	agcagcatat	tgttcagttc	actgacacgc	cttgtcatac	gatagaaatc	tttcatcata
64141	tgttcaacgg	gctcattgcc	ttcaccttcg	tagcgtaaaa	gttgagcaac	gctcagttgg
64201	cggccaacaa	gcaggcgggt	atcgtagcga	gtcaatacca	ggtgcagcgc	aaaacggata
64261	cgccataaaa	aactctggct	ttcattcagt	tcattacgct	cggcgttggt	gagaacacca
64321	aaatcaacca	tttcacttaa	cgatgtcgca	ccgaaatggc	gacgggcaac	ccagagttaat
64381	gtgtggatat	cccgtaatcc	accagggtca	cttttgatat	cgggttccag	attatagctg
64441	gtgccgtgat	agcgtttatg	acgctcttgc	tgttcaacaa	cttttgcatg	gaaaaattga
64501	ggggaggggc	agaaactgtc	actgaaaata	tgtttttgca	tctgtaaaaa	aagggcgaca
64561	tcaccgcaaa	tcaaccgtga	ctcaatcata	ttggtggcta	tggttaaatc	tgcgaggcct
64621	tccagcaagc	actctttccg	tgtgcgcaca	ctatgaccga	cttccagctt	caaattcccac
64681	aataaggtaa	tgagttggcc	aaccgcttgc	gcctgttcac	catttagacg	ctgcttactc
64741	agtactaaca	catcaatata	tgataatgga	tgcagttcgc	cgcgcccata	gccaccgacc
64801	gcaaccagag	ctgtttcttg	caccttgtea	aaaccataga	atgtccacaa	ccgctgtaac
64861	agatgatcga	tataatcact	gcgtgcccga	attaatacct	cggcagaggt	gccactatta
64921	aatgcctctg	cctgccagcg	ttggaaagcg	tcaagccgtt	gcttcagtat	cgggcaatgg
64981	atgtcgctat	caagataagt	gctgggaagt	gcgggctgct	cagaaatagt	gggagtggag
65041	gtcagcgata	gggagtgttc	ggtgtgtattg	tcagacatat	gtttaccgga	tgaggaacgc
65101	agcccataaa	aaagccggcg	gtgccggctt	gtcattatta	ctcgtgcgtt	atgatgttgg
65161	ggatagtgtc	atccttacgc	aacgtcatta	tttcgcagcc	gttatcggtt	accacaatag
65221	tatgctcata	ctgcgccgac	aagttgcat	cttttagttt	taccgtccag	ccgtctttca
65281	tggttccgaat	ccggtaatcc	ccggcggttc	ccatgggctc	gatcgtgaag	gccatacctg
65341	cttgccaggac	gacgcgcgcg	tcataccgat	cgtaatgtaa	aacttgtggc	ttatcggtga
65401	aaccttcacc	gatcccgtga	ccacaatatt	cacgtactac	ggagaagttc	tctgcttcaa
65461	caaatttctg	gatagcttta	cccagcgtcc	gcaggcggat	ccccggttta	accatttttaa
65521	tcgccaggta	caggctctct	tgagtcacgc	ggcacagacg	ttcaccagaa	atggtcgggt
65581	taccaacaat	aaacattttt	gaggtatcgc	catggaagcc	atctttaatc	acggtcacgt
65641	cgatattgac	gatatacccc	tctttcagca	ctttttcatc	gcttgggatg	ccgtggcaga
65701	tcacttctat	taccgagatt	cagaccgatt	tcgggaaacc	gtgatacccc	agcaggcag
65761	aaatagcctg	ttgggtggtg	gtgatattgat	catgacagat	acgatccagt	taccgcgttg
65821	ttaccctctg	tttcacatag	ggttcgatga	tttcacagac	ttcagcagcc	aagcggccag
65881	caacgcgcac	tttttgaata	tcttcagggtg	ttttgattga	gattgccatg	caaaagtgtc
65941	cgtaggggct	gtaaaatagcc	agccgcggtt	attaatgaga	tgagataaat	gaaaagataa
66001	ctgtcgatta	ataaaaaatct	gtggctaagt	gtatcagcca	agcaatttgc	tgccaaattt
66061	tcctttatag	ggcctcaccg	aatacaacaa	aagttgggtg	gttggtggctg	tttatgggat
66121	aaagcgcgcc	ggcgaaccgc	actataattcc	gatgaatatg	aatcttccga	tgacgtattc
66181	tgacgataag	tagccagttt	agccgggcaa	taccaatcgc	actcatatgt	gtaaataaca
66241	cacacgtgtc	gacacataca	ccgggggtgcc	ctaaagtttt	tgattgttat	caatcgctta
66301	tggggctcgg	gttatgggac	acgtggaggc	ataaccccaa	ctgatactat	agaggtttta
66361	atcatggcaa	ctgtttccat	gcgcgacatg	ctccaggctg	gtgttcactt	tggtcaccaa
66421	accggttact	ggaacccgaa	atgaagcct	ttcatcttcg	gcgcacgtaa	caaagttcac
66481	atcatcaacc	tggaaaaaaac	tgtaccaatg	ttcaacgaag	ctctgggtga	gttgactaaa
66541	atcttctccc	gtaaaggtaa	gatacctgttt	gttggtacta	aacgcgcagc	aagcgaagcg
66601	gtaaaagaag	ctgctaacaa	ctgcgaccag	ttcttcgtga	accatcgctg	gttgggcggg
66661	atgctgacta	actggaaaac	tgttcgtcag	tccatcaaac	gtttgaaaga	tttggaatc
66721	cagtctcaag	acggcacctt	tgataagctg	acaaaaaaag	aagcgtgat	gcgtaccctg
66781	gaactgaaca	agctggaaaa	cagcctgggt	ggtatcaaaag	acatgggcgg	cttaccagac
66841	gcactgtttg	ttgttgatgc	tgatcacgaa	cacatcgcta	tcaaagaagc	taataacctg
66901	ggtatcccg	tattctctat	cgttgatact	aactccgatc	cagatggcgt	tgacttcatc
66961	atccctggta	acgatgacgc	aatccgtgca	gttaaactgt	acctaggcgc	tgttgctacc
67021	gccgtccgtg	aaggctcgctc	tcaagatctg	gccgttcagg	cgaagaag	cttcgtagaa

67141	ĕtaġgggggc	ctĕataġġcc	cĕctĕtġcāt	atctaagtgtg	agāĕttttġĕc	ttcacāagāġ
67201	aaccgaggaa	atttaaātgg	ttġctaĕttac	cgctġctĕttg	ġtaaaagaac	tġcgġgagcg
67261	tacagccġca	ġġcatġatġġ	aatġtaaaaa	ġġcgĕttġġtt	ġaagctaatġ	ġtġacattġa
67321	ġctġġccatc	ġacaacatġc	ġtaagtctġġ	tġagġctaaa	ġctġccaaga	aagcagġccġ
67381	tātġtġtġct	ġaagġtatca	tĕctġġctaa	agĕttĕcgct	ġatġġtaagt	acġġtġtġat
67441	tctġġaactġ	aactġcġaaa	ctġactĕtġt	tġctaaagat	ġctġġcttca	aagcattcġġ
67501	cġaġaagtt	atcaacġcag	ctctġġctġa	aaaaatcġct	ġatactġatġ	ttctġaaagc
67561	taagtĕcġaa	ġaacaacġtġ	caaacctġġt	cġctaaaatc	ġġtġagaaca	tcaacattcġ
67621	ccġtġtġcġt	ġtactġġaag	ġcġacattct	ġġġtactĕttac	ctġcatġġcġ	cacġtatcġġ
67681	tġttatġġtt	ġcġġccacġġ	ġtġctġatġa	agaaactġġtt	aagcacattġ	ctatġcacat
67741	cġctġcaagc	aagcctġaat	atġttaagcc	agacġatġtt	cctġctġaag	ttġttġctcġ
67801	cġagcaccaa	atccagĕttġġ	acattġctat	cġaatccġġc	aagccacġtġ	agattġctġa
67861	ġaagatġġtt	ġaagġccġtā	tġcġtaagt	cactġġcġaa	ġtctctctġa	ctġġtcagaa
67921	cttġġttatġ	ġacccaagca	aaactġttġġ	cġatctġttġ	aaagaaaaca	acġctġatġt
67981	cġtġaactĕc	atccġctĕttġ	aagtġġġcġa	agġcattġag	aaagtġġaaa	ctġactĕttġc
68041	tġctġaagtt	ġcagġcaatġa	ġcaaacagġt	ttaatġctcc	aaatġġġġcc	ġccaatagġc
68101	ġġttccattt	tattcactcġ	ataccġtġa	tactĕtcaagt	tġcaagcġcġ	tġactġcct
68161	tĕctataact	cġaattattt	agġġtataaa	cttagĕccġc	tġagtĕtttā	ġcġcacaccġ
68221	ctġctctġag	tactġtġacġġ	tcaagtctcc	aataĕttatta	ctġctġcttā	ġġacacaaca
68281	ccatġġcaac	caatġcaaaa	cccġtatatc	agcġtatcct	ġcttaagctġ	agtġġcġaag
68341	ccctġcaagġ	cġcagaagġt	ttcġġtatcġ	acġctagcġt	tttġġaccġc	atġġctcagġ
68401	aagtĕtaaaġa	ġctġġttġaa	ttġġġcattc	agġtcġġtġt	agtĕattġġc	ġġtġġtaact
68461	tattccġcġġ	tġccġġttġġ	ġcacagġctġ	ġaatġaacġġ	tġtġtġġġc	ġaccacattġġ
68521	ġaatġctġġc	ġactġttatġ	aaatġtctġġ	caatġcġaga	tġctĕttġcac	ġctġcctatġ
68581	tġaacġcccġ	cctaattġtct	ġctattccac	ttaatġġcġt	ttġtġataat	tacagtġġġġ
68641	ccġaagcġat	tagcttġctġ	cġtcataacc	ġtġtġġttat	ttttġctġcġ	ġġtaccġġtā
68701	acccattctt	tacġacġġat	tctġctġcġt	ġtctacġtġġ	tatagaaatt	ġaagccġatġ
68761	ttġtġttāaa	agcaacaaag	ġttġatġġġġ	tttactccġc	agatccġġtġ	aaaaatccġt
68821	acġcaacatt	ġtacġaacag	ttaacctatc	agġatġtttt	agaacaagag	ttġaaagtĕtā
68881	tġġatctġġc	ġġccttĕact	ttġġcccġtġ	accataacct	ġccaattcġġt	ġccttcaaca
68941	tġaataaacc	cġġcġctĕttġ	cġtġcġtġġġ	tġatġġġtġa	ġaatġaagġġ	acattġatcġ
69001	ctaaataagc	ġacagacctt	attatcagġġ	ġtaagcacat	tġttctġtct	ġcccctttag
69061	ccagcaactġ	ttġġtttġtā	tattcaccġġ	ctatactcaa	aagctatġġc	cagccaagġtā
69121	accagtttcc	aagġġttcġc	aacġtġatĕtā	acġaaattag	aaaagatġcc	ġaagtġcġcā
69181	tġġaaaaatġ	tctġġaagca	ttccagaacc	acattagĕtā	aatccġtāa	ġġtġcġcct
69241	ctccaagtat	cctġġatġġc	attcagġttġ	agĕtactacġġ	tacġġcġaca	ccattġcġcc
69301	aattġġctāa	cattġtġatġa	ġaagactccc	ġtactttagc	ġctaacagĕt	ttcġaccġtā
69361	ġcctġagtġc	tġcġġtagag	aagġctatca	tġacttĕcagā	tttġġġġctġ	aatccatcġt
69421	ccġccġġtac	tġttatccġt	ġttccattġc	cagcattġac	ġġaagagcġt	cġtaaaagact
69481	tġattāaaagt	cġtġcġġġcā	ġaagcagagc	agġġġcġtġt	ġtctattcġt	aacġtġcġcc
69541	ġtġatġctāa	cġataaagtġ	aagġcattġc	tġaaagacāa	agaaatcagc	ġaagacġaag
69601	atcġccġttc	acaagacġat	ġtġcaaaagc	tġacġġatġc	ctatatcaag	aaagtġtġatġ
69661	ctġcattġġc	ġġtaaaagāa	ġctġagtĕtġa	tġġatttttā	atctctactc	ġcattġtātā
69721	agcġtġcġct	tagġcġġcġc	tttġcĕtttt	ttccġġtcat	ġttttġtctġ	atcaatġttt
69781	tatctġatca	atġtcttatc	ttcġcġatġt	tttttcġġcā	ġtcactcġcc	ataaaacctġ
69841	ġaacġatġġt	atcġtttġcc	atġcagġcāa	attġatātct	cġcctatcac	caaacagĕtā
69901	ttcagagcġc	cctcatġaag	caactġactā	ttcttġġctc	tactġġctcc	atcġġcaaca
69961	ġcacġttġag	tġttġtġcġt	ġcaaaccctġ	aattattttāa	agtĕacġġcġ	ttagtġcġcġ
70021	ġġcġtaatġt	cagġġaaatġ	ġcġcagcaat	ġccttġagtĕt	ctccccccġc	tatġcagctā
70081	tġtctġatġa	acactcagct	aaatcactġc	ġtttattġtt	ġġcagaacag	ġġttcagaca
70141	ccġagġtctā	ttccġġtġaa	acġġctġcct	ġcġaattġġc	agctttagat	ġatġtġcatc
70201	aagtġatġġc	cġcġattġtt	ġġcattġctġ	ġtttaccctc	aacattġġcc	ġctattcġtġ
70261	cagġtaaaacā	agtcttġctt	ġccaataaag	agtĕcġtġat	tacctġcġġt	aaactcttāa
70321	tġġatġagġt	tāaacġcagc	cġtġctcaat	tactġccaat	tġatagcġag	cataacġcġa
70381	tttttcagag	tttġcctġaa	agaattcagc	ġccaattagġ	ctattcttca	ttaaattġaaa
70441	atġġcġtttc	acġġattatt	ttġactġġct	ctġġtġġccc	atttcġtġaa	actccacttt
70501	cġcagĕtttc	tġatġtĕacc	ccagatcaag	cttġtġctca	tccaaattġġ	tctatġġġġc
70561	ġġaaaatttc	tġtġcagctā	ġcġacġatġa	tġaataaagġ	cctġġagatā	attġagġctc
70621	ġatġġttatt	taattġccagc	ġcagaacagā	tagagġttġt	ġttacatccġ	cagctġġttā
70681	ttcactcġat	ġġttcġctat	catġacġġaa	tġactcctġġc	acaaatġġġġ	actccagaca
70741	tġcġġacacc	ġattġcacat	ġcġatġġctt	acccaatġcġ	agttagctca	ġġtġttġcġc
70801	cattġġattt	ttġcaaagĕtā	ġġcġcġctġa	cctttacaac	cccġġattat	caacġttatc
70861	cġtġcttāaa	ġttġġccatā	ġacġcctġtā	atġcġġġġcā	ġġcagcġaca	acagcġctġa
70921	atġcagcaaa	tġaaatttca	ġtcatġġcat	ttttagattc	aaaaattcġt	ttcactġgātā
70981	ttġaagtġat	taaccġtact	ġttġttġaag	ġtttattatt	atcagaacct	acagġtġġġ
71041	aagagġtġtt	ġġtġattġat	cġcaaagctc	ġtġatġtġcġ	ġġcccaagtĕ	attġcaaaat
71101	tāaaataatta	aaccagġttc	ġctġatccġġ	tcatĕttġttā	ġġġaaagġct	ġagatġġtat
71161	agtcaaccct	atcaatġġat	agatagactġ	ttġattagġġ	acccaatagġ	tatttāaaacc
71221	ġtctattttġġ	ġctġtĕactc	cagaagccġt	ġacttġġtat	acġġcttttt	ttġtġcactt
71281	ġagġcctaat	ġttcġġġacġ	aacaactġat	ttattġagġa	aataagtĕtġ	cġttatġtġcġ
71341	cctġtaaaag	aagatagġġc	taacttġtcc	cccġġagġt	cagctcatġt	tġtatcatt
71401	atġġatġġtā	atġġacġttġ	ġġctāaaat	aagġġtāaat	taagagtttt	cġġccataaa
71461	ġccġġġtġa	agtccġttcġ	acġcġcagġtġ	agtĕtttġctġ	cġaagcātāa	tttagatġcġ
71521	ctcactcttt	atġctttttag	cagġtaaaac	tġġaatcġcc	ctġaccaaga	agtġaccġct
71581	ctġatġġagc	tttttġttcġ	agcactagac	agtġaagĕtāa	aaagcttġcā	tāaacatāt



71701	ċgctgġttcag	aaaaattaāc	gġcaaataāt	gācggatġgā	āācġcaacat	tġcġgġcaat
71761	tātgggtggcc	gġtgggatāt	cātccagggg	gtgġgġcāt	tagġtgaaca	agġtcagaaa
71821	ggggaattgc	aacġtacaga	tātcaġtgaa	gagġcġctca	actġgtatat	ctgġcġtgcāt
71881	gagcaatctc	aggtggacġt	agtgatcaga	accġgtgġtg	aacatġgcāt	cagtaatttc
71941	tġgttġtgġc	aaatagcġta	tġctgaacġt	tactġttacag	atġtġctctg	gġctgatttt
72001	gatgaaaatg	tġtttgaagg	tġcġctgaat	gcattġgcac	aacġcġagcġ	tġcġttcġgg
72061	ggaactacac	ctatġgatġc	cactġcatcc	tagggggaac	ttttġctgaa	gtatġctctc
72121	ataactġctt	tġattttgat	tġcġgttġtc	attġgtġcac	tġttġctġct	tġcġcġgġtt
72181	gġtttġcġta	tġgttactġt	cġtġctġtġc	atġcttġcag	cġtgggaatġ	ggġtcaatta
72241	gġgġgttttġ	ccagġcġtac	tġcagġtatc	tġgttagġga	tactġtġcġg	attġctġctt
72301	gġtġccatġc	tġcttagtġt	ccġtgaatat	cagcattġcac	ctcatcacġt	cttġgtġagt
72361	acaccactāt	ggġtġctāt	ggġctġgtġg	gttġctġcat	tġatġctġgt	gġttacttac
72421	ccġcġctġtġ	ctġtatġttġ	ggġtaactġg	cġcġctġtġc	gcātcatġct	cġgtattġctġ
72481	actattatcc	catttttttġ	gggaatġttt	gġtttacġcc	agtatġġcġta	cġagcagaac
72541	cataataccġ	gġcġttġġtġ	gġtġttatāt	gtcatġttāt	tagtġtġggg	ggcagattġt
72601	ggcġcġtaca	tġtttġgtāa	attġttcġgt	aaacacaaat	tagcġcġtaa	agġtġcacca
72661	ggtaaaacat	gggaaggatt	aattġgġcġt	tġactġagġt	cagġtġtġat	atcattġctġ
72721	tġtġgtġgat	acġcacġgt	ggatatġctġ	ccġgaaaac	tġttaatġctġ	tġcġgtġgtt
72781	gġtġcattġg	cġcġgtact	cġgtġatġctġ	actgaaagta	tġtttaaacġ	tgaagcġgga
72841	atcaaagaca	gtġgtcattt	gattġctġgt	catġgtġgga	tactġgatġcġ	tatġgatagc
72901	ctgaccġcag	ctġtġcġgt	atttġcġtġc	ttaaġtġctġ	tagtġtttāa	atcġgtcact
72961	gacġgggagġ	ttagġgatta	tġatġagġat	actġtġgagġ	ctġgġtġcġt	ttattġtġcġ
73021	actġgggātġ	ttaattacag	tġcatġagġt	tġgtcacttġ	tġggġtġgac	ggcġgtġtġg
73081	tġtġcġgtāa	gagġcttttġ	caattġgttġ	tġgtaaagcġ	tġatġgġcġc	gġactġatġcġ
73141	tġcagġgaac	gagtatġtta	tġcġcġttāt	ccactġggġc	gġttacġtta	aaatġttaga
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73261	tttacaacġt	gġgġcaatġc	tġcagġcġgg	tġctattġct	aacttġcġtt	ttġccatġgt
73321	cġcttactġg	ctġgtġtttāa	tġcatġgġcġt	gġcaaġtġtġ	cġtġcġgtcāa	ttġgtġtatāt
73381	ttġcġccacāa	tġtattġctġ	cġcaaġccāa	tatttġcttġcāa	ggaatġgaac	ttaagġtġgt
73441	tġatġgġcatġ	gaaacġcġtġ	attġggattġc	gttġcġtttġg	gġgttġatcāa	gġcgaattġg
73501	cġgataagcāa	atġcaagġtġg	ggġtġcġtġc	atttġgttġc	gacaaġtġtġg	tagagaaaac
73561	tġtġgatttāa	cġccagġtġgġ	aatttġgaac	cġataaacaāa	gatccagġttġ	tagcactġcġg
73621	tattatccca	cġtġgtġcġc	agattġgaatc	tġtġtġgġct	gaagġtcagġ	cagġgtcagġ
73681	ggcacaāaaġ	gġcġgtttac	aagcagġgga	tagġatġcġt	aaagġtāatġ	gtcāattatt
73741	ggatġcttġg	cagacattġg	tġttacagġt	cġgtāataat	ccġgġcagġc	cġgtġgtatt
73801	agatattġgāa	aggagagġta	ccccattġtġ	ttāaacġttġg	ataccagatāa	cāaaatcġgt
73861	tġgagaaaac	cġtagġgaag	gttttġcġgg	tġtagġcġcġ	aaagġgātac	cacttġcġga
73921	tgaatataāa	acaattġcġc	aatatġggġc	gtttacġgġcāa	gtġtatcāag	ctġgggātāa
73981	aacġtġgġcag	ttġatġcġgt	tġacġgtāag	catġttġggġt	aaactġattāa	ctġgtġatġt
74041	taagġtgaat	aacġtāagġt	gġccġtatāt	tattġcġcāa	ggcġctġggġc	tttġcagġtāa
74101	gtacġgattġg	gtġtactacġ	tġatġtttġt	ggcġtāatc	agġtġcact	tggġcattāt
74161	caatttġttġ	ccattaccag	tattagatġg	tġgcatġctġ	ctġtġcġttġg	cġatagāaaa
74221	gġtġaagġgt	ggġcġgttġt	ctġagġcagġt	gġcagġcttġ	agttatġcġcāa	tġgġctġgat
74281	tttġctġgtġg	ctattāatġg	ggġtġcact	tttġcāatġat	ttġtġcġctġ	tttāacġgġcāa
74341	ggġgatagġt	tagġaagaac	gcataacaac	gatġgġcġatġ	aaaaagttġc	tġatagġctġ
74401	gġtġctġttġ	ggcagġcġcāa	cġgtatācġg	tġcagacġgg	ttġgtāgtāa	acġtatġtġcāa
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74521	aggġcātāc	gtcagġgatġg	atġacatġcġ	tāaaactātġc	cġtġcġttġtġ	ttġctācagġ
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74641	acġccccacġ	attġccagġcāa	tġactttġtġc	cġgtāatāaa	gġgtġgāaag	aagatātġct
74701	caagcagāat	ctġgaagġcġt	ctġgġcġtġcġ	ggġtġgġcag	gġcttġggac	gaaccactāt
74761	atccaacatt	gāaaaaggac	tġgaagattt	ctattācagġt	gtġggġtāat	acagġcġttġc
74821	agġgaaggġt	gttġttācġc	cattāccacġ	taactġgtġt	gacġtġgāat	tġgtġttāc
74881	cgaagġgtġt	tġtġcāaaaāa	ttcagcagāt	taatatġcġta	ggtaatcācāa	gtttcaccac
74941	tġatġagġctt	atġtġcagġct	tġcāactġcġ	tġacġagġtġg	cġttġgtġga	acġtagġcġg
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75121	tāaaaaggġc	atġtatġtġcāa	ccatcāatāt	tactġaaggġc	ccacāattġcāa	agġtāaatāg
75181	tġgtātġgtġg	agġcġcāatġc	tġcagġgġcāa	tġcāactġgāa	gġtġgāagġc	tġacāaaaat
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75301	gatġttġggġc	cġttacġgġct	atġcttāccc	acġtġttġtġc	actcagġccag	aaattāatġgāa
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121441	atgcaacgcc	ccggctaaaa	caactgaagc	accgcgccac	aagggcttgt	aggctctcta
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121621	agttttgaaa	ttttctcgta	ttgatcttgt	aatagtattt	ttcttgcgtc	taatttaatt
121681	acttgagcat	ttgtttttat	ttgctctaag	gctttgtgtt	ccatggcaca	tataacatat
121741	tgccatcat	taatttatgcc	gtcagaaatt	gattttataa	tgttggtata	attcccgcct



121861	ĕccgċtactt	ġttċātaaaċ	ġgċtaataaa	taaccaāggā	ċagccċttgc	atċtttċtġċċ
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121981	acgttaactt	ttaattttgt	tatgtatttc	gataatctat	ċtgċgaagct	ttgċttttatt
122041	tcactttttt	gttċċttgga	tagtatgtca	ċtttgagatt	tttttgċtgt	tttttċttċt
122101	gatttttttaa	tttcaatggg	tatatttttt	ttactattta	tttċgtgtgc	gcggtttttca
122161	aacttatcat	tggggaatga	tattaacgaa	ttggagtcac	tttcaatgac	attattataa
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122341	atcaaaatgc	tagtgċgatg	tgċtatagaa	ttttcatgta	ttggtċċaca	tggtgggcac
122401	tċtatgtcac	catċttċcat	gttttċgacg	gaaaaaatat	aatċtttatċ	tagċtċacta
122461	ataatċċċtt	tggtċtaattt	gattttgċag	tcaagtgċta	ttttttcaac	ttċtaagtta
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122641	gcattattca	gttċagtaac	gċttttċtca	acttċttċta	actċtċtttt	tattacataa
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122761	ggtttttgċċċ	agċtactata	ttgċtgaaga	ttċtċgaaac	tatċċċaagg	tttagċċcat
122821	gttċttttttt	ggċcaatata	aaaggggatg	aagtaatatg	caggtggagg	ggtttċtagt
122881	gttaattgac	ċtttċttagg	gagtaataca	ttaaaattaa	caagtċtċga	aaaataċttt
122941	gaataatcac	ċggttatttt	tgggaaactg	tgtagtttac	cattgtċtatg	ċċtaatttta
123001	atttċattttt	tatatċtatg	aataatgtaa	gggtċcattat	ttatċtċaaa	ċtċtataaatt
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123121	aaaatċattt	ttgċaagċgt	agatttċċċt	acgċtattat	catċatċtċg	tggtatċagt
123181	gttagatgċt	ċtċċgaactċ	gaattgċċċt	gċgċatttttċ	ċtgaatċtċga	gagtatċatg
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123361	tagaaatatt	atċċtċaaac	aaċċaatag	tatċttttga	taagtċtatg	attagċċttt
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123541	aattttatttt	ttgtattatt	tttgċċttaa	tċgtgċċċtt	taaattttaga	tċatċtataa
123601	tgtatttttat	tgċttċaaaa	tttaaactċg	aattacċttt	tgagactatt	ttggttacta
123661	ċċgtatggat	atċttttatag	gtcagtċċt	ttttagtaag	agċatċattċ	ċaattttċat
123721	agtċaaaaac	gttċttċċċt	ċtgatgċgta	atgagtċċat	taatattċta	taaatatċt
123781	tċgtacgaag	tagatgttgt	ggataċactt	ċtċċgacċċt	atċagtċatċ	ċttgatattg
123841	tatgċtċata	atagċtttċt	agaggaatgt	cagaggtagt	gaagtgtatt	atttċttgċg
123901	gaaactttċċ	gaagttagċg	agċtċatċac	ttaggċattt	tataatttċa	ċtagċċċat
123961	ċactacttaa	gċtagacagt	ttatatgaag	ċcaagtttaa	ċttgtttgtt	ttagtċaggt
124021	tgaatċċact	tgtagtata	aaatċtaatt	tttċaacċtt	ttċaaagtat	tttttgċċg
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124141	ataċttttgċ	agtataagtt	ttċtttgċat	tggttttaatt	ttgattgaaa	gtaaatttaa
124201	ċttttattttt	atċtatagaa	ttċgċataga	ċaacatċttċ	atgatattċċ	atgaagattg
124261	caaagtċatt	gċttttċttg	tatgaactga	atgċtttaca	aagagċċċaa	tgatatggg
124321	attċaaatċg	atċataggac	tgggċċċċtċ	ċggactċtċt	ttgċgggtċg	gacaagggat
124381	tgċcagatgt	gtċttċacta	tċċatttttag	tggtċgtċċ	attttatgag	tgataċtaaa
124441	agataataċg	tgċtaaggga	aacgtċtatg	actttċactt	acgttaaata	ċttċtttttag
124501	tgtatatċtċ	taatċċċċac	ċaatċċatta	actċttggċg	ttgtatgaga	taggtagaac
124561	gattataaċg	tttċċtgact	tċattċttat	ċactatgċċg	tagċċgagċċ	tċaatċacat
124621	cagcattaaa	ċċcagċċtċa	ttatċggċtg	tactggċgat	agaacgċtaa	ċċgtgagċaa
124681	ċgagċttċċċ	tċċataacċa	atacgtttċa	aggċtgċatt	tgċtgtttg	ċtattċatgt
124741	gattacgtgg	gtċattgċga	ċttgggaata	ċgtgċtgacg	attaccacta	attggacċga
124801	ttatttċċag	ċaactċtaag	gċttgttċċg	acaacgggac	tatatggċċg	ċgċtttgċtt
124861	tċattċgttċ	tgċċggtata	ċaccactgċt	tattċtċtaa	atċgatċtċt	atċċaagċtg
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124981	ttggcagtga	gagattgċtċ	atggċaatgg	tacċgatgag	tttagċtagt	tċtċcaggtċ
125041	tgatgtggg	catatgtċgċ	ttċttggggċ	gttċaaaagc	attaccgata	ċċtgaagċtg
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125161	ċcaatċgċċt	gacċgtċtċt	aatgċtċċac	gtgċtttgat	tggtċċaat	acttgaatċa
125221	gagttċgtgċ	tttaaagtċt	tggtatgggaa	tattttċgat	gċtgggtaag	atgtċttttt
125281	ċaatagaacg	ċċaaatatċt	ttċgċatggg	ċtgċgċtaac	atggċtttċt	ttċaactċga
125341	accatttgċg	ggċgacattċ	acaaaaatgċ	ttċċċċċgċ	tatċtgagag	ttttcagċċt
125401	ċttcaccagċ	ċċtċgtttga	gggtċtgċċ	ċtċtgactaa	catċgċtagt	ttttċtgċċg
125461	gtatċtċtċt	ggċatċtgċg	agggatagtg	ċtggtgaagċ	accgaggċtg	atċatagtgċ
125521	gċttgċtact	gttgggaagċ	tgatagċgga	aacgċċaaat	tttċttgċċg	gtagttttga
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125761	tggattċagċ	ċggatċċċt	tggaċtacta	ċagacacaaa	taaatatċċt	ċċggċatagċ
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131641	ccttgaatcc	ccggttttga	tccccataat	aagccaagta	gcgagattaa	tgctaaaacg
131701	cggagatatc	cgtgagtgt	aaagaacaga	aaacgccaac	cgagcaagtc	tcggaagaaa
131761	tggaaaatac	agcagagcag	caagtggaag	caacacaaga	gacgggggaa	tgtgtagatc
131821	cgcgtgttgc	agagcttgag	gtgcagttgt	ctgatgctct	acagcgtgag	cgcgaaagcc
131881	tgttacgcgc	taaggctgaa	gttgagaata	tccgtcgtcg	tactgaattg	gatgtcgaga
131941	aagcgcataa	atttgcactg	gagagattct	catctgaatt	attgccagtg	attgacaatc
132001	tggagcgcgc	tctagatacc	gctgataaga	ccaactactg	actgatctca	atgattgaag
132061	gtgtcgaaac	gacactgaaa	tctactgtag	atgtgtcgg	taaatttggg	attgaagttg
132121	tcggcgagac	ccatgtgccg	tttaaccctg	aggtgcatca	ggccatgaca	atgcttgagt
132181	ctgctgatca	cgagccaaac	cacgtaatga	tggtgatgca	aaaaggctat	acgctgaatg
132241	gccggctgtt	acgcccagca	atggttgccg	tatctaaagc	gaaatcgtaa	agtgtcttaa
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132361	gactttgtct	taattttacg	cgttaacgcg	tacctgctta	ttttttcaat	tggtcttggg
132421	aatcacgttc	gttatagcca	gtataaagct	ggcgcgagcg	ggcaatcttg	atgccgtcat
132481	tatgcatttc	gttccagtga	gcaatccaac	cgatggttcg	ggcaatggcg	aatatcaccg
132541	taaacattga	cgatggaatc	cccatggctt	tcaggataat	acctgaatag	aagtcacagt
132601	ttggatacag	ttttttctca	atgaagtaag	gatcggttcag	tcgatgttt	tccaactcca
132661	tcgccacttc	taacaagctg	ttattcagct	tcagctcttc	taacacttca	tgacaggttt
132721	cacgcgatgc	ggtggcacga	gggtcatagt	ttttatagac	acggtgacca	aaacccatca
132781	gacggaatga	gtcattctta	tctttcgcgc	ggcgagataa	ttcagggata	tgctcaacag
132841	ttttaatctc	ttccaacatc	ttcaggcagg	cttcattggc	accaccgtgc	gcagggcccc
132901	acagggatgc	gatccccgcg	gcgatacagg	caaacggggt	agcgccagaa	gagccggcag
132961	tacggacggg	cgatgttgac	gcgttctgtt	cgatgatctgc	gtgcaggatg	agaatacatg
133021	ccatagcgcg	ttccagtact	gggttaactt	catatttctc	acatggcgta	gagaacatca
133081	tgtgtaggaa	gttaccgcgc	taggacagat	cggtacgtgg	ataaacaaac	gggtgacca
133141	gtgaatatct	ataacacatc	gctgcgacag	tcggcatttt	agacaacaga	cggaaggcgg
133201	taatttcacg	atggcgctcg	ttattaacat	ccagagcatc	atggtagaag	gcggctagcg
133261	caccagtaac	cccacatagc	acggccatcg	gatgtgaatc	gcggcggaac	ccatggaaca
133321	gacgggtgat	ctgctcgtgg	atcatggtat	gtcgggtcac	tgtggttttg	aacgttttgt
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133441	aatcttttgc	caactgggca	atcggggaagc	cacgggtgcag	caaaataccc	tgatcaccat
133501	caatataggt	gatttttgat	tcgcaggatg	cggttagaggt	aaaaccgggg	tcaaaggtaa
133561	aataaccctt	agaacctaag	gtgcggacgt	cgatcacgtc	agtgccgagg	gttggggata
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133681	acagtctcct	taagtgtcta	ttttaaaacc	cctaacaacg	gaaacatctt	agatgcccg
133741	ggatatacacc	ttattagcac	tgctctgttt	tattcatcat	taatactctt	ggtagttgaa
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133861	gagtaaatgt	ccaatacggc	ccgcgatccg	aagggttgga	tcaacagcta	gtgttaaaaa
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133981	gatattgact	caatacactg	ttgcataact	taagcttggt	gggaagtgt	tccgttgacc
134041	tttagtgcat	cataggcctt	atttctaccc	tagttgtaat	ggaaatgttt	attctttgtc
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134161	gaaatgttat	caatcagttt	gtgtgggaat	tgtaataaga	atgtgaaccc	cctatactgc
134221	gccaggtct	ccggattacc	ctgaagttag	agcaccacgc	gttatacaga	acatgctgtt
134281	taagcattca	ggatgcaata	cttaaacgtg	cgatgtgaag	ggtttcgact	cttaacgctg
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134521	tctggctgtt	gggtttgtct	gtttctctac	aagaaggatt	catgcaggca	gcaaccatca
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135121	gaatctgcca	atcagagagt	ttgatgcagt	tggtgtcggt	gcaggtgggtg	ccggtatgcg
135181	tgccgcctgt	caaatttcac	aaatgggctt	gtcttgcgcc	ctgatatcta	aagtcttccc
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135301	tgaagataac	tgggaatggc	acatgtacga	tacggtaaag	ggttccgatt	atatcggcga
135361	tcaggatgcc	atcgaatata	tgtgtaaaac	cgggtccggaa	gcggttctgg	aattggagca
135421	catgggttta	cctttctccc	gttttagagga	tgggagcatt	tatcagcgtc	catttggggg



135541	ċggġcatgċg	ttgttaċācā	ċċċċttatċā	gāāāācċctg	āāāāacċacā	ccāctaċttt
135601	ċtċtgaatgg	tatgċactgg	atċttggtgaa	gaatcaggac	ggċgċttttt	tcggttgtag
135661	tgċtattaat	attgaaacċg	gċgaagtċgt	ċtattċcaaa	gċacgggċca	caatattggċ
135721	aactggċggt	gċtgggċgta	tttaccāatċ	aacaacċaat	gċgċacatta	ataccgggtga
135781	ċgggtgtgg	atggċċttgċ	gtgċtggagt	ċċċggtgċag	gacatggāaa	tggtggagtt
135841	ċcāċċgāċc	ggċtattggċg	gtgċgggtgt	attagtċact	gaaggċtggċ	gċgggtgaagg
135901	ggggtatttta	ċtgaataaac	atgggtgaacg	ċttċatggāa	ċgttatggċċ	ċgaacgċcāa
135961	agatttgċgċ	ggċċgtgatg	tagtggċacg	ttċċattatg	attgāaatċċ	gtgaaggacg
136021	tggttggtgac	ggċċċttggg	gċċċacatgċ	ċāaactgāaa	ttggatċact	taggtāaaga
136081	tgtgċttgāa	ttċċċgtċtċ	ċgggtattċt	tgagċtċtċ	ċgċacċttt	ċacacgttga
136141	ċċċgatċāaa	gaacċgatċċ	ċgggttatċċ	tacttgċċat	tatatgatgg	ggggāattċċ
136201	gactāaagtċ	acgggtċagg	ċgattacċgt	āaatgāāaag	gggtgaggatg	ttgtgatċċċ
136261	ċggċttgttt	gċgttagggċ	āaatgċċtċ	tggttċċgċ	ċacgggtgċga	acċgċttggg
136321	agggaactċa	ttactggact	tagtgggtatt	tggtċgtgċt	gċċggtatgċ	acċtgāaaga
136381	atċattgatg	gagċagggċg	ċaagċċgċga	tgċċagtċag	ttċagatātċ	aagċċtċtċ
136441	ggċtċgċatg	aatċgċtggā	ataatāċċċg	ttċagggtgāa	gatċċagttg	āaatċċgtāa
136501	agċattgċāa	gċċtċtatgċ	agaācāattt	ċtċċgtgttċ	ċgċgaaggċg	atgċgatggċ
136561	āāaagggttċ	gaagagċtga	āāactātċċg	tgaacgtttt	ċāāaatgċċċ	gtttggatga
136621	ċacttċcagt	gaattċāata	ċtċagċgtat	tgagtċċċt	gagċtggata	acċtgatgga
136681	aactgċgttt	tċāacċgċtċ	tgċċggċāaa	ċttċċgtacc	gagagċċgag	gtgċċcatag
136741	ċċgċttċgat	ttċċċggatċ	gtgatgatgt	gaactggċtċ	tgċċattċac	tgtatttgċċ
136801	aggċactgag	agċatgāċċċ	gċċgtgaggt	āaacatgċāa	ċċtaagċtāc	gċgaggċatt
136861	ċċċgċċgāaa	gtgċgttċtċ	attgatgċċt	gtgttggtgt	ttċtaagggtt	āaacċċgttċ
136921	ċggaggāata	ggċċatgaag	ttċgagtttt	ċāatttātċg	ċtataāċċċa	gaatċċgata
136981	acċgċċgċca	tatgċāagat	tacagċċtċg	atgċggaaga	aggċċgggāt	atgatgttċg
137041	tggtatgċact	tatċċagttg	āaagāāāaag	atċċgacgtt	gtċattċċgt	ċgċtċatgtċ
137101	gċgaagggtg	gtgtgggttċ	gatggċtċtga	atatgāatgg	ċāāāaatgg	ttggċċtċtga
137161	ttacgċcāat	ċtċagċtttċ	ċāāāaaggċa	ataāāaagat	agtċatċċgċ	ċċtċtċċċg
137221	ggttāacċggt	ggċtċgagat	ttagtċgtċg	atatggggċa	gttttātātċ	ċagtatgaga
137281	āataāāāāc	ttācċgttċg	aatgācggċa	agaattċċāc	agċacgtgag	ċacċtācagt
137341	ċċċggaāca	acgggċāāaa	ċtggatgggt	tgatgāatg	ċatattgtċg	gċttgtċgtċ
137401	ċāacgtċttċ	ttċgtċattċ	tggtggāatċ	ċagācāagtt	tggtggċċċg	gċtgggttāc
137461	tggtċgċċtā	ttċgtttċċtċ	atagatagċċ	gtgatāċċga	āacggċċtċā	ċgtttggatg
137521	acċtgċgāċga	tgċttttċagt	gttttċċgċt	gċċatagċat	tatgāattgt	gtċagtgttt
137581	gtċċtāaagg	ttċtāatċċt	acċāaagċāa	ttċggċatāt	taagtċtātċ	gtgttācāc
137641	gtagċgċatā	gtċgttatċg	ċgtagċċat	āāatagċga	tagċgċtċgt	agtċatgatt
137701	acagtgtagt	gaatgācāat	tatggċcāaa	ċgattgttāt	āacatagċgċ	atāatċattg
137761	ċāacgċagtċ	ċċtgatgtga	gtttattāac	ċċggagaggċ	gattċtċċgċ	gtagċttċac
137821	ggtagggāat	ċtċtāāāagċ	ċggċcātāatg	ttċgtttċtā	gaggttċċtt	gaacgggācċ
137881	gataagggtċċ	atāacgāāac	gtgċattgag	ċacgtċgagt	gaacċgtttt	tācgggāāac
137941	ċgttgatatt	acgggtgtatā	tgttāacċc	ggċgāāāact	gaagċttċāa	agtċtāaggċ
138001	atċcātāatg	agaacggċgċ	aatgāaggċċ	tggttggatt	ċċtċtātċt	ggċgggċgċg
138061	aacċatċċt	acatagāgċā	gċtċtatgāa	gċtttttāa	ċtgatċċtċg	ttċċgttgat
138121	gatagttggċ	gttċāatttt	tċāacagċtā	ċcāacāacgċ	gtgtāāāāc	tgatċagċtċ
138181	ċactċċcāaa	ċgċgtgagta	tttċċgtċgċ	ċtgċggaagg	attċċactċg	ttātāactċċ
138241	tċtatċāatg	atċċtgatāt	tgatgċcāag	ċaggtāagg	tattgċagtt	aatċaatgċċ
138301	ttċċgċttċċ	gtggċċatċā	gċatgċcāat	ċttgāċċċāc	ttċgtttgtg	gaagċaggag
138361	ttċgtttċcāg	acċtċgatċċ	ttċċtāċċat	aatċtgāċċg	aagċtgāċċt	ċcāgaacācċ
138421	ttċāatgtċg	gttċtttttċg	ċatċggċāaa	gāaacgātga	agċtggċtga	tttgatgċċ
138481	gċgċtgaagċ	āāacttattg	ċggttċtċgtg	gggtċtgaat	atātċċācāt	tācāacācċ
138541	gaagāāāāc	gċtggattċā	gċagċgtatt	gāatċggttċ	ttgggāāāc	gacattċagt
138601	gatgċagaga	āacgċċgttt	ċttgagtgaā	ċtgāċċċċg	ċtgaagggtċ	tgagċgttāt
138661	ttaggċgċāa	aatttċċcāg	ċgċcāaggċt	ttċtċtċtċg	agggggggga	ttċactggċ
138721	accatgċtċā	aagagatgāt	ċċgtċatgċċ	ggtaāāāatg	gċacacgtga	agtċgtċċtċg
138781	gggatggċċċ	acċgtggċċg	tttgaacgta	ttgatċāatg	tgċtgggtāa	gāaacċagāa
138841	gacttgtttċg	atgagtttċg	tggtāagċat	āāagaacātċ	ttċgtactgg	tgatgttāag
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138961	gċċtttāācċ	ċatċācāttt	ggāaatgtċ	agċċċggttċ	ttattgggtċ	agtċgċtċgā
139021	ċgtċgċgatċ	gċċtgatga	agċācċgċt	āatātgggtċ	tgċcāatċāc	tattċatgg
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139141	ggċtatgāag	tgggċgggtāc	tgtagċcāt	gttatċācā	acċagattgg	tttċācāācċ
139201	ttċgāācċāc	tggtatgċgċ	ċtċgactċāa	tactgtactċ	atattgċcāa	aatgggtācāg
139261	gċācċgattt	ttċācgtgāa	tgċtgatgat	ċċtgāaggċtċ	tgċcatttċgt	tācċċgtċtċg
139321	gċgttggtt	ttċċgtāatāc	ċtttāāacgt	gācgtgatga	ttċgatċtċgt	ttgttācċgċ
139381	ċgtċatggċċ	atāacgāagċ	ċgatgāgċcā	agtċāacāc	agċċtgatgāt	tgātāgāāa
139441	attāāāāāc	atċċgāācāc	gċgtāāāatċ	tatgtċgācā	āactgattga	gċgāatātċ
139501	gċcāgċċtċg	āagatgċgāc	agāaatggċtċ	āacċtatātċ	gtgatgċatt	agātċācgggt
139561	gactgtgtgg	tggaagagtċ	gċgtċċgatg	āatttgċag	ċttċċacttċ	gtċācċgtāt
139621	ttgāācċatg	agtgggatga	agċgtātċcā	agċāāagggttċ	āaatgāāācċ	ċċtgāāagg
139681	ċtgċgċgċtċ	ggatċāgċtċ	tgċgċċggāa	gċcattgāāa	tgāatċtċg	gggtgċgāag
139741	atātācāgtċ	atċgċgċgtt	gatggċcāgċ	gggtgāagāc	ċatttgactċ	ggggggāgċg
139801	gāāacāctċg	ċttāgċtāc	attggtagāc	gagggċattċ	ċtattċgttt	atċtċggāa
139861	gatgċgggċg	gtgggtacttt	ċttċācċgċ	ċatgċggċtā	ttċātātācā	gāāāaatgg
139921	tċtċgtttatg	tācċactgtċ	āaatātċāc	agtggċcāgg	gtgatttċcā	ggtttgggāc
139981	ttċgtgċtċgt	cagaagaggċ	agtattggċg	ttċgāatācċ	gċtatgċcāc	tgċggāgċċg

140101	aċcgaccaāt	ttattaġtċc	tġgtgaācag	āāatġgggtċ	ggatgġtġg	cttāġtgāt
140161	ttgctaccac	atggctacga	agggcagggg	ccggaacact	cctccgcacg	tctggaacgt
140221	tatttgcagc	tttgtgctga	acaaaatatg	caggtgtgta	ttccatcgac	ccctgcacag
140281	gtttatcaca	tgatccgccc	tcaggcatta	cgtggtatgc	gccggcctct	gattggtatg
140341	tcacctaāt	cattactacg	ccatccatta	gcgacatcat	ctctggatga	atctggtaat
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140461	gtcgtgatgt	gctcaggcaa	agtctactat	gacttgctag	agcagcgtcg	taaaaatggg
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140641	cttaaccaag	gtgcctggta	ttgtagccag	cataacttcc	gcgaagtgat	tccatttggg
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140761	gtacaccaaa	aacaacaaca	agctctgggt	aatgacgcgc	tgaatggtga	atagctagtc
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162121	cagccḡāatc	actḡactcca	ḡḡāagctcat	tḡḡaacḡctc	tḡcḡḡḡḡccḡ	cctḡcctḡcā
162181	actcḡāatḡa	ttḡḡḡḡḡḡāa	tāaatācācā	ttcāatḡatā	attattatcā	ttatattḡcḡ
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172861	gtgcggccct	ggcttcggcg	gtggttgctt	ttcctttgat	ggtcaggcg	attcgcttag
172921	ctctggaggc	cgctcgatacc	cgtttgaggc	tggcgcgcg	cacgttaggg	gcaacgccat
172981	ggcgggtctt	tttcacgata	actctgccgc	tctctttacc	gggggtgatt	gccggtacgg
173041	tgctgtcttt	tgcccgtcga	ttgggggagt	tcggtgcgac	catcacgctt	gtttcgata
173101	tccccgttga	aaccggaacc	attcctctgg	caatgtacac	cctgattgaa	acgccgggtg
173161	cggaagccgc	cgctgcgcgc	ttgtgtgtga	tcgccattat	tttatcggtg	gtgtcattgc
173221	tgttatccga	atggttggct	aatggggta	aaaaacgcac	gggggcccc	tgctagaact
173281	gaatttcagc	caacaatttg	gtgattttaca	cctacaggct	gccaccgatt	taccggcgca
173341	ggggattacc	gcgatttttg	gtttatccgg	tgccggtaaa	acgtcactga	ttaatgtgat
173401	aggggggctg	actcgccac	agcaaggccg	agtgtattctg	aatggccggg	tgatgggtga
173461	tgcgcagaaa	aataatttacc	tgccgcccga	aaagcgccgg	gttggctacg	tgtttcagga
173521	tgccgcgttg	ttccctcatt	atcggtgtcg	gggtaacttg	caatacggta	tggcggcgtc
173581	aatgcgcggg	cagtttgacg	cgattgtggg	cttgctgggc	attgagccgt	tattgaaccg
173641	cttcccgttc	acgctgtcag	gtggcgagaa	acagcgggtt	gccattgggt	gtgcattatt
173701	gaccgctcct	gagttgtctg	taattggatga	gccattggca	tcactggatt	tgccacgtaa
173761	gcgcgagctg	ttgccgtatc	tggaaggct	ggcgaggat	gtgaatacgc	ccattttgta
173821	tgtcagccac	agcatggatg	aaattttgcg	gctggcggat	caagtgggtg	tgatggatgc
173881	cggtaaagtt	cgtgccgtgg	gggggctgga	ggaggtatgg	gccagcagtg	cactgcggcc
173941	gtggttgcaa	cgagaagagc	ctagcagcat	tttgccgggtg	agtgtgattg	gtcatcatga
174001	tcgttatgcy	atgacggcac	tggcgttagg	tgaccagcgg	ttgtgggtgg	gcaagtggga
174061	tgccgctgaa	ggcaattcaa	tgctatccg	tattaatgct	gccgatgtct	cactggcatt
174121	acagccgcgc	cacagcagca	gtattcgtta	tattttgccg	gtaaaagtgg	ctgagtgtct
174181	ggatgtggac	ggcgaggctg	atgttaagtt	agccatcggt	gagcaatgg	tatgggcgcg
174241	gatcacgcca	tgggcacggg	atgaactggg	gctgaaacct	ggtcagtggg	tgtatgcaca
174301	gataaaaagt	gtgtcattta	accgccagaa	tggccctgta	ccagattgag	tgggtgccgt
174361	ttttgtgtag	gcaccaccat	gatgaatctg	tcgctgtgaa	tttatcaggc	taatacatgc
174421	tggcggataa	cggcggcaat	accggcttgc	tcgttatctg	taatcaccag	gtccgccgt
174481	tgtttaatcg	cactgtcgtc	gttaccctga	gcaaccccta	atccagcagc	ctctaacata
174541	ctcagatcgt	taaagttatc	accaaaagcg	atcacctctt	gcatactcag	gccctgagat
174601	tcaaccact	gttggaggcg	tttccccctg	ctgttccccg	cttgggcgat	atccacctga
174661	tcatgccacg	accattcgca	ggccagaccc	atcttctgctt	ctaccctggc	ggcaaacgct
174721	tttaactgtg	cagtatctgg	gtgagagggt	gcaaatttcc	agatggcgg	cgcactgtga
174781	gcggcatcca	gtaagctggt	gacctgaaga	aaggtcgggc	gctgagcggg	cggcaatgac
174841	tcggcccaac	tgaggggtcg	ggtcacatgg	cccgtgatct	gctgatacag	catggcatca
174901	tccacataca	tcaggccatg	gatctgtgtt	ttctccagta	attgcaggac	ttgaaccgcc
174961	tggtgtggag	tgagtgggtt	tgaatccagc	acttttttat	tttgataatc	ataaatataa
175021	gtgccgttac	agcagatagc	gggtgtatcc	agttgcagtg	cctgataaaa	cggatggatc
175081	gcgacatggt	ggcggcctgt	tacgacgatc	acttttcacg	cttcagcccg	ggcttgccgc
175141	agcgcggaca	acgattcaga	caggatgcgt	tttttgtgat	ctaacagtgt	tccttcgaga
175201	tccagtgcca	ttatgcgata	tgtcatagcg	gtccctgtcc	ccattaaagg	ggcgaatgag
175261	aaattatatg	cttgaaaagt	atgttccgat	agtacaccgg	atgggtgatc	gattaaacca
175321	aaccggggga	aaggcctgta	taaacagcta	aaaagaagcc	gcgccgcgag	atgcccgaca
175381	gttggttatgt	ccgtgcagtc	aggtaagcta	ggcttaaaatt	aaccgttaat	aaaagatatt
175441	tggttaaaggc	gaaggggctg	gaacagggtca	attcacctta	atagcgttac	ccaacagggtt
175501	cgactaagga	gtaaagatga	agcaaggcgt	ttacgtggca	agtcagaca	gccaacaaat
175561	ctactgtctgg	caattagatt	cagccgggtga	attaacctta	ttgcaaaccg	tggacgtgcc
175621	gggtcaggta	cagccgatgg	caataagccc	taatcagcgc	catctgtatg	tcgggggttcg
175681	tcctgatttt	ggtattgtca	gctatcacat	tgccgatgat	ggtacgctga	ccgccgcagg
175741	tatggcaccg	cttcccggca	gcccgcactca	cattgacacc	gatcgacaag	gtcgcttctt
175801	gttctctgct	tcttacagtt	tcaattgcgt	cagtatttagc	cctatttgata	cgcattggcgt
175861	agtgcgaagc	cccattcagc	aatgggatga	cctgcccgcg	ccacattcgg	ggaatattga
175921	cccaaccac	cagatcttgc	tggttcttgc	cctgaaagag	gataagggtac	ggctgtttga
175981	tttgagcgcg	gaggggcagt	taacccccca	tgacacaggct	gatattactg	ttgccgcggg
176041	cgctggccca	cgtcatatgg	ctttccaccc	gaatcatcag	ggtgcttatt	gtgttaacga
176101	actcaatagc	tcggtggatg	tgtatcaaatt	cagcaataaac	ggtcagggaat	accacttagt
176161	gcagagcctg	gacgcgatgc	ctgcccgat	caccgggaca	cgttgggcgg	cggatattca
176221	tatcacgcct	aatggccgct	atttatacat	cagtgaaccgt	accgccaacc	tggtgggtat
176281	tttcaccggt	tctgaagatg	gccgggtgat	ttcgttggtc	gggcaccacc	tgaccgaagc
176341	ccaaccgcgt	ggtttcaata	tcgaccacag	tggtaatttc	ctgattgctt	ccggtcagaa
176401	atctgatcat	atcgaaagttt	atcgtatcga	tcagaacacg	ggggagctaa	ccaccctgaa
176461	acgttatccg	gtaggtaagg	ggccgatgtg	ggtcagtatc	cggggggcgc	agaactcata

176581	cttgagtġāc	tgtgcactgċ	ccatgtctāa	attgācġgċġ	aċtġtġggcgc	tgātġtġcġā
176641	gagatcttta	caccagacgg	cggaaaaacc	gġgatġccġt	tacċttaaacc	ggtgaagata
176701	ggcattttagc	ttccġġgatc	taccacġġcc	ġcagtgagcc	gggttaaaggc	ġtġttgagag
176761	ataatataag	ġġġġcatcag	ataaatcag	ttġccaaagg	ġcċtgatcca	cacccċctġt
176821	tcgacaaaac	tġġtġtġcag	ġġġġġcaca	ttaaġġġtt	ttttcatctc	taccacccġġ
176881	atġġcccca	ġtaccġġcac	atġġccacġ	ġtatċttċċ	ġagccagcġġ	cagtaattċċ
176941	ċtttttaact	ġatċttċtat	tttatċcacc	tġġtġttġcc	acġaatċtċ	tġċtaataaa
177001	ċtġagġttġġ	cagagġġġac	tġġġcaagcc	agġġattġġ	ċcataaagġt	tġġcccatġġ
177061	ataaagcagc	ċġġatċċċċ	tttactġatġ	ġtttċtġcca	ċtġcacġġġt	ġġtġagcġtġ
177121	ġġġataaagġ	tġagataaacc	ttċġġtġagc	ġċtttacċta	aacataaaat	atċġġġcacġ
177181	atċtġġġat	ġttcacagġġ	aaacagtttġ	ċċtġttġġġ	caaaccġag	ġġċtatċtca
177241	tcġġcaatca	ataaaatttġ	atġtttatca	cataacġċċ	tġacttċacġ	cagatagctġ
177301	gggtgataaa	ttġġatċċċ	ġġġġċċċċ	tġcacċacġġ	ġttċcagġat	tacġġġġcā
177361	atċtġattġġ	cġtġġtġġġt	tatcagcġġ	acaaaattag	cġatatċttġ	cġġatċċcac
177421	gggtġatcāa	agċġġcactġ	tġġġġcattġ	ġcaaacagat	tċtġġġtāa	atagċċtġa
177481	tacaaactġt	ġcattġaatt	ċtġtġġġtca	cagacġġaca	tġġcacġġaa	cġtatġġġġ
177541	tġġtaaccat	ġġġġcaagġt	caaaatcacġ	tġġġġġġt	cġċċtċtġġ	tġġcagtat
177601	tġcaacġcca	ttttcagġtġ	ġacċtcaacġ	ċtġacġagc	cġġaatġġġ	caaaaaaacġ
177661	cattċcagcġ	ġġġġġġtġt	cacġġġġac	agttġtġġġ	acagċttat	tġġġġġġġa
177721	tġġġtaatġġ	ċċċġaacat	cacġtġġġac	attttatcca	ġttġġtġatġ	cġġġġġāa
177781	ttcagġacġġ	ġġtġġttata	ġċcatġaatġ	ġġtġċċacċ	aagatġacat	accatġġatċ
177841	agċġġġġac	catcagġcāa	ttġcaattca	acacċtċcag	cġċċacċac	ggġġtaacag
177901	ġġcagġġġt	cagġcattġa	ġġtġtagġġa	tġġcagatat	ġġtġttġatċ	aaaaactaag
177961	tġagaagġtġ	tċattagġta	cġġttġtāa	ċcaaaatatc	aatagaattġ	ttġcagtat
178021	atġagtttta	ttttactġta	cġāaactttt	tċtċttċttt	tġagagġcca	tċatġġcāac
178081	ttatċatcac	tġġacagġtag	ġġcaagċċċ	ġġċċtġttt	ġataaaċġġ	tġttġġaatt
178141	attġtttġaa	ġcacaacaag	ttcacġġcca	ġcattttġat	ċġġġtġagġ	tacaagġcag
178201	tacġttġttġ	tġġattāaaa	ċġġtġċċtġ	tċġġaagat	tġtāaatatt	ġċċġcāaag
178261	ċtċċġġtat	aaaaccġġtċ	tġġaaagcġa	acġċtāatġ	cagġttġagc	agġtactġġa
178321	atġġġcāaġ	aaagcāaag	cġġcagġttċ	ġacċġġttċ	tġtatġġġġ	cġġġtġġāa
178381	aaatċċċac	ġagagġġata	tġċċttattt	ġġġāaaatġ	ġttġaagġġ	tcaagġtċt
178441	ggġġatġġāa	acċtġtatġa	cattġġġttċ	ġġtġagġāaa	cagcaagġtċ	atġġġtġġġ
178501	ġġatġġġġġ	ċtġġattatt	acaaccacāa	tċtġġatacc	tċtċcagagġ	tttacġġcag
178561	cattattacġ	acċġġcagġt	atcagġaacġ	tttġġatacġ	tāaaacġagġ	tġġtġacġġ
178621	tġġġatcāaa	ġtġtġttċtġ	ġtġġcatġġt	cġġtġġġāa	ġaaacġġtat	ġġatġtġġ
178681	cġġġġtġttġ	ġtacaactġġ	cġaatġġġc	tāagcċacċ	ġaaagġtġġ	ċcatċaatat
178741	ġttġġtāaaa	ġtġaaagġca	ċċċġġtġġa	aaataacġca	ġagġtġġatġ	ċttttġagtt
178801	tatċġġcacc	attġġġtag	cġġġatċat	ġatġġġtċt	tċċtatġtċċ	ġtċtġtġtġġ
178861	cġġġġġġġ	caaatġaacġ	aacaacċcca	ġġċcatġtġġ	tttatġġtġġ	ġagccaactċ
178921	tattttċtċac	ġġġtġāaat	tactġaccac	acċġaatċċ	ġatġaagata	aagatċtġca
178981	attġttċġt	aaattġġġġ	tāaaċċġca	ġcagacġġca	acatcacacġ	ġtġatġtġa
179041	acaacaacag	ġċċtġacġġ	agcagġtact	ġcattġġġat	acġġccagġ	tttataatġġ
179101	ġġġġtċtāa	tġagġtġġca	agataaaata	ġġcāaagġt	tġcaacġġġġ	acġtġatġġġ
179161	ġġġġttacc	ġtactġġcca	ġġtcaacġag	ġġġġcāatġ	ġġġġtġġġt	acagġcagġġ
179221	ġagġġcāat	atċtcaactt	ċtċcagġaat	ġactatċtag	ġġtāagcca	aaatġacġag
179281	ġtġattġġġġ	catġġcagca	agġtġcagġġ	cġġtatġġġġ	tġġġġagġtġġ	cġġttġġġtġ
179341	catġtġacġġ	ġttatagcca	acċtcatġġt	cġġttġġagc	agcaattagc	tġattġġttġ
179401	ġġtġacġġġ	cġġċċtġġt	atttatċtċt	ġġttatġġġ	cġaatcagġġ	agġtġtġacġ
179461	ġġtġtġacġġ	atġtġatġa	cġġatattġ	ġġġataaac	tġagcċatġġ	ċtċactattġ
179521	ġaagcġġġġ	cġcattċacc	cġġcagttġ	cġġġtttċċ	agcataatca	ġċċġaagcġ
179581	ċtġcāaaatc	tġġtġatcāa	ġċċttġġcag	ġġċcagacġġ	tġġtġġtċac	cġaagġcġta
179641	tttagtatġġ	atġġġatag	tġġġcattġ	ġġġġġtġġ	agcaacagac	ġtġagcġġġ
179701	ġġġġtġġt	tactġġtġġa	ġġatġġcāc	ġġtatġġġġ	ttcatġtġġa	agġġġġġġġ
179761	ggcagġtġġt	ġġttacaagġ	tttcaacċċ	ġagġtġttag	ttġtġcġtt	tġġcāagġġġ
179821	ttġġġtāa	ġġġtġġġġ	ġġtċttġtġt	cagġaacġġġ	ttġtġāata	ċttġttġcag
179881	tatġċċġġġ	acċtġatttā	cagcācġġġ	atġċċċċġġ	cġcaagcċtġ	tġġtċtācāa
179941	ġġġġġttġġ	ġccaagġtġca	acaagġtġat	ġcattacġġġ	aacaacttca	ġcagcġtatċ
180001	cġccaatttġ	ġġacġġġġġ	cġġcatttā	cġġtġcāac	tġġġġġġtġ	aaaaacġġġġ
180061	atccaacġġ	tġttġġtġġġ	cġataatcag	caagġtġta	tċtġġġcāġa	ġcaactġġtġ
180121	ġġtġġġġġ	tatġġtġġac	ġġcaatcġġ	ċċċċacġġġ	tġċcācāġġ	aagcġġcāġa
180181	ttġġġcattā	ċċtġcagġġ	ġġtġcācāa	ċċġagġġatā	tġġatagatt	attġġagġtġ
180241	ċtttatġġġġ	tċtġtġcactġ	agcācġġcā	atġġġġġtġt	ġġġtġttac	cġċcactġāa
180301	cġttġatāaa	cagġġġattġ	cġġtġcatt	cagċġġġġġ	ġċġagagġt	acġacagġġġ
180361	ġġġtāatttā	cagġġāāāā	cġġtġcatġġ	ġttagġtġcag	tġġġġcāġġ	agcācācġġġ
180421	ttttġtġġtġ	tġġatġġġġ	ġttġtġġcāc	ġġġcatttċ	agcġagcatt	ġġġġtġtt
180481	ggġtāagcġġ	ġtġattġġġt	tġġattġġġ	ġġcagġtatġ	tġġġattatġ	cġġcācācā
180541	ġcagġtġġt	ġacġactatċ	tġġtġġġġā	tattġaacat	attċcactġġ	ċtġatcagġtġ
180601	ġġtġġatātċ	tġġtttagca	atttġġġġt	ġcaatġġtġt	tġagatċtġġ	ġġġcġġcatt
180661	ġagġāattċ	tacġagġtġa	cġġċċċġġ	cġġġatċatċ	ċtattttċtā	ċtttġġcāġa
180721	agġġċċċtt	ġatġāattag	ġġcāagcġtġ	ġcaacagġtġ	ġatġġtġcagc	ġtġatġtāaa
180781	tġatttttġtġ	ċcattġcāac	atātċcāġac	ġġċtġcāa	tattatġġġ	atcacġtāac
180841	aacġġġtā	tatcagċcāc	ġġttċtċtāa	cġtġatagcġ	ċtġatġġġġ	cġttācāagġ
180901	cattġġtġġġ	acġcacttġġ	atġatġġġġ	tġagġtġġġ	ttacagġġġ	ġtcaacġtċt
180961	ġġġġġġtā	caacġġġġt	atġtġatġca	atċtġġġġġ	tatċcactġa	ġttatġtat
181021	ġġtttatġġġ	ġttatċtatċ	ġtġactāaac	ġttġġtttat	cacġġtāac	ġatactġatġ

181141	ctgctggccta	tāaaācgggta	gāatcccggtg	gācagātāāc	cgctgacggc	ttgācgaāta
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L3 ANSWER 101 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AF276872 GenBank (R)  
GenBank ACC. NO. (GBN): AF276872  
GenBank VERSION (VER): AF276872.2 GI:13162669  
CAS REGISTRY NO. (RN): 306927-06-0  
SEQUENCE LENGTH (SQL): 1743  
MOLECULE TYPE (CI): mRNA; linear  
DIVISION CODE (CI): Rodents  
DATE (DATE): 28 Feb 2001  
DEFINITION (DEF): Mus musculus sodium and chloride-dependent \*\*\*high\*\*\*  
- \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
\*\*\*transporter\*\*\* mRNA, complete cds.

SOURCE: house mouse.  
ORGANISM (ORGN): Mus musculus  
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NUCLEIC ACID COUNT (NA): 406 a 409 c 410 g 518 t  
COMMENT:

On Feb 28, 2001 this sequence version replaced gi:11527247.  
REFERENCE: 1 (bases 1 to 1743)  
AUTHOR (AU): Apparsundaram,S.; Ferguson,S.M.; Blakely,R.D.  
TITLE (TI): Molecular cloning and characterization of \*\*\*human\*\*\*  
and murine high-affinity choline transporters  
JOURNAL (SO): Unpublished  
REFERENCE: 2 (bases 1 to 1743)  
AUTHOR (AU): Apparsundaram,S.; Ferguson,S.M.; Blakely,R.D.  
TITLE (TI): Direct Submission  
JOURNAL (SO): Submitted (09-JUN-2000) Department of Pharmacology and  
Center for Molecular Neuroscience, Vanderbilt  
University, 23rd Avenue South at Pierce, Nashville, TN  
37232-6420, USA  
REFERENCE: 3 (bases 1 to 1743)  
AUTHOR (AU): Apparsundaram,S.; Ferguson,S.M.; Blakely,R.D.  
TITLE (TI): Direct Submission  
JOURNAL (SO): Submitted (28-FEB-2001) Department of Pharmacology and  
Center for Molecular Neuroscience, Vanderbilt  
University, 23rd Avenue South at Pierce, Nashville, TN  
37232-6420, USA

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L3 ANSWER 102 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AB043997 GenBank (R)  
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 GenBank VERSION (VER): AB043997.1 GI:11231080  
 CAS REGISTRY NO. (RN): 304428-43-1  
 SEQUENCE LENGTH (SQL): 5158  
 MOLECULE TYPE (CI): mRNA; linear  
 DIVISION CODE (CI): Primates  
 DATE (DATE): 19 Nov 2000  
 DEFINITION (DEF): Homo sapiens mRNA for \*\*\*high\*\*\* - \*\*\*affinity\*\*\*  
 \*\*\*choline\*\*\* \*\*\*transporter\*\*\* CHT1, complete  
 cds.  
 SOURCE: Homo sapiens spinal cord cDNA to mRNA.  
 ORGANISM (ORGN): Homo sapiens  
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 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;  
 Hominidae; Homo

REFERENCE: 1 (sites)  
 AUTHOR (AU): Okuda,T.; Haga,T.  
 TITLE (TI): Functional characterization of the \*\*\*human\*\*\*  
 \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\*  
 JOURNAL (SO): FEBS Lett., 484 (2), 92-97 (2000)  
 REFERENCE: 2 (bases 1 to 5158)  
 AUTHOR (AU): Okuda,T.  
 TITLE (TI): Direct Submission  
 JOURNAL (SO): Submitted (30-MAY-2000) Takashi Okuda, University of  
 Tokyo, Faculty of Medicine, Department of  
 Neurochemistry; 7-3-1 Hongo, Bunkyo-ku, Tokyo 1130033,  
 Japan (E-mail:okuda@m.u-tokyo.ac.jp,  
 URL:http://park.ecc.u-tokyo.ac.jp/neurochemistry,  
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L3 ANSWER 103 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

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LOCUS (LOC): AF276871 GenBank (R)
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GenBank VERSION (VER): AF276871.1 GI:10998441
CAS REGISTRY NO. (RN): 392136-26-4
SEQUENCE LENGTH (SQL): 1743
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Primates
DATE (DATE): 27 Nov 2000
DEFINITION (DEF): Homo sapiens ***high*** ***affinity***
***choline*** ***transporter*** (SLC5A7) mRNA,
complete cds.
SOURCE: ***human***

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;  
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;  
Hominidae; Homo

NUCLEIC ACID COUNT (NA): 412 a 393 c 406 g 532 t

REFERENCE: 1 (bases 1 to 1743)

AUTHOR (AU): Apparsundaram,S.; Ferguson,S.M.; George,A.L. Jr.;  
Blakely,R.D.

TITLE (TI): Molecular cloning of a \*\*\*human\*\*\*  
hemicholinium-3-sensitive choline transporter  
JOURNAL (SO): Biochem. Biophys. Res. Commun., 276 (3), 862-867 (2000)  
OTHER SOURCE (OS): CA 134:52827

REFERENCE: 2 (bases 1 to 1743)

AUTHOR (AU): Apparsundaram,S.; Ferguson,S.M.; Blakely,R.D.

TITLE (TI): Direct Submission

JOURNAL (SO): Submitted (09-JUN-2000) Department of Pharmacology and  
Center for Molecular Neuroscience, Vanderbilt  
University, 23rd Avenue South at Pierce, Nashville, TN  
37232-6420, USA

#### FEATURES (FEAT):

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CDS	1..1743	/gene="SLC5A7" /note="hCHT; solute carrier family 5 member 7" /codon-start=1 /product="high affinity choline transporter" /protein-id="AAG25940.1" /db-xref="GI:10998442" /translation="MAFHVEGLIAIIVFYLLILL VGIWAAWRTKNSGSAEERSEAIIV GGRDIGLLVGGFTMTATWVGGGYINGTAEAVYVP GYGLAWAQAPIGYSLSLILGGLFF AKPMRSKGYVTMLDPFQOIYKRMGGLLFIPALM GEMFWAAAIIFSALGATISVIIDVD MHISVIIISALIATLYTLVGGLYSVAYTDVVQLFC IFVGLWISVPFALSHPAVADIGFT AVHAKYQKPWLGTVDSSSEVYSWLDSFLLMLGGI PWQAYFQVRLSSSSATYAQVLSFL AAFGCLVMAIPAILIGAIGASTDWNQTAYGLPDP KTTEEADMILPIVLQYLCPVYISF FGLGAVSAAVMSSADSSILSASSMFARNIYQLSF RQNASDKEIVWVMRITVFVFGASA TAMALLTKTVYGLWYLSSDLVIYVIFPQLLCVLF VKGTNTYGAVAGYVSGFLFRITGG EPYLYLQPLIFYPGYYPDDNGIYNQKFPFKTLAM VTSFLTNICISYLAHYLFESGTLF PKLDVFDVAVARHSEENMDKTILVKNENIKLDEL ALVKPRQSMTLSSFTNKEAFLDV DSSPEGSGTEDNLQ"

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gene                1..1743         /gene="CHT1"
CDS                 1..1743         /gene="CHT1"
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L3 ANSWER 105 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): HSA401466 GenBank (R)  
 GenBank ACC. NO. (GBN): AJ401466  
 GenBank VERSION (VER): AJ401466.1 GI:9843753  
 CAS REGISTRY NO. (RN): 286923-93-1  
 SEQUENCE LENGTH (SQL): 1813  
 MOLECULE TYPE (CI): mRNA; linear  
 DIVISION CODE (CI): Primates  
 DATE (DATE): 16 Aug 2000  
 DEFINITION (DEF): Homo sapiens mRNA for \*\*\*high\*\*\* \*\*\*affinity\*\*\*  
 \*\*\*choline\*\*\* \*\*\*transporter\*\*\* (CHT1 gene).  
 SOURCE: \*\*\*human\*\*\*  
 ORGANISM (ORGN): Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;  
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;  
 Hominidae; Homo  
 NUCLEIC ACID COUNT (NA): 440 a 406 c 417 g 550 t  
 REFERENCE:  
 1 (bases 1 to 1813)  
 AUTHOR (AU): Wieland,A.; Bonisch,H.; Bruss,M.  
 TITLE (TI): Molecular cloning of the \*\*\*human\*\*\* and murine  
 high affinity choline transporters and characterization  
 of the \*\*\*human\*\*\* gene-structure  
 JOURNAL (SO): Unpublished  
 REFERENCE:  
 2 (bases 1 to 1813)  
 AUTHOR (AU): Bruess,M.  
 TITLE (TI): Direct Submission  
 JOURNAL (SO): Submitted (14-AUG-2000) Bruess M., University of Bonn,  
 Pharmacology and Toxicology, Reuter str. 2b, D-53113  
 Bonn, GERMANY

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CDS 19..1761

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L3 ANSWER 106 OF 111 MEDLINE on STN  
AN 2003541411 MEDLINE  
DN PubMed ID: 12827517  
TI Organic cation transporters.  
AU Koepsell H; Schmitt B M; Gorboulev V  
CS Institut fur Anatomie und Zellbiologie, Bayerischen Julius-Maximilians-

SO Hermann@Koepsell.de  
 Reviews of physiology, biochemistry and pharmacology, (2003) 150 36-90.  
 Ref: 390  
 Journal code: 0434624. ISSN: 0303-4240.  
 CY Germany: Germany, Federal Republic of  
 DT Journal; Article; (JOURNAL ARTICLE)  
 General Review; (REVIEW)  
 (REVIEW, ACADEMIC)  
 LA English  
 FS Priority Journals  
 EM 200404  
 ED Entered STN: 20031119  
 Last Updated on STN: 20040501  
 Entered Medline: 20040430

L3 ANSWER 107 OF 111 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN  
 AN 2004:343483 SCISEARCH  
 GA The Genuine Article (R) Number: 802CT  
 TI Expression of \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* CHT1 in the \*\*\*human\*\*\* leukemic T cell line  
 MOLT-3  
 AU Fujii T (Reprint); Okuda T; Haga T; Kawashima K  
 CS Kyoritsu Coll Pharmaceut Sci, Dept Pharmacol, Tokyo 1058512, Japan; Univ  
 Tokyo, Fac Med, Dept Neurochem, Tokyo 1170033, Japan; Gakushuin Univ, Fac  
 Sci, Inst Biomol Sci, Tokyo 1718588, Japan  
 CYA Japan  
 SO JOURNAL OF PHARMACOLOGICAL SCIENCES, (10 MAR 2004) Vol. 94, Supp. [1], pp.  
 202P-202P.  
 Publisher: JAPANESE PHARMACOLOGICAL SOC, EDITORIAL OFF, KANTOHYA BLDG  
 GOKOMACHI-EBISUGAWA NAKAGYO-KU, KYOTO, 604, JAPAN.  
 ISSN: 1347-8613.  
 DT Conference; Journal  
 LA English  
 REC Reference Count: 0

L3 ANSWER 108 OF 111 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN  
 AN 2004:105139 SCISEARCH  
 GA The Genuine Article (R) Number: 753PR  
 TI Characterization of the \*\*\*human\*\*\* \*\*\*high\*\*\* - \*\*\*affinity\*\*\*  
 \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 AU Haga T (Reprint); Okuda T; Kaitsuka C; Okamura M; Osawa C; Nishiyama N;  
 Yamada H; Nakamura T; Kobayashi Y  
 CS Gakushuin Univ, Inst Biomol Sci, Tokyo 171, Japan; Univ Tokyo, Fac Med,  
 Tokyo 113, Japan; Kyorin Univ, Fac Med, Tokyo, Japan  
 CYA Japan  
 SO JOURNAL OF NEUROCHEMISTRY, (DEC 2003) Vol. 87, Supp. [1], pp. 43-43.  
 Publisher: BLACKWELL PUBLISHING LTD, 9600 GARSINGTON RD, OXFORD OX4 2DG,  
 OXON, ENGLAND.  
 ISSN: 0022-3042.  
 DT Conference; Journal  
 LA English  
 REC Reference Count: 0

L3 ANSWER 109 OF 111 USPATFULL on STN  
 AN 2004:63743 USPATFULL  
 TI Invertebrate choline transporter nucleic acids, polypeptides and uses  
 thereof  
 IN Raming, Klaus, Leverkusen, GERMANY, FEDERAL REPUBLIC OF  
 PI US 2004048261 A1 20040311  
 AI US 2002-241784 A1 20020911 (10)  
 DT Utility  
 FS APPLICATION  
 LN.CNT 2653  
 INCL INCLM: 435/006.000  
 INCLS: 435/069.100; 435/320.100; 435/348.000; 530/350.000; 536/023.500;  
 800/008.000  
 NCL NCLM: 435/006.000  
 NCLS: 435/069.100; 435/320.100; 435/348.000; 530/350.000; 536/023.500;  
 800/008.000  
 IC [7]  
 ICM: C12Q001-68  
 ICS: A01K067-033; C07H021-04; C07K014-705  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 110 OF 111 USPATFULL on STN

TI 18F-labeled choline analogs  
IN DeGrado, Timothy R., Durham, NC, UNITED STATES  
Coleman, R. Edward, Durham, NC, UNITED STATES  
Baldwin, Steven W., Durham, NC, UNITED STATES  
Price, David T., Greenwood, LA, UNITED STATES  
Orr, Matthew D., Durham, NC, UNITED STATES  
Wang, Shuyan, Durham, NC, UNITED STATES

PI US 2002061279 A1 20020523  
US 6630125 B2 20031007  
AI US 2001-844674 A1 20010430 (9)  
PRAI US 2000-200347P 20000428 (60)  
US 2000-231303P 20000908 (60)

DT Utility  
FS APPLICATION

LN.CNT 1576

INCL INCLM: 424/001.890

NCL NCLM: 424/001.890

IC [7]

ICM: A61K051-00

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 111 OF 111 USPATFULL on STN

AN 1999:85438 USPATFULL

TI Decahydroquinoline-based anti-cholinergic agents

IN Efange, S. Mbua Ngale, Plymouth, MN, United States

Parsons, Stanley M., Santa Barbara, CA, United States

PA Regents of the University of Minnesota, Minneapolis, MN, United States  
(U.S. corporation)

PI US 5929087 19990727

AI US 1997-826830 19970408 (8)

DT Utility

FS Granted

LN.CNT 857

INCL INCLM: 514/314.000

INCLS: 514/278.000; 546/017.000; 546/154.000; 546/158.000; 546/164.000

NCL NCLM: 514/314.000

NCLS: 514/278.000; 546/017.000; 546/154.000; 546/158.000; 546/164.000

IC [6]

ICM: A61K031-47

ICS: C07D401-04

EXF 546/164; 546/154; 546/158; 546/17; 514/314; 514/312

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

STN INTERNATIONAL LOGOFF AT 10:22:35 ON 21 MAY 2004